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OM protein - protein search, using sw model

(without alignments)
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31

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database : A_Geneseq_36: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

44	29	93.5	810	1	R04574	Derived amino acid
45	29	93.5	218	1	W40287	Human Tfsl protein

ALIGNMENTS						
RESULT	1					
ID	R06511	standard; protein; 507 AA.				
AC	R06511;					
DT	04-JAN-1991	(first entry)				
DE	EPO receptor sequence deduced from DNA of clone 190.					
KM	Erythropoietin; Diamond Blackfan anaemia; polycythemia vera.					
OS	Mus musculus.					
FT	Key	Location/Qualifiers				
FT	peptide	1..24				
FT	domain	/label-signal peptide				
FT	domain	25..248				
FT	domain	/label-extracellular domain				
FT	domain	/note-EPO binding region				
FT	domain	248..271				
FT	domain	/label-transmembrane domain				
FT	domain	272..507				
FT	modified_site	/label-intracellular domain				
FT	modified_site	75..77				
FT	modified_site	/label-N-linked_glycos				
FT	modified_site	182..184				
FT	modified_site	/label-N-linked_glycos				
PN	MO9008822-A.					
PD	09-AUG-1990.					
PF	01-FEB-1990; U00635.					
PR	03-FEB-1989; US-306503.					
PA	(GENE-) GENETICS INST INC.					
PA	(WHIT-) WHITEHEAD INST.					
PI	D'Andrea A; Wong G;					
DR	WPI; 90-260931/34.					
DR	N-PSDB; Q05747.					
PT	Erythropoietin receptor and gene - used for developing reagents					
PS	and systems to control and study erythropoiesis.					
PS	Disclosure; Fig 1; 53pp; English.					
CC	The sequence was deduced from DNA from a clone isolated from a					
CC	cDNA library prep. from uninduced murine erythroleukemia cells.					
CC	It is a type I transmembrane protein with binding affinity for EPO.					
CC	The gene and recombinant EPO receptor produced on expression of					
CC	the DNA are used to develop reagents and systems to control and					
CC	study erythropoiesis. It is believed that the EPO receptor is					
CC	dysfunctional in individuals with Diamond Blackfan anaemia, and					
CC	may be hyperactive in polycythemia vera.					
CC	See also R06512 (human EPO receptor).					
CC	Sequence	507 AA.				
SQ	Sequence	507 AA.				

Query Match	96.8%;	Score 30;	DB 1;	Length 507;
Best Local Similarity	80.0%;	Pred. No. 4.4e+02;		
Matches	4;	Conservative	0;	Mismatches 1;
			Indels	0;
			Gaps	0

QY	1	WSXWS	5
DB	232	WSAWS	236

RESULT	2		
ID	R06512	standard; protein; 508 AA.	
AC	R06512;		
DT	04-JAN-1991	(first entry)	
DE	EPO receptor.		
KM	Erythropoietin; Diamond Blackfan anaemia; polycythemia vera.		
OS	Homo sapiens.		
PN	MO9008822-A.		
PD	09-AUG-1990.		
PD	01-FEB-1990; U00635.		

PR 03-FEB-1989; US-306503.
 PA (GENE-) GENETICS INST INC.
 PA (WHIT-) WHITEHEAD INST.
 PI D'andrea A, Mong G;
 DR WPI; 90-260931/34.
 DR N-PSDB; 005748.
 PT Erythropoietin receptor and gene - used for developing reagents
 PT and systems to control and study erythropoiesis.
 PS Disclosure; Fig 2; 53pp; English.
 CC The sequence was deduced from DNA obid. from a clone isolated from
 CC a commercially available human genomic cDNA library in phage
 CC Lambda Fix (Stratagene). The sequence encodes a type I trans-
 CC membrane protein with binding affinity for EPO. The gene and
 CC recombinant EPO receptor produced on expression of the DNA are
 CC used to develop reagents and systems to control and study
 CC erythropoiesis. It is believed that the EPO receptor is dys-
 CC functional in individuals with Diamond Blackfan anaemia, and may
 CC be hyperactive in polycythemia vera.
 CC See also R06511 (murine EPO receptor).
 SQ Sequence 508 AA;

Query Match 96.8%; Score 30; DB 1; Length 508;
 Best Local Similarity 80.0%; Pred. No. 4,4e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXMS 5
 DB 233 WSAMS 237

RESULT 3
 R24017
 ID R24017 standard; Protein; 552 AA.
 AC R24017;
 DT 26-NOV-1992 (first entry)
 DE Fusion protein GM-CSFRFC.
 KW Granulocyte macrophage-colony stimulating factor; GM-CSF; IgG1;
 KM Immunoglobulin G1.
 OS Synthetic.
 FH Key
 FT region Location/Qualifiers
 FT 1..318 "human GM-CSF receptor"
 FT 319..336 /note="linker and hinge"
 FT 337..445 /note="19G1 CH2"
 FT 446..552 /note="19G1 CH3"
 FT region
 PN EP-488170-A.
 PD 03-JUN-1992.
 PE 26-NOV-1991; 120187.
 PR 28-NOV-1990; DE-037637.
 PA (BEHW) BEHRINGERKE AG.
 PI Lauffer L, Oquendo P, Zettlmeissl G;
 DR WPI; 92-185084/23.
 PT Cell free receptor binding test contg. recombinant fusion protein -
 PT comprising carrier bound to fusion partner coupled to fixed support,
 PT and second, labelled binding partner, for receptor or antibody
 PT screening etc.
 PS Example; Fig 12; 24pp; German.
 CC The sequence is that of fusion protein GM-CSFRFC comprising the
 CC extracellular domain of granulocyte macrophage-colony stimulating
 CC factor (GM-CSF) fused via a hinge region to the Fc part of the heavy
 CC chain of human IgG1. It may be used as part of a cell free receptor
 CC binding test which can be used for the identification of agonists,
 CC antagonists, antibodies, biological activity of soluble cellular
 CC receptors, functional analysis of modified ligands and diagnostic or
 CC therapeutic substances. See also R24016.
 SQ Sequence 552 AA;

Query Match

96.8%; Score 30; DB 1; Length 552;

Best Local Similarity 80.0%; Pred. No. 4,4e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXMS 5
 DB 306 WSAMS 310

RESULT 4
 R10795
 ID R10795 standard; Protein; 622 AA.
 AC R10795;
 DT 25-APR-1991 (first entry)
 DE Human prolactin receptor.
 KW Human prolactin receptor; PRL; assay; antibody; growth hormone.
 OS Homo sapiens.
 FH Key
 FT peptide Location/Qualifiers
 FT 1..24 /label="sig_peptide"
 FT 25..622 /label="mat_protein"
 FT protein
 PN US4992378-A.
 PD 12-FEB-1991.
 PE 16-DEC-1988; 286445.
 PR 16-DEC-1988; US-286445.
 PA (ROYA-) ROYAL INST ADVAN LE.
 PI Kelly PA, Dlane J;
 DR WPI; 91-065341/09.
 DR N-PSDB; Q10550.
 PT Isolated cDNA sequence encoding human prolactin receptor - useful
 PT for expressing the receptor, e.g. for screening assays and antibody
 PT prodn.
 PS Disclosure; Fig. 1 (A-E); 11pp; English.
 CC The human PRL receptor cDNA is isolated by screening a lambda gt 10
 CC library prepared from normal human hepatoma Hep G2 and T47-D breast
 CC cancer cells. Initially, 1x10⁶ recombinants are screened with the
 CC following probe: a complementary RNA of the F3 cDNA of the rat
 CC prolactin receptor. One positive recombinant was isolated from the
 CC Hep G2 library, which was later used as a probe to rescreen the
 CC library. Five additional cDNAs were identified, and by combining
 CC two of the six cDNAs, a PRL receptor cDNA of 2.5 kb was constructed,
 CC contg. a single ORF of 1866 bp. Similar partial length cDNA were
 CC isolated from the T47-D library.
 CC Several regions of sequence identity between the human growth
 CC hormone and PRL receptors can be found, both in the extracellular
 CC and cytoplasmic domains.
 CC The sequence is an important genetic engineering tool which may be
 CC used for the screening of growth hormone variants, for the development
 CC of test kits to measure PRL receptor levels in human breast and prostate
 CC cancer biopsies, for the measurement of bioactive forms of prolactin,
 CC and for the development of drugs to induce stimulation or inhibition of
 CC the immune system.
 SQ Sequence 622 AA;

Query Match 96.8%; Score 30; DB 1; Length 622;
 Best Local Similarity 80.0%; Pred. No. 5,4e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXMS 5
 DB 215 WSAMS 219

RESULT 5
 R10919
 ID R10919 standard; Protein; 400 AA.
 AC R10919;
 DT 08-MAY-1991 (first entry)
 DE Human GM-CSF receptor.
 KW Granulocyte-macrophage colony-stimulating factor; myeloid leukaemia;
 KW autoimmune disease.
 FH Key
 FT region Location/Qualifiers

KM haematopoietic cell; growth factor receptor; gene rearrangement;
 KM Friend replication competent ecotropic murine leukaemia virus.
 OS Myeloproliferative leukaemia virus.
 OS Friend murine leukaemia virus.
 PH Key
 FT peptide
 FT 1.34
 FT /label= signal
 FT /note= "from F-MuLV"
 FT region
 FT 1.64
 FT /note= "N-terminal region of F-MuLV gp70"
 FT 65.100
 FT /note= "central region of F-MuLV env"
 FT 101.284
 FT /note= "MPLV-specific mpl"
 FT 144.165
 FT domain
 FT /note= "putative transmembrane domain"
 PN MO9207074-A.
 PD 30-APR-1992.
 PE 19-OCT-1990; F00762.
 PR 19-OCT-1990; MO-F07623.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PI Charon M, Gisselbrecht S, Penciolelli JF, Souyri M;
 PI Tambourin P, Varlet P, Vigon I, Wendling F;
 DR MPI; 92-167154/20.
 DR N-PSDB; Q24677.
 PT Polypeptides similar to v-mpl protein of MPLV - for diagnosis and
 treatment of myeloproliferative diseases
 PS Claim 8; Fig 2b; 75pp; French.
 CC The rearranged env MPLV gene has an open reading frame of 284 amino
 acids and deduced mol.wt. of 31kD. The env-mpl fusion protein
 CC comprises the N-terminal 64 amino acids from F-MuLV gp70, including
 CC the signal peptide, 36 amino acids from the central region of the
 CC F-MuLV env gene and 184 amino acids specific to MPLV.
 CC See R23970, Q24674-7.
 SQ Sequence 284 AA;

QY 1 WSXWS 5
 DB 126 WSAMS 130

RESULT 9
 R23970
 ID R23970 standard; protein; 635 AA.
 AC R23970;
 DT 05-NOV-1992 (first entry)
 DE MPLV env protein with growth factor receptor properties.
 KM Myeloproliferative leukaemia virus; haematopoietic cell.
 OS Myeloproliferative leukaemia virus.
 PH Key
 FT region
 FT 449.635
 FT /note= "gp70 of MPLV"
 PN MO9207074-A.
 PD 30-APR-1992.
 PE 19-OCT-1990; F00762.
 PR 19-OCT-1990; MO-F07623.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PI Charon M, Gisselbrecht S, Penciolelli JF, Souyri M;
 PI Tambourin P, Varlet P, Vigon I, Wendling F;
 DR MPI; 92-167154/20.
 DR N-PSDB; Q24674.
 PT Polypeptides similar to v-mpl protein of MPLV - for diagnosis and
 treatment of myeloproliferative diseases
 PS Claim 1; Page 28; 75pp; French.
 CC This polypeptide is encoded by clone MPV107, isolated from a
 CC genomic bank prepared from clones of Mus dunni cells containing
 CC a unique copy of the MPLV provirus. The bank was screened with two
 CC 300bp long clones specific for MPLV env region. Restriction enzyme

Query Match 96.8%; Score 30; DB 1; Length 284;
 Best Local Similarity 80.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC analysis showed that clone MPLV107 contained the entire MPLV genome
 CC except for the 3'UTR.
 CC See R23971 and Q24674-7.
 SQ Sequence 635 AA;

QY 1 WSXWS 5
 DB 474 WSAMS 478

RESULT 10
 R27659
 ID R27659 standard; protein; 382 AA.
 AC R27659;
 DT 05-NOV-1992 (first entry)
 DE MPLV-env related polypeptide.
 KM Myeloproliferative leukaemia virus; envelope protein; gp70;
 KM haematopoietic cell; growth factor receptor.
 OS Myeloproliferative leukaemia virus.
 PN MO9207074-A.
 PD 30-APR-1992.
 PE 19-OCT-1990; F00762.
 PR 19-OCT-1990; MO-F07623.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PI Charon M, Gisselbrecht S, Penciolelli JF, Souyri M;
 PI Tambourin P, Varlet P, Vigon I, Wendling F;
 DR MPI; 92-167154/20.
 DR N-PSDB; Q24675.
 PT Polypeptides similar to v-mpl protein of MPLV - for diagnosis and
 treatment of myeloproliferative diseases
 PS Claim 3; Page 30; 75pp; French.
 CC This polypeptide is an example of a fragment related to the MPLV
 CC env protein having the amino acid sequence assigned GENESQ
 CC accession number R23970. The protein is involved in the
 CC ligand-fixing or signal-transmitting function of haematopoietic
 CC growth factor receptors; is recognised by antibodies to the
 CC protein R23970; when produced from the MPLV genome it can induce/
 CC promote proliferation of haematopoietic cells and/or is involved
 CC in differentiation of haematopoietic cells.
 CC See also Q24674-7.
 SQ Sequence 382 AA;

QY 1 WSXWS 5
 DB 222 WSAMS 226

RESULT 11
 R27660
 ID R27660 standard; protein; 184 AA.
 AC R27660;
 DT 05-NOV-1992 (first entry)
 DE Partial MPLV-env related polypeptide.
 KM Myeloproliferative leukaemia virus; envelope protein; gp70;
 KM haematopoietic cell; growth factor receptor.
 OS Myeloproliferative leukaemia virus.
 PN MO9207074-A.
 PD 30-APR-1992.
 PE 19-OCT-1990; F00762.
 PR 19-OCT-1990; MO-F07623.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PI Charon M, Gisselbrecht S, Penciolelli JF, Souyri M;
 PI Tambourin P, Varlet P, Vigon I, Wendling F;

Query Match 96.8%; Score 30; DB 1; Length 382;
 Best Local Similarity 80.0%; Pred. No. 3.3e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DR WPI: 92-167154/20.
 DR N-PSDB: Q24676.
 PT Polypeptides similar to v-mpl protein of MPLV - for diagnosis and
 PT treatment of myeloproliferative diseases
 CC Claim 4; Page 31; 75pp; French.
 CC This polypeptide is an example of a fragment related to the MPLV
 CC accession number R23970. The protein is involved in the
 CC ligand-fixing or signal-transmitting function of haematopoietic
 CC growth factor receptors; is recognised by antibodies to the
 CC protein R23970; when produced from the MPLV genome it can induce/
 CC promote proliferation of haematopoietic cells and/or is involved
 CC in differentiation of haematopoietic cells.
 CC See also Q24674-7.
 SO Sequence 184 AA;

Query Match 96.8%; Score 30; DB 1; Length 184;
 Best Local Similarity 80.0%; Pred. No. 1.6e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSXWS 5
 II II
 DB 26 WSAWS 30

RESULT 12

R47517
 ID R47517 standard; Protein; 507 AA.

AC R47517;
 DT 24-JUN-1994 (first entry)

DE MEL EPO receptor.
 KW Erythropoietin receptor; recombinant; murine; anaemia.
 CS Mus musculus.

FT Key Location/Qualifiers
 FT peptide 1..24
 FT protein 25..507
 FT modified_site 75
 FT modified_site 383
 FT modified_site 250..271
 FT region /note- "putative transmembrane region"

US5278065-A.
 11-JAN-1994.
 03-FEB-1989; 306503.
 03-FEB-1989; US-306503.
 25-MAR-1991; US-678877.
 (CHIL-) CHILDRENS MEDICAL CENT.
 (GENY) GENETICS INST INC.
 (WHEE) WHITEHEAD INST BIOMEDICAL RES.
 D'Andrea A, Jones SS, Wong GG;
 WPI: 94-025409/03.
 N-PSDB: Q53994.
 T Recombinant DNA encoding erythropoietin receptor - used to
 T develop prods. for study, treatment or diagnosis of disorders in
 T which receptor is dysfunctional.
 T Disclosure Fig 2; 24pp; English.
 T Mouse erythroleukemia (MEL) cells were used to construct a cDNA
 T library. The cDNA was used to transfect COS-1 cells and these were
 T screened for radiolabeled erythropoietin (EPO) binding to isolate
 T cDNA encoding the EPO receptor. The cDNA may be used to isolate
 T EPO receptor from other sources and to study, treat or diagnose
 T disorders in which the EPO receptor is dysfunctional. The EPO
 T receptor may also be used to raise antibody or for treating
 T hypersensitivity to EPO or who have elevated levels of EPO. The prod.
 T is pref. used for treating anaemias, primary proliferative polycythemia
 T and secondary polycythemia.
 T See also R47518.
 C Sequence 507 AA;

Query Match 96.8%; Score 30; DB 1; Length 507;
 Best Local Similarity 80.0%; Pred. No. 4.4e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSXWS 5
 II II
 DB 232 WSAWS 236

RESULT 13

R47518
 ID R47518 standard; Protein; 508 AA.

AC R47518;
 DT 24-JUN-1994 (first entry)

DE Human EPO receptor.
 KW Erythropoietin receptor; recombinant; murine; anaemia.
 CS Homo sapiens.

FT Key Location/Qualifiers
 FT peptide 1..24
 FT protein 25..508
 FT modified_site 251..272
 FT region /note- "mature EPO receptor"

US5278065-A.
 11-JAN-1994.
 03-FEB-1989; 306503.
 03-FEB-1989; US-306503.
 25-MAR-1991; US-678877.
 (CHIL-) CHILDRENS MEDICAL CENT.
 (GENY) GENETICS INST INC.
 (WHEE) WHITEHEAD INST BIOMEDICAL RES.
 D'Andrea A, Jones SS, Wong GG;
 WPI: 94-025409/03.
 N-PSDB: Q53995.
 T Recombinant DNA encoding erythropoietin receptor - used to
 T develop prods. for study, treatment or diagnosis of disorders in
 T which receptor is dysfunctional.
 T Disclosure Fig 9; 24pp; English.
 T Mouse erythroleukemia (MEL) cells were used to construct a cDNA
 T library. The cDNA was used to transfect COS-1 cells and these were
 T screened for radiolabeled erythropoietin (EPO) binding to isolate
 T cDNA encoding the EPO receptor. This cDNA was used as a probe to
 T screen a human genomic cDNA library to obtain DNA encoding the human
 T EPO receptor. The cDNA may be used to study, treat or diagnose
 T disorders in which the EPO receptor is dysfunctional. The EPO
 T receptor may also be used to raise antibody or for treating
 T hypersensitivity to EPO or who have elevated levels of EPO. The prod.
 T is pref. used for treating anaemias, primary proliferative polycythemia
 T and secondary polycythemia.
 T See also R47517.
 C Sequence 508 AA;

Query Match 96.8%; Score 30; DB 1; Length 508;
 Best Local Similarity 80.0%; Pred. No. 4.4e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSXWS 5
 II II
 DB 233 WSAWS 237

RESULT 14

R50326
 ID R50326 standard; Protein; 265 AA.

AC R50326;
 DT 19-OCT-1994 (first entry)

DE Mouse soluble EPO receptor protein fragment.
 KW Murine; soluble; erythropoietin; EPO; receptor protein; sEPO-R; drug;
 KW antigen; diagnostic agent; biochemical reagent.
 CS Mus musculus.

US5278065-A.
 11-JAN-1994.
 03-FEB-1989; 306503.
 03-FEB-1989; US-306503.
 25-MAR-1991; US-678877.
 (CHIL-) CHILDRENS MEDICAL CENT.
 (GENY) GENETICS INST INC.
 (WHEE) WHITEHEAD INST BIOMEDICAL RES.
 D'Andrea A, Jones SS, Wong GG;
 WPI: 94-025409/03.
 N-PSDB: Q53994.
 T Recombinant DNA encoding erythropoietin receptor - used to
 T develop prods. for study, treatment or diagnosis of disorders in
 T which receptor is dysfunctional.
 T Disclosure Fig 2; 24pp; English.
 T Mouse erythroleukemia (MEL) cells were used to construct a cDNA
 T library. The cDNA was used to transfect COS-1 cells and these were
 T screened for radiolabeled erythropoietin (EPO) binding to isolate
 T cDNA encoding the EPO receptor. The cDNA may be used to isolate
 T EPO receptor from other sources and to study, treat or diagnose
 T disorders in which the EPO receptor is dysfunctional. The EPO
 T receptor may also be used to raise antibody or for treating
 T hypersensitivity to EPO or who have elevated levels of EPO. The prod.
 T is pref. used for treating anaemias, primary proliferative polycythemia
 T and secondary polycythemia.
 T See also R47518.
 C Sequence 507 AA;

Query Match 96.8%; Score 30; DB 1; Length 507;
 Best Local Similarity 80.0%; Pred. No. 1.6e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSXWS 5
 II II
 DB 233 WSAWS 237

Job time: 301 sec

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FH Key Location/Qualifiers
FT Peptide 1..25
FT /note="Signal peptide"
FT protein 26..265
FT /note="Mature EPO-R fragment"
PN J06038787-A.
PD 15-FEB-1994.
PF 04-MAR-1992; 082865.
PR 04-MAR-1992; JP-082865.
PA (SNOW) SNOW BRAND MILK PROD CO LTD.
DR WPI: 94-094847/12.
DR N-PSDB: 044853.
PT Soluble erythropoietin receptor protein - and DNA coding for
PT SEPO-R, useful as diagnostic reagent
PS Disclosure; page 5-6; 9pp; Japanese.
CC This sequence represents a fragment of the murine soluble erythro-
CC poietin (EPO) receptor protein (SEPO-R). This protein is able to
CC bind to EPO and has antigenicity as an EPO receptor. The molecular
CC weight of the full length protein is pref 33 or 29 kD. The protein
CC is useful as a drug, as a diagnostic agent and a biochemical reagent.
SQ Sequence 265 AA;

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Query Match 96.8%; Score 30; DB 1; Length 265;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 MSXMS 5
DB 232 WSAMS 236

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RESULT 15
R50327
ID R50327 standard; Protein; 507 AA.
AC R50327;
DT 19-OCT-1994 (first entry)
DE Mouse soluble EPO receptor protein.
KW Murine; soluble; erythropoietin; EPO; receptor protein; SEPO-R; drug;
KW antigen; diagnostic agent; biochemical reagent.
OS Mus musculus.
FH Key Location/Qualifiers
FT modified_site 75..77
FT /note="N-linked glycosylation site"
PN J06038787-A.
PD 15-FEB-1994.
PF 04-MAR-1992; 082865.
PR 04-MAR-1992; JP-082865.
PA (SNOW) SNOW BRAND MILK PROD CO LTD.
DR WPI: 94-094847/12.
DR N-PSDB: 044854.
PT Soluble erythropoietin receptor protein - and DNA coding for
PT SEPO-R, useful as diagnostic reagent
PS Disclosure; fig 1; 9pp; Japanese.
CC This sequence represents the murine soluble erythropoietin (EPO)
CC receptor protein (SEPO-R). This protein is able to bind to EPO and
CC has antigenicity as an EPO receptor. The molecular weight of the
CC full length protein is pref 33 or 29 kD. The protein is useful as a
CC drug, as a diagnostic agent and a biochemical reagent.
SQ Sequence 507 AA;

```

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Query Match 96.8%; Score 30; DB 1; Length 507;
Best Local Similarity 80.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 MSXMS 5
DB 232 WSAMS 236

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Search completed: September 17, 1999, 03:08:10

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OW protein - protein search, using sw model

Run on: September 16, 1999, 19:10:31 ; Search time 53.94 Seconds
(Without alignments)
0.915 Million cell updates/sec

Title: US-09-037-657-1

Perfect score: 31

Sequence: 1 MSXWS 5

Scoring table: BLOSUM62

Searched: 106577 seqs, 9868381 residues

Database :

Issued_Patents_AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/prodata/2/1aa/PCTUS9_COMB.pep.*
4: /cgn2_6/prodata/2/1aa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	96.8	185	1	US-07-676-647-10 Sequence 10, Appl
2	30	96.8	185	1	US-07-676-647-13 Sequence 13, Appl
3	30	96.8	185	1	US-08-184-327A-2 Sequence 2, Appl
4	30	96.8	185	1	US-08-184-327A-4 Sequence 4, Appl
5	30	96.8	482	1	US-08-184-327A-8 Sequence 8, Appl
6	30	96.8	633	1	US-08-250-859-17 Sequence 17, Appl
7	30	96.8	400	1	US-08-351-149-6 Sequence 6, Appl
8	30	96.8	552	1	US-08-243-010-6 Sequence 6, Appl
9	30	96.8	185	1	US-08-449-329-10 Sequence 10, Appl
10	30	96.8	185	1	US-08-449-329-13 Sequence 13, Appl
11	30	96.8	633	1	US-08-490-803-17 Sequence 17, Appl
12	30	96.8	400	1	US-08-384-828-6 Sequence 6, Appl
13	30	96.8	584	2	US-08-313-288B-17 Sequence 17, Appl
14	30	96.8	508	2	US-08-850-293-5 Sequence 5, Appl
15	30	96.8	185	2	US-08-445-073-10 Sequence 10, Appl
16	30	96.8	185	2	US-08-445-073-13 Sequence 13, Appl
17	30	96.8	32	2	US-08-280-864A-13 Sequence 13, Appl
18	30	96.8	185	3	PCT-US91-03896-13 Sequence 13, Appl
19	30	96.8	633	3	PCT-US91-03896-13 Sequence 13, Appl
20	30	96.8	633	3	PCT-US94-08806-17 Sequence 17, Appl
21	30	96.8	626	3	PCT-US95-00670-2 Sequence 2, Appl
22	30	96.8	633	3	PCT-US95-00670-4 Sequence 4, Appl
23	30	96.8	482	3	PCT-US95-00670-8 Sequence 8, Appl
24	30	96.8	633	3	PCT-US95-01775-17 Sequence 17, Appl
25	30	96.8	27	3	PCT-US95-04570-47 Sequence 47, Appl
26	30	96.8	27	3	PCT-US95-04589-47 Sequence 47, Appl
27	30	96.8	633	3	PCT-US95-16626-7 Sequence 7, Appl
28	29	93.5	23	1	US-07-646-531D-6 Sequence 6, Appl
29	29	93.5	60	1	US-07-646-531D-12 Sequence 12, Appl
30	29	93.5	708	1	US-07-797-556-2 Sequence 2, Appl
31	29	93.5	1001	1	US-07-797-556-6 Sequence 6, Appl
32	29	93.5	807	1	US-07-862-021B-10 Sequence 10, Appl
33	29	93.5	568	1	US-07-862-021B-12 Sequence 12, Appl
34	29	93.5	568	1	US-07-862-021B-14 Sequence 14, Appl
35	29	93.5	56	1	US-07-862-021B-19 Sequence 19, Appl
36	29	93.5	1001	1	US-07-943-843-2 Sequence 2, Appl
37	29	93.5	719	1	US-07-943-843-4 Sequence 4, Appl
38	29	93.5	1097	1	US-07-943-843-6 Sequence 6, Appl
39	29	93.5	372	1	US-07-865-878A-4 Sequence 4, Appl

40	29	93.5	17	1	US-07-801-812A-19	Sequence 19, Appl
41	29	93.5	11	1	US-07-801-812A-22	Sequence 22, Appl
42	29	93.5	372	1	US-07-676-647-2	Sequence 2, Appl
43	29	93.5	188	1	US-07-676-647-8	Sequence 8, Appl
44	29	93.5	185	1	US-07-676-647-9	Sequence 9, Appl
45	29	93.5	184	1	US-07-676-647-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-07-676-647-10
Sequence 10, Application US/07676647
Patent No. 5426177

GENERAL INFORMATION:

APPLICANT: Davis, Samuel
APPLICANT: Squinto, Stephen P.
APPLICANT: Furth, Mark E.
TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Penite & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/676,647
FILING DATE: 19910328
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Mastro, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENITE

SEQUENCE CHARACTERISTICS:

LENGTH: 185 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-676-647-10

Query Match

Best Local Similarity: 96.8%; Score 30; DB 1; Length 185;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 181 MSXWS 185

OY 1 MSXWS 5

RESULT 2

US-07-676-647-13
Sequence 13, Application US/07676647
Patent No. 5426177
GENERAL INFORMATION:
APPLICANT: Davis, Samuel
APPLICANT: Squinto, Stephen P.
APPLICANT: Furth, Mark E.

```

; APPLICANT: Yancopoulos, George D.
; TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/676,647
; FILING DATE: 19910328
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6526-048
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
;
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
; US-07-676-647-13
;
; Query Match          96.8%; Score 30; DB 1; Length 185;
; Best Local Similarity 80.0%; Pred. No. 1.5e+02;
; Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; OY 1 MSXWS 5
; DB 181 WSSWS 185
;
; RESULT 3
; US-08-184-327A-2
; Sequence 2, Application US/08184327A
; Patent No. 5498599
;
; GENERAL INFORMATION:
; APPLICANT: Chol, Esther S.
; APPLICANT: Hokom, Martha M.
; APPLICANT: Hunt, Pamela
; APPLICANT: Nichol, Janet L.
; TITLE OF INVENTION: Compositions And Methods For Stimulating
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc., U.S. Patent Operations/RRC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: USA
; ZIP: 91320-1789
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/184,327A
; FILING DATE: 20-JAN-1994
; CLASSIFICATION: 514
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 635 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-184-327A-4
;
; Query Match          96.8%; Score 30; DB 1; Length 635;
; Best Local Similarity 80.0%; Pred. No. 4.5e+02;
; Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; OY 1 MSXWS 5
; DB 474 WSSWS 478
;
; RESULT 5
; US-08-184-327A-8
; Sequence 8, Application US/08184327A
; Patent No. 5498599
;
; GENERAL INFORMATION:
; APPLICANT: Chol, Esther S.
; APPLICANT: Hokom, Martha M.
; APPLICANT: Hunt, Pamela

```

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; CLASSIFICATION: 514
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 626 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-184-327A-2
;
; Query Match          96.8%; Score 30; DB 1; Length 626;
; Best Local Similarity 80.0%; Pred. No. 4.4e+02;
; Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; OY 1 MSXWS 5
; DB 466 WSSWS 470
;
; RESULT 4
; US-08-184-327A-4
; Sequence 4, Application US/08184327A
; Patent No. 5498599
;
; GENERAL INFORMATION:
; APPLICANT: Chol, Esther S.
; APPLICANT: Hokom, Martha M.
; APPLICANT: Hunt, Pamela
; APPLICANT: Nichol, Janet L.
; TITLE OF INVENTION: Compositions And Methods For Stimulating
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc., U.S. Patent Operations/RRC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: USA
; ZIP: 91320-1789
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/184,327A
; FILING DATE: 20-JAN-1994
; CLASSIFICATION: 514
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 635 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-184-327A-4
;
; Query Match          96.8%; Score 30; DB 1; Length 635;
; Best Local Similarity 80.0%; Pred. No. 4.5e+02;
; Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; OY 1 MSXWS 5
; DB 474 WSSWS 478
;
; RESULT 5
; US-08-184-327A-8
; Sequence 8, Application US/08184327A
; Patent No. 5498599
;
; GENERAL INFORMATION:
; APPLICANT: Chol, Esther S.
; APPLICANT: Hokom, Martha M.
; APPLICANT: Hunt, Pamela

```

APPLICANT: Nichol, Janet L.
TITLE OF INVENTION: Compositions And Methods For Stimulating
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc., U.S. Patent Operations/RRC
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: CA
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,327A
FILING DATE: 20-JAN-1994
CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 482 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-184-327A-8

Query Match 96.8%; Score 30; DB 1; Length 482;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 466 WSXWS 470

RESULT 6
US-08-250-859-17
Sequence 17, Application US/08250859
Patent No. 5541085
GENERAL INFORMATION:
APPLICANT: Holly, Richard D.
APPLICANT: Burkhead, Steven K.
TITLE OF INVENTION: METHOD FOR PREPARING ORPHAN RECEPTOR LIGANDS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,859
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E.
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 94-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-632-4009
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 633 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-250-859-17

Query Match 96.8%; Score 30; DB 1; Length 633;
Best Local Similarity 80.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 473 WSXWS 477

RESULT 7
US-08-351-149-6
Sequence 6, Application US/08351149
Patent No. 5628283
GENERAL INFORMATION:
APPLICANT: Nicola, Nicos A.
APPLICANT: Gough, Nicholas M.
APPLICANT: Gearing, David P.
APPLICANT: Metcalf, Donald
APPLICANT: King, Julie Ann
TITLE OF INVENTION: Improvements in Granulocyte-Macrophage
NUMBER OF SEQUENCES: 6
TITLE OF INVENTION: Colony-Stimulating Factor Receptor and Derivatives Thereof
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 New York Ave., NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351,149
FILING DATE: 23-NOV-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fox, Samuel L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 1256.0030001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-351-149-6

Query Match 96.8%; Score 30; DB 1; Length 400;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 306 WSXWS 310

RESULT 8
US-08-243-010-6
Sequence 6, Application US/08243010
Patent No. 5639597

GENERAL INFORMATION:

APPLICANT: Lauffer, Leander
APPLICANT: Zeitlmeissel, Gerd
APPLICANT: Oquendo, Patricia
TITLE OF INVENTION: Cell-free Receptor Binding Assays, The
TITLE OF INVENTION: Production and Use Thereof
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,010
FILING DATE: 13-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/798,564
FILING DATE: 26-NOV-1991
APPLICATION NUMBER: DE P 40 37 837.3
FILING DATE: 28-NOV-1990

ATTORNEY/AGENT INFORMATION:

NAME: Einsauid, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 02481-1132-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-243-010-6

Query Match 96.8%; Score 30; DB 1; Length 552;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSXMS 5
1111
Db 306 MSSMS 310

RESULT 9
US-08-449-329-10

Sequence 10, Application US/08449329
Patent No. 5648334

GENERAL INFORMATION:

APPLICANT: Davis, Samuel
APPLICANT: Squinto, Stephen P.
APPLICANT: Furch, Mark E.
APPLICANT: Yancopoulos, George D.
TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennile & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,329
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/700,677
FILING DATE: 15-MAY-1991

ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-065
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-449-329-10

US-08-449-329-10

Query Match

Best Local Similarity 96.8%; Score 30; DB 1; Length 185;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSXMS 5
1111
Db 181 MSAMS 185

RESULT 10
US-08-449-329-13

Sequence 13, Application US/08449329
Patent No. 5648334

GENERAL INFORMATION:

APPLICANT: Davis, Samuel
APPLICANT: Squinto, Stephen P.
APPLICANT: Furch, Mark E.
APPLICANT: Yancopoulos, George D.
TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennile & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,329
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/700,677
FILING DATE: 15-MAY-1991

ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-065
TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-449-329-13

Query Match 96.8%; Score 30; DB 1; Length 185;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WSXWS 5
DB 181 WSSWS 185

RESULT 11
US-08-490-803-17
Sequence 17, Application US/08490803
Patent No. 5705349
GENERAL INFORMATION:
APPLICANT: Holly, Richard D.
APPLICANT: Burkhead, Steven K.
TITLE OF INVENTION: METHOD FOR PREPARING ORPHAN RECEPTOR LIGANDS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/490,803
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 94-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-632-4009
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 633 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-490-803-17

Query Match 96.8%; Score 30; DB 1; Length 633;
Best Local Similarity 80.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WSXWS 5
DB 473 WSWMS 477

RESULT 12

US-08-384-828-6
Sequence 6, Application US/08384828
Patent No. 5726036
GENERAL INFORMATION:
APPLICANT: Nicola, Micos A.
APPLICANT: Gough, Nicholas M.
APPLICANT: Gearing, David P.
APPLICANT: Metcalf, Donald
APPLICANT: King, Julie Ann
TITLE OF INVENTION: Improvements in Granulocyte-Macrophage
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 New York Ave., NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,828
FILING DATE: 07-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/351,149
FILING DATE: 23-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fox, Samuel L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 1256.0030001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-384-828-6

Query Match 96.8%; Score 30; DB 1; Length 400;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WSXWS 5
DB 306 WSSWS 310

RESULT 13
US-08-313-288B-17
Sequence 17, Application US/08313288B
Patent No. 5750502
GENERAL INFORMATION:
APPLICANT: Jessell, Thomas M. and Avihu Klar
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,288B
FILING DATE: January 5, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-313-288B-17

Query Match
Best Local Similarity 96.8%; Score 30; DB 2; Length 584;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 545 WSXWS 549

RESULT 14
US-08-850-293-5
Sequence 5, Application US/08850293
Patent No. 5843726
GENERAL INFORMATION:
APPLICANT: Lee, Jong Y.
TITLE OF INVENTION: PURIFIED HUMAN ERYTHROPOIETIN RECEPTOR
NUMBER OF SEQUENCES: 5
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C., P.A.
STREET: 60 South Sixth Street, Suite 3300
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,293
FILING DATE: 05-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/499,643
FILING DATE: 07-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,815
FILING DATE: 16-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 07004/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/335-5070
TELEFAX: 612/288-9696

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 508 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-850-293-5

Query Match
Best Local Similarity 96.8%; Score 30; DB 2; Length 508;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 233 WSXWS 237

RESULT 15
US-08-445-073-10
Sequence 10, Application US/08445073
Patent No. 5849897
GENERAL INFORMATION:
APPLICANT: Davis, Samuel
APPLICANT: Squinto, Stephen P.
APPLICANT: Futh, Mark E.
TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,073
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,647
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-445-073-10

Query Match
Best Local Similarity 96.8%; Score 30; DB 2; Length 185;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 181 WSXWS 185

- Fri Sep 17 14:52:34 1999

Search completed: September 16, 1999, 20:41:05
Job time: 5434 sec

us-09-037-657-1.ra1

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 16, 1999, 19:12:07 ; Search time 49.27 Seconds

(without alignments)
4.066 Million cell updates/sec

Title: US-09-037-657-1

Perfect score: 31
Sequence: 1 MSXMS 5

Scoring table: BLOSUM62

Searched: 122810 seqs, 40065486 residues

Database:

PIR-60:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	96.8	508	1 ZOHUR	erythropoietin rec
2	30	96.8	507	1 A32385	erythropoietin rec
3	30	96.8	583	1 C8HUA	unc-5 protein, lon
4	30	96.8	947	1 B44294	unc-5 protein, lon
5	30	96.8	494	2 S60028	ferredoxin-NADP-
6	30	96.8	140	2 S20914	lysozyme (EC 3.2.1
7	30	96.8	140	2 S41573	lysozyme (EC 3.2.1
8	30	96.8	140	2 S41574	lysozyme (EC 3.2.1
9	30	96.8	140	2 S41577	lysozyme (EC 3.2.1
10	30	96.8	81	2 S41580	lysozyme (EC 3.2.1
11	30	96.8	437	2 S69881	phosphopyruvate hy
12	30	96.8	437	2 S67305	phosphopyruvate hy
13	30	96.8	222	2 A26489	placental lactogen
14	30	96.8	507	2 A46713	erythropoietin rec
15	30	96.8	265	2 S14081	erythropoietin rec
16	30	96.8	197	2 JH0602	beta-crystallin A2
17	30	96.8	934	2 A43372	complement C6 prec
18	30	96.8	843	2 A27340	complement C7 prec
19	30	96.8	584	2 I37213	complement 8 alpha
20	30	96.8	191	2 S41317	hypothetical prote
21	30	96.8	284	2 S27931	En/v-mpl fusion p
22	30	96.8	2529	2 B64635	toxin-like outer m
23	30	96.8	2399	2 H1879	toxin-like outer m
24	30	96.8	218	2 S02828	allicidin resistan
25	30	96.8	394	2 A70504	probable PPE prote
26	30	96.8	2894	2 C64474	hypothetical prote
27	30	96.8	455	2 S66765	hypothetical prote
28	30	96.8	691	2 J60150	acetylcholinestera
29	30	96.8	1584	2 T00026	brain-specific an
30	30	96.8	1522	2 T00028	granulocyte-macrop
31	30	96.8	333	2 S13684	granulocyte-macrop
32	30	96.8	400	2 S06945	granulocyte-macrop
33	30	96.8	137	2 S47568	granulocyte-macrop
34	30	96.8	378	2 S50040	granulocyte-macrop
35	30	96.8	984	2 T00326	hypothetical prote
36	30	96.8	422	2 I37891	interleukin-11 rec
37	30	96.8	579	2 B45266	MPL-K protein prec
38	30	96.8	635	2 A45266	MPL-K protein prec
39	30	96.8	206	2 A57018	prolactin receptor

40	30	96.8	622	2 A40144	prolactin receptor
41	30	96.8	625	2 S35317	hematopoietic grow
42	30	96.8	432	2 I48343	interleukin-11 rec
43	30	96.8	437	2 S05478	properdin - mouse
44	30	96.8	626	2 S37622	proto-oncogene - m
45	30	96.8	367	2 G71178	hypothetical prote

ALIGNMENTS

RESULT 1

ZOHUR

erythropoietin receptor precursor - human

C.Species: Homo sapiens (man)

C.Date: 12-Feb-1993 #sequence revision 05-Apr-1995 #text-change 26-Feb-1999

C.Accession: A43799; A60160; A49824; A53958; A55280; I52563

R.Jones, S.S.; D'Andrea, A.D.; Haines, L.L.; Wong, G.G.

Blood 76, 31-35, 1990

A.Title: Human erythropoietin receptor: cloning, expression, and biologic characteriz

A.Reference number: A43799; MUID:90304340

A.Accession: A43799

A.Molecule type: mRNA

A.Residues: 1-508 <JON>

A.Cross-references: GB:M60459; NID:g182244; PID:g182245

R.Winkelmann, J.C.; Penny, L.A.; Deaven, L.L.; Forget, B.G.; Jenkins, R.B.

Blood 76, 24-30, 1990

A.Title: The gene for the human erythropoietin receptor: analysis of the coding seque

A.Reference number: A60160; MUID:90304334

A.Accession: A60160

A>Status: not compared with conceptual translation

A.Molecule type: mRNA, DNA

A.Residues: 1-101, 'R', 103-168, 'RP', 191-243, 'E', 245-508 <WIN>

R.Noguchi, C.T.; Bae, K.S.; Chiu, K.; Wade, Y.; Schechter, A.N.; Hankins, W.D.

Blood 78, 2548-2556, 1991

A.Title: Cloning of the human erythropoietin receptor gene.

A.Reference number: A49824; MUID:92399733

A.Accession: A49824

A.Molecule type: DNA

A.Residues: 1-508 <NOG>

A.Cross-references: GB:S45333; NID:g255496; PID:g255497

A.Experimental source: placenta

A.Note: sequence extracted from NCBI backbone (NCBI:113293, NCBI:113294)

R.Ehmann, K.; St. John, T.

Exp. Hematol. 19, 973-977, 1991

A.Title: The erythropoietin receptor gene: cloning and identification of multiple tra

A.Reference number: A53958

A.Accession: A53958

A.Molecule type: mRNA

A.Residues: 1-508 <ENR>

R.Penny, L.A.; Forget, B.G.

Genomics 11, 974-980, 1991

A.Title: Genomic organization of the human erythropoietin receptor gene.

A.Reference number: A55280; MUID:92147143

A.Accession: A55280

A.Molecule type: DNA

A.Residues: 1-17, 381-387, 'LLEQOQDA', 391-395, 504-508 <PEN>

A.Note: sequence modified after extraction from NCBI backbone

A.Note: the authors translated the codon GAT for residue 31 as B

R.Maouche, L.; Tournamille, C.; Hattab, C.; Boffa, G.; Cartton, J.P.; Chretien, S.

Blood 78, 2557-2563, 1991

A.Title: Cloning of the gene encoding the human erythropoietin receptor.

A.Reference number: I52563; MUID:92399734

A.Accession: I52563

A>Status: translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Residues: 1-96 <RES>

A.Cross-references: GB:M76595; NID:g182147; PID:g553281

C.Genetics:

A.Gene: GDB:EPOR

A.Cross-references: GDB:125242; OMIM:133171

A.Map position: 19p13.3-19p13.2

A:introns: 39/1; 84/2; 143/1; 195/3; 247/1; 276/2; 305/3
 C:superfamily: erythropoietin receptor; cytokine receptor homology
 C:keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-508/Product: erythropoietin receptor #status predicted <MAT>
 F:52-250/Domain: extracellular #status predicted <EXT>
 F:52-239/Domain: cytokine receptor homology <CRS>
 F:233-237/Region: WSXWS motif
 F:251-272/Domain: transmembrane #status predicted <TM>
 F:273-508/Domain: intracellular #status predicted <INT>
 F:52-62,91-107/Disulfide bonds: #status predicted
 F:76/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 96.8%; Score 30; DB 1; Length 508;
 Best Local Similarity 80.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 WSXWS 5
 Db 233 WSXWS 237

RESULT 2
 A:32385
 erythropoietin receptor precursor, membrane-bound form - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 28-Sep-1990 #sequence_revision 05-Apr-1995 #text_change 05-Sep-1997
 C:Accession: A41686; A32385; S13249
 R:Rino, M.; Tojo, A.; Misawa, Y.; Moril, H.; Takaku, F.; Shibuya, M.
 Mol. Cell. Biol. 11, 5527-5533, 1991
 A:Title: Unregulated expression of the erythropoietin receptor gene caused by insertion
 A:Reference number: A41686; MIMD:92017832
 A:Accession: A41686
 A:Molecule type: mRNA
 A:Residues: 1-507 <HIN>
 A:Cross-references: GB:S59388; NID:9237036; PID:9237037
 A:Experimental source: murine erythroleukemia (MEU) cell line F5-5
 R:D'Andrea, A.D.; Lodish, H.F.; Wong, G.C.
 Cell 57, 277-285, 1989
 A:Title: Expression cloning of the murine erythropoietin receptor.
 A:Reference number: A32385; MIMD:89195238
 A:Accession: A32385
 A:Molecule type: mRNA
 A:Residues: 1-507 <DA>
 A:Cross-references: GB:J04843; NID:9193090; PID:9309219
 A:Experimental source: murine erythroleukemia (MEU) cells, subclone 745
 R:Kuramochi, S.; Ikawa, Y.; Todokoro, K.
 J. Mol. Biol. 216, 567-575, 1990
 A:Title: Characterization of murine erythropoietin receptor genes.
 A:Reference number: S13249; MIMD:91080149
 A:Accession: S13249
 A:Molecule type: DNA
 A:Residues: 1-507 <RUR>
 A:Cross-references: EMBL:X53081; NID:950861; PID:950862
 A:Experimental source: murine erythroleukemia K-1 cells
 C:Genetics: 39/1; 83/2; 142/1; 194/3; 246/1; 275/2; 304/3
 C:superfamily: erythropoietin receptor; cytokine receptor homology
 C:keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-507/Product: erythropoietin receptor #status predicted <MAT>
 F:52-249/Domain: extracellular #status predicted <EXT>
 F:52-238/Domain: cytokine receptor homology <CRS>
 F:550-271/Domain: transmembrane #status predicted <TM>
 F:272-507/Domain: intracellular #status predicted <INT>
 F:52-62,91-106/Disulfide bonds: #status predicted
 F:75/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 96.8%; Score 30; DB 1; Length 507;
 Best Local Similarity 80.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 WSXWS 5
 Db 232 WSXWS 236

RESULT 3
 C8HUA
 complement C8 alpha chain precursor - human
 C:Species: Homo sapiens (man)
 C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 07-Aug-1998
 C:Accession: A26704
 R:Rao, A.G.; Howard, O.M.2.; Ng, S.C.; Whitehead, A.S.; Colten, H.R.; Sodetz, J.M.
 Biochemistry 26, 3556-3564, 1987
 A:Title: Complementary DNA and derived amino acid sequence of the alpha subunit of
 A:Reference number: A26704; MIMD:88000560
 A:Accession: A26704
 A:Molecule type: mRNA
 A:Residues: 1-583 <RA>
 A:Note: part of the sequence was confirmed by protein sequencing
 C:Comment: C8, a constituent of the cytolytic (membrane attack) complex C5b-C9, con
 C:Comment: The alpha chain binds to the beta chain, gamma chain, and component C9 a
 C:Genetics:
 A:Gene: GDB:C8A
 A:Cross-references: GDB:119735; OMIM:120950
 A:Map position: 1p32-1p32
 C:superfamily: complement C9; EGF homology; LDL receptor ligand-binding repeat hom
 C:keywords: complement pathway; cytolytic; glycoprotein; membrane attack complex; p
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-10/Domain: propeptide #status predicted <PRO>
 F:31-583/Product: complement C8 alpha chain #status predicted <MP>
 F:37-91/Domain: thrombospondin type 1 repeat homology <THR1>
 F:96-130/Domain: LDL receptor ligand-binding repeat homology <LDL2>
 F:496-527/Domain: EGF homology <EGF>
 F:537-583/Domain: thrombospondin type 1 repeat homology <THR2>
 F:43,437/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 96.8%; Score 30; DB 1; Length 583;
 Best Local Similarity 80.0%; Pred. No. 3.1e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 WSXWS 5
 Db 544 WSXWS 548

RESULT 4
 B44294
 unc-5 protein, long form - Caenorhabditis elegans
 N:Contains: unc-5 protein, short form
 C:Species: Caenorhabditis elegans
 C>Date: 30-Apr-1993 #sequence_revision 28-Jul-1995 #text_change 20-Mar-1998
 C:Accession: B44294; A44294
 R:Leung-Hagstedt, C.; Spence, A.M.; Stern, B.D.; Zhou, Y.; Su, M.W.; Hedgecock, E
 Cell 71, 283-299, 1992
 A:Title: UNC-5, a transmembrane protein with immunoglobulin and thrombospondin type
 A:Reference number: A44294; MIMD:93046629
 A:Contents: variety Bergerac
 A:Accession: B44294
 A:Molecule type: DNA
 A:Residues: 1-947 <LEU>
 A:Cross-references: GB:S47168; NID:9258527; PID:9258529
 A:Note: sequence extracted from NCBI backbone (NCBIN:116668, NCBIN:116670, NCBIN:116
 A:Note: authors translated the codon CMA for residue 642 as Val; sequence shown fol
 A:Note: mRNA lacking the first exon is equally prevalent
 C:Genetics:
 A:Gene: unc-5
 A:introns: 28/1; 69/3; 136/1; 170/3; 229/1; 351/2; 581/1; 886/3
 C:Function:
 A:Description: required for guidance of pioneering axons and cells migrating dorsall
 C:superfamily: unc-5 protein; immunoglobulin homology; SH3 homology; thrombospondin
 C:keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane

F:30-947/Product: unc-5 protein, short form #status predicted <ALT>
 F:46-116/Domain: immunoglobulin homology <IG>
 F:153-211/Domain: immunoglobulin homology <IG2>
 F:229-300/Domain: thrombospondin type 1 repeat homology <THR1>
 F:301-354/Domain: thrombospondin type 1 repeat homology <THR2>
 F:365-390/Domain: transmembrane #status predicted <TM>
 F:512-559/Domain: SH3 homology <SH3>
 F:53-114,65-112,160-209/Disulfide bonds: #status predicted
 F:206/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 96.8%; Score 30; DB 1; Length 947;
 Best Local Similarity 80.0%; Pred. No. 4.8e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXWS 5
 || ||
 Db 305 WSAWS 309

RESULT 5
 S60028
 ferredoxin--NADP+ reductase (PC 1.18.1.2) precursor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 15-Feb-1996 #sequence_revision 08-Nov-1996 #text_change 16-Feb-1997
 C:Accession: S60028; 149671
 R:Itch, S.; Iemura, O.; Yamada, E.; Yoshimura, T.; Tsujikawa, K.; Kohama, Y.; Malmure, T.
 Biochim. Biophys. Acta 1264, 159-162, 1995
 A>Title: cDNA cloning of mouse ferredoxin reductase from kidney.
 A:Reference number: 149671; MUID:96085117
 A:Accession: S60028
 A:Molecule type: mRNA
 A:Residues: 1-494 <IT0>
 A:Cross-references: EMBL:D4920; NID:g108468; PID:g108469
 C:Genetics:
 A:Genome: nuclear
 C:Superfamily: human ferredoxin--NADP+ reductase
 C:Keywords: FAD; mitochondrion; NADP; oxidoreductase
 F:1-34/Domain: transit peptide (mitochondrion) #status predicted <MP>
 F:35-494/Product: ferredoxin--NADP+ reductase #status predicted <MP>

Query Match 96.8%; Score 30; DB 2; Length 494;
 Best Local Similarity 80.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXWS 5
 || ||
 Db 11 WSAWS 15

RESULT 6
 S20914
 lysozyme (EC 3.2.1.17) D precursor - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Sep-1997
 C:Accession: S20914; S41576
 R:Kyllsten, P.; Kimbrell, D.A.; Daffre, S.; Samakovlis, C.; Hultmark, D.
 Mol. Gen. Genet. 232, 335-343, 1992
 A>Title: The lysozyme locus in Drosophila melanogaster: different genes are expressed in
 A:Reference number: S20914; MUID:92269751
 A:Accession: S20914
 A:Molecule type: DNA
 A:Residues: 1-140 <KYL>
 A:Cross-references: EMBL:X58382; NID:g9197; PID:g9198
 R:Daffre, S.; Kyllsten, P.; Samakovlis, C.; Hultmark, D.
 Mol. Gen. Genet. 242, 152-162, 1994
 A>Title: The lysozyme locus in Drosophila melanogaster: an expanded gene family adapted
 A:Reference number: S41573
 A:Accession: S41576
 A:Molecule type: mRNA
 A:Residues: 1-140 <DAF>
 C:Genetics:

A:Gene: lyso
 A:Cross-references: FlyBase:FBgn0004427
 A:Map position: 3
 C:Superfamily: lysozyme C
 C:Keywords: bacteriolytic enzyme; glycosidase; hydrolase; polysaccharide degradation
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-140/Product: lysozyme D #status predicted <MP>

Query Match 96.8%; Score 30; DB 2; Length 140;
 Best Local Similarity 80.0%; Pred. No. 81;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXWS 5
 || ||
 Db 120 WSAWS 124

RESULT 7
 S41573
 lysozyme (EC 3.2.1.17) precursor - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 25-Dec-1994 #sequence_revision 23-Feb-1996 #text_change 08-Sep-1997
 C:Accession: S41573; S41575; S32651; S32726
 R:Daffre, S.; Kyllsten, P.; Samakovlis, C.; Hultmark, D.
 Mol. Gen. Genet. 242, 152-162, 1994
 A>Title: The lysozyme locus in Drosophila melanogaster: an expanded gene family adapt
 A:Reference number: S41573
 A:Accession: S41573
 A:Molecule type: mRNA
 A:Residues: 1-140 <DAF>
 A:Cross-references: EMBL:Z22223; NID:g288920; PID:g288921
 A:Genetics: LYSA
 A:Accession: S41575
 A:Molecule type: mRNA
 A:Residues: 1-140 <DA>
 A:Cross-references: EMBL:Z22226; NID:g296038; PID:g296039
 A:Genetics: LYSC
 A:Genetics: <LYSA>
 A:Gene: lyso
 A:Map position: 3
 C:Genetics: <LYSC>
 A:Gene: lyso
 A:Map position: 3
 C:Genetics: <LYSC>
 A:Map position: 3
 C:Superfamily: lysozyme C
 C:Keywords: bacteriolytic enzyme; glycosidase; hydrolase; polysaccharide degradation
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-140/Product: lysozyme A #status predicted <MP>

Query Match 96.8%; Score 30; DB 2; Length 140;
 Best Local Similarity 80.0%; Pred. No. 81;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXWS 5
 || ||
 Db 120 WSAWS 124

RESULT 8
 S41574
 lysozyme (EC 3.2.1.17) B precursor - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 25-Dec-1994 #sequence_revision 23-Feb-1996 #text_change 26-Feb-1998
 C:Accession: S41574; S32643; S32620
 R:Daffre, S.; Kyllsten, P.; Samakovlis, C.; Hultmark, D.
 Mol. Gen. Genet. 242, 152-162, 1994
 A>Title: The lysozyme locus in Drosophila melanogaster: an expanded gene family adapt
 A:Reference number: S41574
 A:Accession: S41574
 A:Molecule type: mRNA
 A:Residues: 1-140 <DAF>
 A:Cross-references: EMBL:Z22225; NID:g289001; PID:g289002

A:Genetics: LYSB
 R:Daftre, S.; Kysten, P.; Samakovlis, C.; Hultmark, D.
 Submitted to the EMBL Data Library, April 1993
 A:Description: The lyszyme locus in Drosophila melanogaster; an expanded gene family ad
 A:Reference number: S32620
 A:Accession: S32643
 A:Molecule type: DNA
 A:Residues: 1-140 <DA2>
 A:Cross-references: EMBL:Z22226
 A:Genetics: LYSB
 C:Genetics: <LYSB>
 A:Gene: LYSB
 A:Cross-references: FlyBase:FBgn0004425
 A:Map position: 3
 C:Genetics: <LYSC>
 A:Gene: FlyBase:LYSC
 A:Cross-references: FlyBase:FBgn0004426
 A:Map position: 3
 C:Superfamily: lyszyme C
 C:Keywords: bacteriolytic enzyme; glycosidase; hydrolase; polysaccharide degradation
 F:1-18/Domain: signal sequence #status predicted <Sig>
 F:19-140/Product: lyszyme B #status predicted <Mat>

Query Match 96.8%; Score 30; DB 2; Length 140;
 Best Local Similarity 80.0%; Pred. No. 81;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXMS 5
 || ||
 Db 120 WSAMS 124

RESULT 9
 S41577
 lyszyme (EC 3.2.1.17) E precursor - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 25-Dec-1994 #sequence_revision 23-Feb-1996 #text_change 24-Sep-1998
 C:Accession: S41577; S32634
 R:Daftre, S.; Kysten, P.; Samakovlis, C.; Hultmark, D.
 Mol. Gen. Genet. 242, 152-162, 1994
 A:Title: The lyszyme locus in Drosophila melanogaster: an expanded gene family adapted
 A:Reference number: S41577
 A:Accession: S41577
 A:Molecule type: mRNA
 A:Residues: 1-140 <DAF>
 A:Cross-references: EMBL:Z22227; NID:g289003; PID:g289004
 C:Genetics:
 A:Gene: LysE
 A:Cross-references: FlyBase:FBgn0004428
 A:Map position: 3
 C:Superfamily: lyszyme C
 C:Keywords: bacteriolytic enzyme; glycosidase; hydrolase; polysaccharide degradation
 F:1-18/Domain: signal sequence #status predicted <Sig>
 F:19-140/Product: lyszyme E #status predicted <Mat>

Query Match 96.8%; Score 30; DB 2; Length 140;
 Best Local Similarity 80.0%; Pred. No. 81;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXMS 5
 || ||
 Db 120 WSAMS 124

RESULT 10
 S41580
 lyszyme (EC 3.2.1.17) X - fruit fly (Drosophila melanogaster) (fragment)
 C:Species: Drosophila melanogaster
 C>Date: 25-Dec-1994 #sequence_revision 19-Oct-1995 #text_change 24-Sep-1998
 C:Accession: S41580; S32650
 R:Daftre, S.; Kysten, P.; Samakovlis, C.; Hultmark, D.

Mol. Gen. Genet. 242, 152-162, 1994
 A:Title: The lyszyme locus in Drosophila melanogaster: an expanded gene family ad
 A:Reference number: S41573
 A:Accession: S41580
 A:Molecule type: mRNA
 A:Residues: 1-81 <DAF>
 A:Cross-references: EMBL:Z22224; NID:g288922; PID:g288923
 C:Genetics:
 A:Gene: LysP
 A:Cross-references: FlyBase:FBgn0004431
 A:Map position: 3
 C:Superfamily: lyszyme C
 C:Keywords: bacteriolytic enzyme; glycosidase; hydrolase; polysaccharide degradation

Query Match 96.8%; Score 30; DB 2; Length 81;
 Best Local Similarity 80.0%; Pred. No. 49;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXMS 5
 || ||
 Db 60 WSAMS 64

RESULT 11
 S69881
 phosphopyruvate hydratase (EC 4.2.1.11) YMR323w - yeast (Saccharomyces cerevisiae)
 C:Species: Saccharomyces cerevisiae
 C>Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 22-May-1998
 C:Accession: S69881
 R:Churcher, C.M.
 Submitted to the EMBL Data Library, November 1995
 A:Reference number: S69876
 A:Accession: S69881
 A:Molecule type: DNA
 A:Residues: 1-437 <CHD>
 A:Cross-references: EMBL:Z54141; NID:g1072408; PID:g1072413; MIPS:YMR323w
 C:Genetics:
 A:Map position: 13R
 A:Note: YMR323w
 C:Superfamily: enolase
 C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; magnesium
 F:40/Binding site: magnesium 2 (Ser) #status predicted
 F:212,346/Active site: Glu, Lys #status predicted
 F:247,296,321/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 96.8%; Score 30; DB 2; Length 437;
 Best Local Similarity 80.0%; Pred. No. 2,3e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXMS 5
 || ||
 Db 304 WSAMS 308

RESULT 12
 S67305
 phosphopyruvate hydratase (EC 4.2.1.11) ERRI - yeast (Saccharomyces cerevisiae)
 N:Alternate names: ERRI protein; protein O6788; protein P0304; protein YOR393w; pro
 C:Species: Saccharomyces cerevisiae
 C>Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 22-May-1998
 C:Accession: S67305; S67306; S59000; S65314; S65335
 R:Delius, H.; Hedling, U.; Hofmann, B.
 Submitted to the Protein Sequence Database, July 1996
 A:Reference number: S67261
 A:Accession: S67305
 A:Molecule type: DNA
 A:Residues: 1-330 <DEU>
 A:Cross-references: EMBL:Z75301; MIPS:YOR393w
 A:Experimental source: strain S288C
 A:Genetics: C15
 R:Wambutt, R.; Medler, H.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S67306
 A:Accession: S67306
 A:Molecule type: DNA
 A:Residues: 177-437 <NAME>
 A:Cross-references: EMBL:Z75301; MIPS:YOR393w
 A:Experimental source: strain S286C
 A:Genetics: C15
 R:Pyde, F.E.; Huckle, T.C.; Louis, E.J.
 Yeast 11, 371-382, 1995
 A:Title: Sequence analysis of the right end of chromosome XV in *Saccharomyces cerevisiae*
 A:Reference number: S59000; MUID:95304651
 A:Accession: S59000
 A:Molecule type: DNA
 A:Residues: 120-230, 'K', 232-437 <PRX>
 A:Cross-references: EMBL:U23472; NID:g775202; PID:g775203
 A:Genetics: C15
 R:Diastheoef, A.; Floeth, M.; Fritz, M.; Hilbert, H.; Moestl, D.
 submitted to the Protein Sequence Database, May 1996
 A:Reference number: S65292
 A:Accession: S65314
 A:Molecule type: DNA
 A:Residues: 1-437 <DUE>
 A:Cross-references: EMBL:Z73937; MIPS:YPL281c; NID:g1370577; PID:e246987; PID:g1370578
 A:Experimental source: strain S286C (AB972)
 A:Genetics: C16
 A:Gene: SGD:ERR1
 A:Cross-references: MIPS:YOR393w; SGD:S0005920
 A:Map position: 15R
 A:Note: YOR393w
 C:Genetics: <C16>
 A:Gene: SGD:ERR2
 A:Cross-references: MIPS:YPL281c; SGD:S0006202
 A:Map position: 16L
 A:Note: YPL281c
 C:Superfamily: enolase
 C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; magnesium
 F:40/Binding site: magnesium 2 (Ser) #status predicted
 F:212/346/Active site: Glu, Lys #status predicted
 F:247/296/321/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 96.8%; Score 30; DB 2; Length 437;
 Best Local Similarity 80.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXWS 5
 ||||
 Db 304 WSSWS 308

RESULT 13
 A26489
 Placental lactogen II precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Oct-1988 #sequence, revision 05-Oct-1988 #text, change 17-Mar-1999
 C:Accession: A44090; A26489; B23159
 R:Shida, M.M.; Jackson-Grusby, L.L.; Ross, S.R.; Linzer, D.I.H.
 Proc. Natl. Acad. Sci. U.S.A. 89, 3864-3868, 1992
 A:Title: Placental-specific expression from the mouse placental lactogen II gene promoter
 A:Reference number: A44090; MUID:92237269
 A:Accession: A44090
 A:Molecule type: DNA

A:Residues: 1-222 <SHI>
 A:Cross-references: GB:M85062
 R:Jackson, L.L.; Colosi, P.; Talamantes, F.; Linzer, D.I.H.
 Proc. Natl. Acad. Sci. U.S.A. 83, 8496-8500, 1986
 A:Title: Molecular cloning of mouse placental lactogen CDNA.
 A:Reference number: A26489; MUID:87041482
 A:Accession: A26489
 A:Molecule type: mRNA
 A:Residues: 1-222 <JAC>
 A:Cross-references: GB:M4647; NID:9200404; PID:9200405
 R:Linzer, D.I.H.; Lee, S.J.; Ogren, L.; Talamantes, F.; Nathans, D.
 Proc. Natl. Acad. Sci. U.S.A. 82, 4356-4359, 1985
 A:Title: Identification of proliferin mRNA and protein in mouse placenta.
 A:Reference number: A94049; MUID:85242683
 A:Accession: B23159
 A:Molecule type: protein
 A:Residues: 32-50 <LIN>
 C:Comment: Placental lactogen II can bind to mammary gland prolactin receptors.
 C:Superfamily: prolactin
 C:Keywords: hormone; placenta
 F:1-31/Domain: signal sequence #status predicted <SIG>
 F:32-222/Product: Placental lactogen II #status experimental <MAT>

Query Match 96.8%; Score 30; DB 2; Length 222;
 Best Local Similarity 80.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXWS 5
 ||||
 Db 173 WSAMS 177

RESULT 14
 A46713
 erythropoietin receptor precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 21-Sep-1993 #sequence, revision 18-Nov-1994 #text, change 20-Mar-1998
 C:Accession: A46713
 R:Masuda, S.; Nagao, M.; Takahata, K.; Konishi, Y.; Gallyas Jr., F.; Tabira, T.; Sase
 J. Biol. Chem. 268, 11208-11216, 1993
 A:Title: Functional erythropoietin receptor of the cells with neural characteristics.
 A:Reference number: A46713; MUID:93265574
 A:Accession: A46713
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-507 <MAS>
 A:Cross-references: GB:D13566; NID:g286209; PID:d1003266; PID:g286210
 A:Experimental source: PC12 and erythroid cells
 A:Note: sequence extracted from NCBI backbone (NCBI:132811, NCBI:132813)
 C:Superfamily: erythropoietin receptor; cytokine receptor homology
 C:Keywords: cytokine receptor; glycoprotein; transmembrane protein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-507/Product: erythropoietin receptor #status predicted <MAT>
 F:25-246/Domain: extracellular receptor #status predicted <EXT>
 F:32-238/Domain: cytokine receptor homology <CRS>
 F:250-271/Domain: transmembrane #status predicted <TM>
 F:272-507/Domain: intracellular #status predicted <INT>
 F:75/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 96.8%; Score 30; DB 2; Length 507;
 Best Local Similarity 80.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXWS 5
 ||||
 Db 232 WSAMS 236

RESULT 15
 S14081
 erythropoietin receptor - mouse

C:Species: Mus musculus (house mouse)
 C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-May-1997
 C:Accession: S14081; I49653
 R:Kuramochi, S.; Ikawa, Y.; Todokoro, K.
 J. Mol. Biol. 216, 567-575, 1990
 A:title: Characterization of murine erythropoietin receptor genes.
 A:Reference number: S13249; MUID:91080149
 A:Accession: S14081
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-265 <KUR>
 R:Jacobs, C.; Chretien, S.; Lemarchandel, V.; Mayeux, P.; Romeo, P.
 J. Biol. Chem. 266, 6952-6956, 1991
 A:title: Spleen focus-forming virus long terminal repeat insertional activation of the m
 A:Reference number: I49653; MUID:91201346
 A:Accession: I49653
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-24 <RBS>
 A:Cross-references: GB:M62360; NID:q193199; PID:q193200
 C:Superfamily: erythropoietin receptor; cytokine receptor homology
 C:Keywords: cytokine receptor; transmembrane protein
 F:52-238/Domain: cytokine receptor homology <CRS>

Query Match 96.8%; Score 30; DB 2; Length 265;
 Best Local Similarity 80.0%; Pred. No. 1.5e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSXMS 5
 |||||
 DB 232 MSAMS 236

Search completed: September 16, 1999, 20:42:05
 Job time: 5398 sec

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OM protein - protein search, using sw model

Run on: September 17, 1999, 03:05:20 ; Search time 35.09 Seconds

(without alignments)
4.028 Million cell updates/sec

Title: US-09-037-657-1

Perfect score: 31

Sequence: 1 WSXMS 5

Scoring table: BLOSUM62

Searched: 77977 seqs, 28268293 residues

Database: SwissProt_37.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	96.8	494	1	ADRO_MOUSE
2	30	96.8	218	1	ALBR_KLEBOX
3	30	96.8	934	1	ALBR_MOUSE
4	30	96.8	843	1	CO7_HUMAN
5	30	96.8	584	1	CO8A_HUMAN
6	30	96.8	586	1	CO9_FUGRU
7	30	96.8	195	1	CRBB_BOVIN
8	30	96.8	972	1	CTRL_BACCI
9	30	96.8	508	1	EPOR_HUMAN
10	30	96.8	507	1	EPOR_MOUSE
11	30	96.8	507	1	ERR1_YEAST
12	30	96.8	437	1	GMCR_HUMAN
13	30	96.8	400	1	LYSD_DROME
14	30	96.8	140	1	LYSD_DROME
15	30	96.8	140	1	LYSD_DROME
16	30	96.8	140	1	LYSD_DROME
17	30	96.8	140	1	LYSD_DROME
18	30	96.8	81	1	LYSD_DROME
19	30	96.8	184	1	MYL_MPV
20	30	96.8	222	1	PLC2_MOUSE
21	30	96.8	622	1	PROR_HUMAN
22	30	96.8	437	1	PROR_MOUSE
23	30	96.8	867	1	SSPO_BOVIN
24	30	96.8	635	1	TPOR_HUMAN
25	30	96.8	625	1	TPOR_MOUSE
26	30	96.8	625	1	TPOR_MOUSE
27	29	93.5	507	1	AL15_TOBAC
28	29	93.5	510	1	CEAB_ECOLI
29	29	93.5	697	1	CEAB_ECOLI
30	29	93.5	362	1	CNTR_CHICK
31	29	93.5	372	1	CNTR_HUMAN
32	29	93.5	372	1	CNTR_RAT
33	29	93.5	591	1	CO8B_HUMAN
34	29	93.5	590	1	CO8B_RABIT
35	29	93.5	140	1	CO8B_RAT
36	29	93.5	547	1	CO9_HORSE
37	29	93.5	559	1	CO9_HUMAN
38	29	93.5	528	1	CO9_MOUSE
39	29	93.5	574	1	CO9_MOUSE
40	29	93.5	557	1	CO9_ONCMY
41	29	93.5	554	1	CO9_RABIT
42	29	93.5	494	1	CPSL_HUMAN
43	29	93.5	391	1	CPSD_STRAC

ALIGNMENTS

44 29 93.5 897 1 CYR2_HUMAN P32827 homo sapien
45 29 93.5 517 1 YXWL_CAEEL Q20806 caenorhabdi

RESULT 1
ID ADRO_MOUSE STANDARD; PRT; 494 AA.
AC 061578;
DT 15-JUL-1998 (REL. 36, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE NADPH:ADRENODOXIN OXIDOREDUCTASE PRECURSOR (EC 1.18.1.2) (ADRENODOXIN REDUCTASE) (FERREDOXIN-NADP(+) REDUCTASE).
GN FDXR.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIROGNATHI; MORIDAE; MORINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6; TISSUE-KIDNEY;
RX MEDLINE; 96085117.
RA ITOH S., IEMURA O., YAMADA E., YOSHIMURA T., TSUJIKAWA K., KOHANA Y., MIKURA T.;
RT "CDNA cloning of mouse ferredoxin reductase from kidney.";
RL BIOCHIM. BIOPHYS. ACTA 1264:159-162(1995).
CC -1- CATALYTIC ACTIVITY: REDUCED ADRENODOXIN + NADP(+) = OXIDIZED ADRENODOXIN + NADPH.
CC -1- CORRECTOR: FAD FLAVOPROTEIN.
CC -1- PATHWAY: CHOLESTEROL SIDE-CHAIN-CLEAVAGE SYSTEM.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE ADRENAL, TESTIS AND OVARY AND TO A LESSER EXTENT IN THE LIVER AND KIDNEY.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
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CC
CC EMBL; D49920; E212200;
DR MGD; MGI:104724; FDXR.
KW OXIDOREDUCTASE; FLAVOPROTEIN; NADP; FAD; MITOCHONDRION;
KW TRANSIT PEPTIDE.
FT TRANSIT 1 34 MITOCHONDRION (POTENTIAL).
FT CHAIN 35 494 ADRENODOXIN REDUCTASE.
SQ SEQUENCE 494 AA; 54202 MW; 81A18E21 CRC32;

Query Match 96.8%; Score 30; DB 1; Length 494;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WSXMS 5
DB 11 WSXMS 15

RESULT 2
ID ALBR_KLEBOX STANDARD; PRT; 218 AA.
AC P10488;
DT 01-JUL-1989 (REL. 11, CREATED)
DT 01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
DT 01-JUL-1989 (REL. 11, LAST ANNOTATION UPDATE)
DE ALBICIDIN RESISTANCE PROTEIN
OS KLEBSIELLA OXYTOCA.
OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
OC KLEBSIELLA.

[1] SEQUENCE FROM N.A.
 RC STRAIN-JMP4505;
 RX MEDLINE; 89013885.
 RA WALKER M.J., BIRCH R.G., PEMBERTON J.M.;
 RT "Cloning and characterization of an albicidin resistance gene from
 RL Klebsiella oxytoca.";
 RM MOL. MICROBIOL. 2:443-454(1988).
 CC -1- FUNCTION: ALBICIDIN RESISTANCE PROTEIN BINDS TO FORM A COMPLEX
 CC WITHOUT ANTIBIOTIC ACTIVITY BUT WITHOUT CATALYZING ANY FURTHER
 CC CHEMICAL MODIFICATIONS TO ALBICIDIN.
 CC -1- SUBCELLULAR LOCATION: PERIPLASMIC.
 CC
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 CC
 CC EMBL; Y00558; G43786;
 DR PIR; S02828; S02828.
 KW ANTIBIOTIC RESISTANCE; PERIPLASMIC.
 SQ SEQUENCE 218 AA; 25838 MW; 87C032C5 CRC32;

Query Match 96.8%; Score 30; DB 1; Length 218;
 Best Local Similarity 80.0%; Pred. No 80;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
 1111
 Db 57 WSSWS 61

RESULT 3
 CO6_HUMAN STANDARD; PRT; 934 AA.
 AC P13671;
 DT 01-JAN-1990 (REL. 13, CREATED)
 DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE COMPLEMENT COMPONENT C6 PRECURSOR.
 GN C6.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 22-31 AND 633-640.
 RX MEDLINE; 90036879.
 RA HAEFLIGER J.-A., TSCHOP J., VIAL N., JENNE D.E.;
 RT "Complete primary structure and functional characterization of the
 RT sixth component of the human complement system. Identification of the
 RT C5b-binding domain in complement C6.";
 RL J. BIOL. CHEM. 264:18041-18051(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89380223.
 RA DISCIPPIO R.G., HUGLI T.E.;
 RT "The molecular architecture of human complement component C6.";
 RL J. BIOL. CHEM. 264:16197-16206(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE-BLOOD;
 RX MEDLINE; 93291175.
 RA HOBART M.J., PERNIE B., DISCIPPIO R.G.;
 RT "Structure of the human C6 gene.";
 RL BIOCHEMISTRY 32:6198-6205(1993).
 RN [4]
 RP SEQUENCE OF 1-491 FROM N.A.
 RX MEDLINE; 89202413.
 RA CHAKRAVARTI D.N., CHAKRAVARTI B., PARRA C.A., MOELLER-EBERHARD H.J.;

RT "Structural homology of complement protein C6 with other
 RT channel-forming proteins of complement.";
 RL PROC. NATL. ACADE. SCI. U.S.A. 86:2799-2803(1989).
 RN [5]
 RP VARIANT ALLOTYPES C6 A AND B.
 RX MEDLINE; 93326158.
 RA DEMARD G., NOTHEN M.M., CICHON S.;
 RT Polymorphism of human complement component C6: an amino acid
 RT substitution (Glu/Ala) within the second thrombospondin repeat
 RT differentiates between the two common allotypes C6 A and C6 B.";
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 194:458-464(1993).
 CC -1- DOMAIN: INVOLVED IN THE FORMATION OF THE LYtic C5b-9m COMPLEX.
 CC -1- DOMAIN: C6 CONTAINS NINE DISTINCT STRUCTURAL UNITS (CYSTEINE-RICH)
 CC WHICH HAVE THE CHARACTERISTIC FEATURES OF MODULES.
 CC -1- PTM: ALL CYSTEINE RESIDUES ARE ASSUMED TO BE CROSS-LINKED TO ONE
 CC ANOTHER. INDIVIDUAL MODULES CONTAINING AN EVEN NUMBER OF CONSERVED
 CC CYSTEINE RESIDUES ARE SUPPOSED TO HAVE DISULFIDE LINKAGES ONLY
 CC WITHIN THE SAME MODULE.
 CC -1- POLYMORPHISM: THE SEQUENCE SHOWN IS THAT OF ALLOTYPIC C6 A.
 CC -1- SIMILARITY: TO COMPLEMENT FACTORS C7, C8, C9, AND TO PERFORIN.
 CC -1- SIMILARITY: CONTAINS 2 SUSHT (SCR) REPEATS.
 CC -1- SIMILARITY: CONTAINS 3 TYPE-1 TSP REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.
 CC
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 CC EMBL; J05054; G179704;
 DR EMBL; J05024; G307228;
 DR EMBL; X72177; G825633;
 DR EMBL; J04506; G618466;
 DR PIR; A32109; A32109.
 DR PIR; A34235; A34235.
 DR PIR; A34372; A34372.
 DR MIM; 217050;
 DR PROSITE; P500279; MAC PERFORIN; 1.
 DR PROSITE; P500022; EGF_1; 1.
 DR PROSITE; P501186; EGF_2; FALSE_NEG.
 DR PROSITE; P501209; LDLRA_1; 1.
 DR PROSITE; P50068; LDLRA_2; 1.
 DR PFAM; PF00057; ldl_recept_a; 1.
 DR PFAM; PF00084; sushi; 2.
 DR PFAM; PF00090; tsp_1; 3.
 DR HSP; P01130; 1A07.
 KW COMPLEMENT PATHWAY; GLYCOPROTEIN; PLASMA; MEMBRANE ATTACK COMPLEX;
 KW CYTOLYSIS; SUSHT; REPEAT; SIGNAL; POLYMORPHISM; EGF-LIKE DOMAIN;
 KW TRANSMEMBRANE.
 FT SIGNAL 1 21
 FT CHAIN 934
 FT REPEAT 22 80
 FT REPEAT 81 137
 FT DOMAIN 138 175
 FT TRANSMEM 331 349
 FT TRANSMEM 354 373
 FT DOMAIN 517 553
 FT REPEAT 562 611
 FT DOMAIN 642 934
 FT DOMAIN 643 762
 FT REPEAT 643 700
 FT REPEAT 703 762
 FT DOMAIN 766 840
 FT DOMAIN 858 934
 FT DISULFID 140 151
 FT DISULFID 146 164
 FT DISULFID 158 173
 FT DISULFID 399 420

COMPLEMENT COMPONENT C6.
 TYPE-1 TSP 1.
 TYPE-1 TSP 2.
 LDL-RECEPTOR CLASS A.
 POTENTIAL.
 EGF-LIKE.
 TYPE-1 TSP 3.
 C5b-BINDING DOMAIN.
 2 x SUSHT (SCR) REPEATS.
 SUSHT 1.
 SUSHT 2.
 COMPLEMENT CONTROL FACTOR I MODULE.
 COMPLEMENT CONTROL FACTOR I MODULE.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.

FT DISULFID 533 539 BY SIMILARITY.
 FT DISULFID 526 541 BY SIMILARITY.
 FT DISULFID 543 552 BY SIMILARITY.
 FT DISULFID 644 666 BY SIMILARITY.
 FT DISULFID 672 699 BY SIMILARITY.
 FT DISULFID 704 746 BY SIMILARITY.
 FT DISULFID 732 761 BY SIMILARITY.
 FT CARBOHYD 324 324 POTENTIAL.
 FT CARBOHYD 855 855 POTENTIAL.
 FT VARIANT 119 119 E -> A (IN ALLOTYPIC C6 B).
 SQ SEQUENCE 934 AA; 104843 MW; D03BD9D CRC32;
 Query Match 96.8%; Score 30; DB 1; Length 934;
 Best Local Similarity 80.0%; Pred. No. 3.1e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSXWS 5
 DB 571 MSXWS 575
 RESULT 4
 CO7_HUMAN STANDARD; PRT; 843 AA.
 AC P10643;
 DT 01-JUL-1989 (REL. 11, CREATED)
 DT 01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE COMPLEMENT COMPONENT C7 PRECURSOR.
 GN C7.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE; 88087145.
 RA DISCIPLO R.G., CHAKRAVARTI D.N., MUELLER-BERHARD H.J., FEY G.H.;
 RT "The structure of human complement component C7 and the C5b-7 complex."
 J. BIOL. CHEM. 263:549-560(1988).
 CC -1- FUNCTION: C7 IS A CONSTITUENT OF THE MEMBRANE ATTACK COMPLEX.
 C7 BINDS TO C5b FORMING THE C5b-7 COMPLEX, WHERE IT SERVES
 AS A MEMBRANE ANCHOR.
 CC -1- SUBUNIT: MONOMER OR DIMER; AS A C5b-7 COMPLEX IT CAN ALSO
 FORM MULTIMERIC ROSETTES.
 CC -1- PTM: C7 HAS 28 DISULFIDE BRIDGES.
 CC -1- SIMILARITY: TO COMPLEMENT FACTORS C6, C8, C9, AND TO PERFORIN.
 CC -1- SIMILARITY: CONTAINS 2 SUSHI (SCR) REPEATS.
 CC -1- SIMILARITY: CONTAINS 2 TYPE-1 TSP REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
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 or send an email to license@isb-sib.ch).
 CC EMBL; J03507; G179716;
 CC MIR; A27340; A27340.
 DR PIR; 217070;
 DR PROSITE; PS00279; MAC_PERFORIN.1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01209; LDLRA_1; 1.
 DR PROSITE; PS00068; LDLRA_2; 1.
 DR PFM; PF00057; Idl_recept_a; 1.
 DR PFM; PF00084; sush1; 2.
 DR PFM; PF00090; tsp_1; 2.
 DR HSP; P10998; IYVC.
 DR

KM COMPLEMENT PATHWAY; COMPLEMENT ALTERNATE PATHWAY; GLYCOPROTEIN;
 KM PLASMA; MEMBRANE ATTACK COMPLEX; CYTOLYSIS; SIGNAL; EGF-LIKE DOMAIN;
 KM REPEAT; SUSHI; TRANSMEMBRANE.
 FT SIGNAL 1 22
 FT CHAIN 23 843
 FT REPEAT 24 83 TYPE-1 TSP 1.
 FT DOMAIN 83 121 LDL-RECEPTOR CLASS A.
 FT TRANSMEM 271 287 POTENTIAL.
 FT TRANSMEM 292 311 POTENTIAL.
 FT DOMAIN 451 487 EGF-LIKE.
 FT REPEAT 497 545 TYPE-1 TSP 2.
 FT DOMAIN 570 689
 FT REPEAT 570 627
 FT REPEAT 630 689 SUSHI 1.
 FT DOMAIN 695 770 SUSHI 2.
 FT DOMAIN 771 843 COMPLEMENT CONTROL FACTOR I MODULE.
 FT DISULFID 85 96 COMPLEMENT CONTROL FACTOR I MODULE.
 FT DISULFID 91 109 BY SIMILARITY.
 FT DISULFID 103 119 BY SIMILARITY.
 FT DISULFID 337 353 BY SIMILARITY.
 FT DISULFID 571 613 BY SIMILARITY.
 FT DISULFID 599 626 BY SIMILARITY.
 FT DISULFID 631 673 BY SIMILARITY.
 FT DISULFID 659 688 BY SIMILARITY.
 FT CARBOHYD 202 202 POTENTIAL.
 FT CARBOHYD 754 754 POTENTIAL.
 SQ SEQUENCE 843 AA; 93514 MW; 0A16E9B4 CRC32;
 Query Match 96.8%; Score 30; DB 1; Length 843;
 Best Local Similarity 80.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSXWS 5
 DB 506 MSXWS 510
 RESULT 5
 CO8A_HUMAN STANDARD; PRT; 584 AA.
 AC P07357; Q13668;
 DT 01-APR-1988 (REL. 07, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE COMPLEMENT COMPONENT C8 ALPHA CHAIN PRECURSOR.
 GN C8A.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE-LIVER.
 RX MEDLINE; 88000560.
 RA RAO A.G., HOWARD O.M.Z., NG S.C., WHITEHEAD A.S., COLTEN H.R.,
 RA SODETZ J.M.;
 RT "Complementary DNA and derived amino acid sequence of the alpha
 subunit of human complement protein C8: evidence for the existence of
 a separate alpha subunit messenger RNA."
 RL BIOCHEMISTRY 26:3536-3564(1987).
 RN [2]
 RP REVISIONS TO 467-479.
 RA SODETZ J.M.;
 RL SUBMITTED (FEB-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BLOOD;
 RX MEDLINE; 95278905.
 RA MICHELOTTI G.A., SNIDER J.V., SODETZ J.M.;
 RT "Genomic organization of human complement protein C8 alpha and
 further examination of its linkage to C8 beta."
 RL HUM. GENET. 95:513-518(1995).
 CC -1- FUNCTION: C8 IS A CONSTITUENT OF THE MEMBRANE ATTACK COMPLEX.
 CC

RESULT

QY 1 WSXWS 5
11111.

DB 549 WSSWS 553

RESULT 7

CRBB_BOVIN STANDARD; PRT; 196 AA.
 AC P26444;
 DT 01-AUG-1992 (REL. 23, CREATED)
 DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE BETA CRYSTALLIN A2.
 GN CRBA2.
 OS BOS TAURUS (BOVINE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVIDAE; BOVINAE; BOS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LENS;
 RX MEDLINE: 91340151.
 RA VAN RENS G.L., DRIESSEN H.P.C., NALINI V., SLINGSBY C., DE JONG W.W.,
 RA BLOEMENDAL H.;
 RT "Isolation and characterization of cDNAs encoding beta A2- and beta
 A4-crystallins: heterologous interactions in the predicted beta
 A4-beta B2 heterodimer".
 RL GENE 102:179-188(1991).
 CC [2]
 CC SEQUENCE OF 133-196.
 CC TISSUE-LENS CORTEX;
 RX MEDLINE: 84132067.
 RA BERBERS G.A.M., HOEKMAN W.A., BLOEMENDAL H., DE JONG W.W.,
 RA KLEINSCHMIDT T., BRAUNITZER G.;
 RT "Homology between the primary structures of the major bovine beta-
 crystallin chains.".
 RL EUR. J. BIOCHEM. 139:467-479(1984).
 CC [1]
 CC -1- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS
 OF THE VERTEBRATE EYE LENS.
 CC -1- SUBUNIT: HOMO/ETERODIMER, OR COMPLEXES OF HIGHER ORDER. THE
 STRUCTURE OF BETA-CRYSTALLIN OLIGOMERS SEEMS TO BE STABILIZED
 THROUGH INTERACTIONS BETWEEN THE N-TERMINAL ARMS (BY SIMILARITY).
 CC -1- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR
 VERY SIMILAR GREEK KEY MOTIFS.
 CC -1- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: M60329; G162727; .
 CC PIR: D27898; D27898.
 CC PIR: JH0602; JH0602.
 CC PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; 3.
 CC PFM: PF00030; CRYSTALL; 2.
 CC HSSP: P02822; 1B1B.
 CC EYE LENS PROTEIN; DUPLICATION.
 GN INIT_MET 0
 GN BY SIMILARITY.
 FT DOMAIN 1 10 N-TERMINAL ARM.
 FT DOMAIN 11 51 MOTIF 1.
 FT DOMAIN 52 99 MOTIF 2.
 FT DOMAIN 100 104 CONNECTING PEPTIDE.
 FT DOMAIN 105 146 MOTIF 3.
 FT DOMAIN 147 196 MOTIF 4.
 FT CONFLICT 182 184 OAH -> HAQ (IN REF. 2).
 FT SEQUENCE 196 AA; 22099 MW; 9867FEC9 CRC32;

QY 1 WSXWS 5
 1111
 DB 77 WSXWS 81

RESULT 8

CTAL_BACCI STANDARD; PRT; 972 AA.
 AC P94286;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE CYCLOISOMALTOLIGOSACCHARIDE GLUCANOTRANSFERASE PRECURSOR (EC 2.4.1.-)
 DE (CI)TASE)
 OS BACILLUS CIRCULANS.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 OC BACILLUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-T-3040.
 RX OGURA T., KUROKAWA T., TOBE K., KOBAYASHI M.;
 RA SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDP DATA BANKS.
 CC -1- FUNCTION: PRODUCES CYCLOISOMALTOLIGOSACCHARIDE FROM DEXTRAN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 66 OF GLYCOSYL HYDROLASES.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: D61382; G1780754; .
 CC DR TRANSFERASE; GLYCOSYLTRANSFERASE; SIGNAL.
 FT SIGNAL 1 38
 FT CHAIN 39 972 CYCLOISOMALTOLIGOSACCHARIDE
 FT GLUCANOTRANSFERASE.
 FT SEQUENCE 972 AA; 107431 MW; E0E01311 CRC32;

Query Match 96.8%; Score 30; DB 1; Length 972;
 Best Local Similarity 80.0%; Pred. No. 3.3e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 WSXWS 5
 1111
 DB 832 WSXWS 836

RESULT 9

EPOR_HUMAN STANDARD; PRT; 508 AA.
 AC P19235;
 DT 01-NOV-1990 (REL. 16, CREATED)
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE ERYTHROPOIETIN RECEPTOR PRECURSOR (EPO-R).
 GN EPOR.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CARNIVORINIA; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 91372359.
 RA EHRENNAN K., ST JOHN T.;
 RT "The erythropoietin receptor gene: cloning and identification of
 multiple transcripts in an erythroid cell line OCIM1.".
 RL EXP. HEMATOL. 19:973-977(1991).
 CC [2]
 CC SEQUENCE FROM N.A.
 RX MEDLINE: 90304340.
 RA JONES S.S., D'ANDREA A., HAINES L.L., WONG G.G.;

RT "Human erythropoietin receptor: cloning, expression, and biologic
RT characterization.";
RL BLOOD 76:31-35(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-PLACENTA;
RX MODOCHI C.T., BAE K.S., CHIN K., WADA Y., SCHECHTER A.N.,
RA HARKINS W.D.;
RT "Cloning of the human erythropoietin receptor gene.";
RL BLOOD 78:2548-2556(1991).
RN [4]
RP SEQUENCE OF 1-96 FROM N.A.
RC TISSUE-PLACENTA;
RX MEDLINE; 9239734.
RA MODOCHI L., TOURNAMILLE C., HATTAB C., BOFFA G., CARTRON J.P.,
RT "Cloning of the gene encoding the human erythropoietin receptor.";
RL BLOOD 78:2557-2563(1991).
RN [5]
RP SEQUENCE OF 1-17 FROM N.A.
RX MEDLINE; 92147143.
RA PENNY L.A., FORGET B.G.;
RT "Genomic organization of the human erythropoietin receptor gene.";
RL GENOMICS 11:974-980(1991).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 34-244.
RX MEDLINE; 96291992.
RA LYNNH O., STURA E.A., JOHNSON D.L., MIDDLETON S.A., MOLICAHY L.S.,
RT "Functional mimicry of a protein hormone by a peptide agonist: the
RT EPO receptor complex at 2.8 A.";
RL SCIENCE 273:464-471(1996).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 34-244.
RX MEDLINE; 99023198.
RA LYNNH O., JOHNSON D.L., STURA E.A., FARRELL F.X., BARBONE F.P.,
RT YOU Y., LIU K.D., GOLDSMITH M.A., HE W., KRAUSE C.D., PESTRA S.,
RA JOLLIFFE L.K., WILSON I.A.;
RT "An antagonist peptide-EPO receptor complex suggests that receptor
RT dimerization is not sufficient for activation.";
RL NAT. STRUCT. BIOL. 5:993-1004(1998).
CC -1- FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY A ROLE IN THE
CC MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST PROLIFERATION
CC AND DIFFERENTIATION.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC
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CC
CC EMBL; M34986; G182301;
CC EMBL; M60453; G182245;
CC EMBL; S43532; G253497;
CC EMBL; M76595; G553281;
CC EMBL; M77244; G182134;
CC PIR; A43799; A43799.
CC PIR; A49824; A49824.
CC PIR; A53958; A53958.
CC PDB; 1EBP; 29-JUL-97.
CC PDB; 1EBA; 18-NOV-98.
CC DR MIM; 133171;
CC DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
CC DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
CC DR PFAM; PF00041; fn3; 1.
CC KM RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; 3D-STRUCTURE.
CC SIGNAL 1 24

FT CHAIN 25 508 ERYTHROPOIETIN RECEPTOR.
FT DOMAIN 25 250 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 251 273 POTENTIAL.
FT DOMAIN 274 508 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 148 213 FIBRONECTIN TYPE-III.
FT DISULFID 52 62
FT DISULFID 91 107
FT CARBOHYD 76 76 POTENTIAL.
SQ SEQUENCE 508 AA; 55065 MW; A567A994 CRC32;

Query Match 96.8%; Score 30; DB 1; Length 508;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
DB 233 WSXWS 237

RESULT 10
ID EPO_MOUSE STANDARD; PRT; 507 AA.
AC P14753; Q63852;
DT 01-APR-1990 (REL. 14, CREATED)
DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE ERYTHROPOIETIN RECEPTOR PRECURSOR (EPO-R).
OS EPO.
GN MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89195238.
RA D'ANDREA A.D., LODISH H.F., WONG G.G.;
RT "Expression cloning of the murine erythropoietin receptor.";
RL CELL 57:277-285(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-LIVER;
RX MEDLINE; 9180149.
RA KURAMOCCHI S., IKAWA Y., TOOKORO K.;
RT "Characterization of murine erythropoietin receptor genes.";
RL J. MOL. BIOL. 216:567-575(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92017832.
RA HINO M., TOJO A., MISAWA Y., MORII H., TAKAYU F., SHIBUYA M.;
RT "Unregulated expression of the erythropoietin receptor gene caused by
RT insertion of spleen focus-forming virus long terminal repeat in a
RT murine erythroleukemia cell line.";
RL MOL. CELL. BIOL. 11:5527-5533(1991).
RN [4]
RP SEQUENCE OF 1-27 FROM N.A.
RX MEDLINE; 90287158.
RA YOUSOUFIAN H., ZON L.I., ORKIN S.H., D'ANDREA A.D., LODISH H.F.;
RT "Structure and transcription of the mouse erythropoietin receptor
RT gene.";
RL MOL. CELL. BIOL. 10:3675-3682(1990).
RN [5]
RP SEQUENCE OF 1-24 FROM N.A.
RX MEDLINE; 91201346.
RA LACOMBE C., CHRETIEN S., LEMARCHANDEL V., MAYEUX P., ROMEO P.H.,
RA GISELBRECHT S., CARTRON J.P.;
RT "Spleen focus-forming virus long terminal repeat insertional
RT activation of the murine erythropoietin receptor gene in the T3C1-2
RT friend leukemia cell line.";
RL J. BIOL. CHEM. 266:6952-6956(1991).
RN [6]
RP MUTAGENESIS.
RX MEDLINE; 93180826.
RA MURA O., CLEVELAND J.L., IHLE J.N.;

RT Inactivation of erythropoietin receptor function by point mutations
 RT in a region having homology with other cytokine receptors."
 RL MOL. CELL. BIOL. 13:1788-1795(1993).
 CC -1- FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY A ROLE IN THE
 CC MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST PROLIFERATION
 CC AND DIFFERENTIATION.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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 CC -----
 CC EMBL: J04843; G309219; -
 CC EMBL: X53081; G50862; -
 CC EMBL: M38133; G193093; -
 CC EMBL: M62360; G193200; -
 CC EMBL: S59388; E90908; -
 CC PIR: A32385; A32385.
 CC PIR: A41686; A41686.
 CC PIR: S13249; S13249.
 CC PIR: S14081; S14081.
 CC MGI: MGI:55408; EPOR.
 CC PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
 CC PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 CC PFM: PFM:PF00041; fn3; 1.
 CC HSSP: P19235; 1EBP.
 CC RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
 KW SIGNAL 1 24
 FT CHAIN 1 25
 FT DOMAIN 25 507 ERYTHROPOIETIN RECEPTOR.
 FT TRANSMEM 250 272 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 273 507 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 147 212 FIBRONECTIN TYPE-III.
 FT DISULFID 52 62 BY SIMILARITY.
 FT DISULFID 90 106 BY SIMILARITY.
 FT CARBOHYD 75 75 POTENTIAL.
 FT CONFLICT 291 291 E -> D (IN E90908).
 FT SEQUENCE 507 AA; 55194 MW; C90C07B8 CRC32;
 SO
 QY 1 MSXMS 5
 DB 232 WSAMS 236
 Query Match 96.8%; Score 30; DB 1; Length 507;
 Best Local Similarity 80.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 RESULT 11
 EPOR_RAT STANDARD; PRT; 507 AA.
 AC Q07303;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE ERYTHROPOIETIN RECEPTOR PRECURSOR (EPO-R).
 GN EPOR.
 OS RATTUS NORVEGICUS (RAT).
 CC EUKARYOTA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; RATTUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 9326574.
 RX MASUDA S., NAGAO M., TAKAHATA K., KONISHI Y., GALLYAS F.,
 RA TABIRA T., SASAKI R.,
 "Functional erythropoietin receptor of the cells with neural

RT characteristics. Comparison with receptor properties of erythroid
 RT cells."
 RL J. BIOL. CHEM. 268:11208-11216(1993).
 CC -1- FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY A ROLE IN THE
 CC MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST PROLIFERATION
 CC AND DIFFERENTIATION.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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 CC -----
 CC EMBL: D13566; G286210; -
 CC PIR: A46713; A46713.
 CC PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
 CC PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 CC PFM: PFM:PF00041; fn3; 1.
 CC HSSP: P19235; 1EBP.
 CC RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
 KW SIGNAL 1 24
 FT CHAIN 1 25
 FT DOMAIN 25 507 ERYTHROPOIETIN RECEPTOR.
 FT TRANSMEM 250 272 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 273 507 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 147 212 FIBRONECTIN TYPE-III.
 FT DISULFID 52 62 BY SIMILARITY.
 FT DISULFID 90 106 BY SIMILARITY.
 FT CARBOHYD 75 75 POTENTIAL.
 FT SEQUENCE 507 AA; 55499 MW; 3C20ECC3 CRC32;
 SO
 QY 1 MSXMS 5
 DB 232 WSAMS 236
 Query Match 96.8%; Score 30; DB 1; Length 507;
 Best Local Similarity 80.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 RESULT 12
 ERRL_YEAST STANDARD; PRT; 437 AA.
 AC P42222;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE ENOLASE RELATED PROTEIN 1 (EC 4.2.1.11).
 GN ERRL OR YMR33W OR YMR924.15.
 OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 CC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOCETES; SACCCHAROMYCETALES;
 CC SACCCHAROMYCETACEAE; SACCCHAROMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-S288C / AB972;
 RX CHORCHER C.M., LOUIS E.J., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
 RL SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE OF 120-437 FROM N.A.
 RX STRAIN-S288C / TP1;
 RX MEDLINE; 95304851.
 RX PRYDE F.E., HUCKLE T.C., LOUIS E.J.;
 "Sequence analysis of the right end of chromosome XV in Saccharomyces
 RT cerevisiae: an insight into the structural and functional
 RT significance of sub-telomeric repeat sequences."
 RL YEAST 11:371-382(1995).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE - PHOSPHOENOLPYRUVATE

+ H(2)O.
 - SIMILARITY: BELONGS TO THE ENOLASE FAMILY.

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 DR EMBL: 254141; G1072413;
 DR EMBL: 023412; G775203;
 DR SGD: L0002735; ERR1.
 DR PROSITE: PS00164; ENOLASE; 1.
 DR PFM: PF00113; enolase; 1.
 DR HSP: P00924; INEL.
 DR LYSASE, GLYCOLYSIS; MAGNESIUM.
 KM ACT SITE 160 160 BY SIMILARITY.
 FT METAL 247 247 MAGNESIUM (BY SIMILARITY).
 FT METAL 296 296 MAGNESIUM (BY SIMILARITY).
 FT METAL 321 321 MAGNESIUM (BY SIMILARITY).
 SO SEQUENCE 437 AA; 47312 MW; FEE64B47 CRC32;

 Query Match 96.8%; Score 30; DB 1; Length 437;
 Best Local Similarity 80.0%; Pred. No. 1.5e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 OY 1 WSXWS 5
 DB 304 WSXWS 308

 RESULT 13
 GPCR_HUMAN STANDARD; PRT; 400 AA.
 ID P15509; Q14429; Q14430;
 AC 01-APR-1990 (REL. 14, CREATED)
 DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DE GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR RECEPTOR ALPHA
 DE CHAIN PRECURSOR (GM-CSF-R-ALPHA) (CD116) (CD116 ANTIGEN).
 GN CSF2RA OR CSF2R.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A. (GM-CSF-R-ALPHA-1).
 RC TISSUE-PLACENTA;
 RX MEDLINE: 90059966.
 RA GEARING D.P., KING J.A., GOUGH N.M., NICOLA N.A.;
 RT "Expression cloning of a receptor for human granulocyte-macrophage
 RT colony-stimulating factor.";
 RL EMBO J. 8:3667-3676(1989).
 RN [2]
 RP SEQUENCE FROM N.A. (GM-CSF-R-ALPHA-2 AND GM-CSF-R-ALPHA-3).
 RC TISSUE-BLOOD.
 RX MEDLINE: 94368898.
 RA HU X., EMMANUEL P.D., ZUCKERMAN K.S.;
 RT "Cloning and sequencing of the cDNAs encoding two alternative
 RT splicing-derived variants of the alpha subunit of the
 RT granulocyte-macrophage colony-stimulating factor receptor.";
 RL BIOCHIM. BIOPHYS. ACTA 1223:306-308(1994).
 RN [3]
 RP SEQUENCE OF 1-385 FROM N.A.
 RX MEDLINE: 94193800.
 RA NAKAGAWA Y., KOSUGI H., MIYAJIMA A., ARAI K.I., YOKOTA T.;
 RT "Structure of the gene encoding the alpha subunit of the human
 RT granulocyte-macrophage colony stimulating factor receptor.
 RT Implications for the evolution of the cytokine receptor
 RT superfamily.";
 RL J. BIOL. CHEM. 269:10905-10912(1994).

CC -1- FUNCTION: RECEPTOR FOR GRANULOCYTE-MACROPHAGE COLONY-STIMULATING
 CC FACTOR.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
 CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. GM-CSF-R-ALPHA-2
 CC IS PROBABLY SOLUBLE.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS, GM-CSF-R-ALPHA-1 (SHOWN
 CC HERE) TO GM-CSF-R-ALPHA-3, ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

 DR EMBL: X17648; G32089;
 DR EMBL: D26628; G522102;
 DR EMBL: D26618; G522102; JOINED.
 DR EMBL: D26619; G522102; JOINED.
 DR EMBL: D26620; G522102; JOINED.
 DR EMBL: D26621; G522102; JOINED.
 DR EMBL: D26622; G522102; JOINED.
 DR EMBL: D26623; G522102; JOINED.
 DR EMBL: D26624; G522102; JOINED.
 DR EMBL: D26625; G522102; JOINED.
 DR EMBL: D26626; G522102; JOINED.
 DR EMBL: D26627; G522102; JOINED.
 DR EMBL: D26628; G522102; JOINED.
 DR EMBL: L29348; G463106;
 DR EMBL: L29349; G463107;
 DR PIR: S06945; S06945.
 DR MIN: 306250;
 DR MIM: 425000;
 DR PROSITE: PS00241; RECEPTOR CYTOKINES 1; 1.
 DR PROSITE: PS00340; RECEPTOR CYTOKINES 2; 1.
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; ALTERNATIVE SPLICING.
 FT SIGNAL 1 22
 FT CHAIN 23 400
 FT DOMAIN 23 320
 FT TRANSSEM 321 346
 FT DOMAIN 347 400
 FT DISULFID 126 136
 FT DISULFID 165 178
 FT CARBOHYD 46 46
 FT CARBOHYD 54 54
 FT CARBOHYD 99 99
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 FT CARBOHYD 195 195
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 FT CARBOHYD 229 229
 FT CARBOHYD 272 272
 FT CARBOHYD 305 305
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 FT VASPLIC 271 286
 FT VASPLIC 287 400
 FT VASPLIC 316 400
 FT VASPLIC 400 400

 SO SEQUENCE 400 AA; 46206 MW; F5C2EF6D.CRC32;

 Query Match 96.8%; Score 30; DB 1; Length 400;
 Best Local Similarity 80.0%; Pred. No. 1.4e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 OY 1 WSXWS 5

1111

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RESULT 15
ID      LYSB_DROME      STANDARD      PRT:      140 AA.
AC      008694; P37158;
DT      01-OCT-1994 (REL. 30, CREATED)
DT      01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT      01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE      LYSOZYME B/C PRECURSOR (EC 3.2.1.17) (1,4-BETA-N-ACETYLMURAMIDASE).
GN      LYSB AND LYSCL.
OS      DROSOPHILA MELANOGASTER (FRUIT FLY).
OC      EDUARDO; METACOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
OC      PTERYOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYROIDEA;
RN      DROSOPHILIDAE; DROSOPHILA.
[1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-CANTON-S;
RX      MEDLINE; 94211204.
RA      DAFRE S., KILSTEN P., SAMAKOVLIS C., HULTMARK D.;
RT      "The lysozyme locus in Drosophila melanogaster: an expanded gene
RT      family adapted for expression in the digestive tract.";
RL      MOL. GEN. GENET. 242:152-162(1994).
CC      -1- FUNCTION: UNLIKELY TO PLAY AN ACTIVE ROLE IN THE HUMORAL IMMUNE
CC      DEFENSE. MAY HAVE A FUNCTION IN THE DIGESTION OF BACTERIA IN THE
CC      FOOD.
CC      -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES BETWEEN
CC      N-ACETYL-D-GLUCOSAMINE AND N-ACETYLMURAMIC ACID IN PEPTIDOGLYCAN
CC      HETEROPOLYMERS OF THE PROKARYOTES CELL WALLS.
CC      -1- TISSUE SPECIFICITY: FOUND IN THE MIDGUT.
CC      -1- DEVELOPMENTAL STAGE: MAXIMAL EXPRESSION IS FOUND DURING THE THIRD
CC      LARVAL INSTAR. IT DROPS TO BECOME UNDETECTABLE IN THE LATE PUPAL
CC      STAGE. THE EXPRESSION IN ADULTS IS SIMILAR TO THAT OF FIRST AND
CC      SECOND LARVAL INSTARS.
CC      -1- SIMILARITY: BELONGS TO FAMILY 22 OF GLYCOSYL HYDROLASES.
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CC      THE SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.1sb-sib.ch/announce/).
CC      or send an email to license@1sb-sib.ch).
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DR      EMBL; Z22322; G289002; -
DR      EMBL; Z22226; G296039; -
DR      PIR; S32620; S32620.
DR      PIR; S32643; S32643.
DR      FLYBASE; FBgn00004425; LYSB.
DR      FLYBASE; FBgn00004426; LYSB.
DR      PROSITE; P500128; LACTALBUMIN_LYSOZYME; 1.
DR      PRAM; PF00062; Lys; 1.
HSP; P11941; ILIC.
KW      HYDROLASE; GLYCOSIDASE; BACTERIOLYTIC ENZYME; SIGNAL,
KW      MULTIGENE FAMILY.
LN      CHAIN      1      18      BY SIMILARITY.
LN      FT      19      140      LYSOZYME B.
LN      FT      24      139      BY SIMILARITY.
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LN      FT      158
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Query Match      96.88;  Score 30;  DB 1;  Length 140;
Best Local Similarity 80.08;  Pred. No. 53;
Matches      4;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0

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Fri Sep 17 14:52:37 1999

us-09-037-657-1.rsp

Page 10

QY 1 WSXNS 5
11 11
Db 120 WSXNS 124

Search completed: September 17, 1999, 03:10:11
Job time: 291 sec

09/11/97 doc to back

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 17, 1999, 03:08:10 ; Search time 64.1 Seconds

(without alignments)
152.611 Million cell updates/sec

Title: US-09-037-657-13

Sequence: 1 MPAGRGPVAVQASARRPPRL.....WRAMKSHKTRNOVLPAKL 413

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database: A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2251	98.9%	413	1	M55011	Novel haemopoietin
2	2226.5	98.9%	425	1	M55012	Novel haemopoietin
3	2222.5	98.9%	425	1	M55012	Nucleotide sequence
4	2197.5	97.6	425	1	M70862	Rat zcytoirs protei
5	2098	93.2	425	1	M70861	Allelic variant of
6	2032	92.9	422	1	M70860	Human zcytoirs prot
7	2036	90.4	408	1	M53805	Amino acid sequenc
8	2006.5	89.1	385	1	M70841	Human zcytoirs vari
9	1982	88.0	392	1	M70840	Human zcytoirs vari
10	1970.5	87.5	388	1	M70839	Human zcytoirs vari
11	1967	87.4	389	1	M70850	Human zcytoirs vari
12	1966	87.3	389	1	M70844	Human zcytoirs vari
13	1965	87.3	389	1	M70851	Human zcytoirs vari
14	1964	87.3	389	1	M70851	Human zcytoirs vari
15	1963	87.2	389	1	M70846	Human zcytoirs vari
16	1963	87.2	389	1	M70846	Human zcytoirs vari
17	1963	87.2	389	1	M70849	Human zcytoirs vari
18	1962	87.2	389	1	M70848	Human zcytoirs vari
19	1961	87.1	389	1	M70853	Human zcytoirs vari
20	1954.5	86.8	385	1	M70842	Human zcytoirs vari
21	1772	78.7	350	1	M55015	Human zcytoirs vari
22	1602	77.2	303	1	M55015	Amino acid sequenc
23	1598	71.0	303	1	M70843	Human zcytoirs vari
24	1505	66.9	278	1	M55014	Human zcytoirs vari
25	696	30.9	185	1	M55016	Protein sequence o
26	577	25.6	155	1	M55016	Amino acid sequenc
27	331	14.7	622	1	R10793	Novel haemopoietin
28	331	14.7	622	1	R10793	Human prolactin re
29	330.5	14.7	211	1	R24273	Human gp130-delta-
30	329	14.6	918	1	R10545	Truncated human pr
31	329	14.6	918	1	R46233	Recombinant human
32	329	14.6	658	1	R45576	Human soluble glyce
33	329	14.6	918	1	R75368	Human gp130 splice
34	329	14.6	918	1	R85911	Human gp130 protei
35	329	14.6	951	1	M70798	gp130 N-terminal f
36	329	14.6	859	1	M70796	Human gp130-C-gamm
37	327.5	14.5	329	1	M17859	Human gp130-FC-His
38	324.5	14.4	211	1	R22228	Rheumatoid arthrit
39	320.5	14.2	917	1	R26334	Truncated human pr
40	316	14.0	917	1	R26334	gp130. New mouse G
41	261.5	11.6	708	1	R37804	Human gp130 N-term
42	261.5	11.6	606	1	R31120	Tilapia prolactin
43	254.5	11.3	783	1	R11741	Granulocyte colony

ALIGNMENTS

44 254.5 11.3 801 1 R11742 Clone 25-1 encoded
45 254.5 11.3 836 1 R14255 Human GCSF recepto

RESULT 1

ID W55011 standard; Protein; 413 AA.
AC M55011;
DE 29-SEP-1998 (first entry)
DT Novel haemopoietin receptor NR6.1 protein.
KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
KW cell survival; therapeutic; neuronal proliferation; drug screening;
KW Mouse.
OS Mus sp.
PN M09811225-A2.
PD 19-MAR-1998.
PE 11-SEP-1997; G02479.
PR 11-SEP-1996; AD-002246.
PA (AMRA-7) AMRAD OPERATIONS PTY LTD.
PA (DZIR/) DZIRGLMSKA H E.
PI Alexander W, Fedri L, Farley A, Hilton DJ, Kikuchi Y,
PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willison T,
PI Zhang J;
DR WPI; 98-260970/23.
DR N-PSDB; V27140.
PT New isolated haemopoietin receptor - used for developing products
PT for modulating proliferation, differentiation and survival of cells,
PT e.g. neuronal cells
PS Claim 14; Page 77-81; 182pp; English.
CC The haemopoietin receptor (HR) NR6.1 is a form of the novel HR NR6.
CC Interaction between the novel HR and a ligand facilitates proliferation,
CC differentiation and survival of a wide variety of cells. The HR and it's
CC derivatives can be used for modulating the activity of the receptors e.g.
CC to regulate development, maintenance or regeneration in an array of
CC different cells and tissues in vitro and in vivo. They can be present in
CC therapeutics used for modulating neuronal proliferation, differentiation
CC and survival. The products can also be used for detection and diagnosis,
CC e.g. for cancers or predisposition to cancers, or for drug screening.
SQ Sequence 413 AA;

Query Match 100.0%; Score 2251; DB 1; Length 413;
Best local similarity 100.0%; Pred. No. 5.4e-186;
Matches 413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAGRGPVAVQASARRPPRLSSLSMSPLLCYLGVPRGSGAHAVSPDPDLLIGSSIQ 60
DB 1 MPAGRGPVAVQASARRPPRLSSLSMSPLLCYLGVPRGSGAHAVSPDPDLLIGSSIQ 60
QY 61 AFGSHGTPGATAEGLYTLNGRLPSELRLNTSTLALANLNGSROQGNLYCH 120
DB 61 AFGSHGTPGATAEGLYTLNGRLPSELRLNTSTLALANLNGSROQGNLYCH 120
QY 121 AFGSHGTPGATAEGLYTLNGRLPSELRLNTSTLALANLNGSROQGNLYCH 120
DB 121 AFGSHGTPGATAEGLYTLNGRLPSELRLNTSTLALANLNGSROQGNLYCH 120
QY 122 AFGSHGTPGATAEGLYTLNGRLPSELRLNTSTLALANLNGSROQGNLYCH 120
DB 122 AFGSHGTPGATAEGLYTLNGRLPSELRLNTSTLALANLNGSROQGNLYCH 120
QY 181 YGQDNTCEHYTGVPHSCHIRPDALFFPYEIVEATNRIGSARSDVLTLDVDTDP 240
DB 181 YGQDNTCEHYTGVPHSCHIRPDALFFPYEIVEATNRIGSARSDVLTLDVDTDP 240
QY 241 PPDVAVSRVGGLEDOLSVRWVSPALKDFLFOAKYQIRVEDSDVMKVVYDVSNQISCR 300
DB 241 PPDVAVSRVGGLEDOLSVRWVSPALKDFLFOAKYQIRVEDSDVMKVVYDVSNQISCR 300
QY 301 IAGLPGVTVFYOVACNPGIYGSKKAIVSMHPTAASIPRSPRPPGGGVCPEPRGGE 360
DB 301 IAGLPGVTVFYOVACNPGIYGSKKAIVSMHPTAASIPRSPRPPGGGVCPEPRGGE 360
QY 361 PSSGFVRRELKQFLGMLKKHAYCSNLSPRLYDWRANMOKSHKTRNOVLPAKL 413

Db 361 PSSGPVRRRLKQFLGLKKAHAYCSNLSFRLYDQWRAMQSKRTNRQVLPATL 413

RESULT 2
ID W55012 standard; Protein; 425 AA.
AC W55012; (first entry)
DE 29-SEP-1998 (first entry)
DE Novel haemopoietin receptor NR6.2 protein.
KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
KW cell survival; therapeutic; neuronal proliferation; drug screening;
KW Mouse.
OS Mus sp.
PN W09611225-A2.
PD 19-MAR-1998.
PF 11-SEP-1997; G02479.
PR 11-SEP-1996; AU-002246.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PA (DZIE/) DZIEGEMSKA H E.
PI Alexander W, Fabry U, Farley A, Hilton DJ, Kikuchi Y,
PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willison T,
PI Zhang J.
DR WPI: 98-260970/23.
DR N-PSDB: V27141.
PT New isolated haemopoietin receptor - used for developing products
PT for modulating proliferation, differentiation and survival of cells,
PT e.g. neuronal cells.
PS Claim 84-87; 182pp; English.
CC The haemopoietin receptor (HR) NR6.2 is a form of the novel HR NR6.
CC Interaction between the novel HR and a ligand facilitates proliferation,
CC differentiation and survival of a wide variety of cells. The HR and its
CC derivatives can be used for modulating the activity of the receptors e.g.
CC to regulate development, maintenance or regeneration in an array of
CC different cells and tissues in vitro and in vivo. They can be present in
CC therapeutics used for modulating neuronal proliferation, differentiation
CC and survival. The products can also be used for detection and diagnosis,
CC e.g. for cancers or predisposition to cancers, or for drug screening.
SQ Sequence 425 AA.

Query Match 98.9%; Score 2226.5; DB 1; Length 425;
Best Local Similarity 98.8%; Pred. No. 7.2e-184;
Matches 409; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

QY 1 MPAGRPVPAQASARRPPRLSSLSWSPLLLCVGVPRGSGGATAVISPDPTLLIGSSIQ 60
DB 1 MPAGRPVPAQASARRPPRLSSLSWSPLLLCVGVPRGSGGATAVISPDPTLLIGSSIQ 60
QY 61 ATCSIHGDTPGATAGLWTNLGRRLPSELRLNTSTLALANLNGSGDNLVCH 120
DB 61 ATCSIHGDTPGATAGLWTNLGRRLPSELRLNTSTLALANLNGSGDNLVCH 120
QY 121 ARDGSILAGSCLYVGLPEKPPENISCSWRNMKDLTCRMTPGAHGETFLHTNYSKYKLMW 180
DB 121 ARDGSILAGSCLYVGLPEKPPENISCSWRNMKDLTCRMTPGAHGETFLHTNYSKYKLMW 180
QY 121 ARDGSILAGSCLYVGLPEKPPENISCSWRNMKDLTCRMTPGAHGETFLHTNYSKYKLMW 180
DB 121 ARDGSILAGSCLYVGLPEKPPENISCSWRNMKDLTCRMTPGAHGETFLHTNYSKYKLMW 180
QY 181 YGQDNTCEHYHTVGHSHCHIPDLALFTPEYELWEATNRLGARSVDLTLVDLVYTTDP 240
DB 181 YGQDNTCEHYHTVGHSHCHIPDLALFTPEYELWEATNRLGARSVDLTLVDLVYTTDP 240
QY 241 PPDVAVSRVGGLEDOLSTRWVSPALKNFLFOAKQIRRVSDVDMKYVDVSNQTSR 300
DB 241 PPDVAVSRVGGLEDOLSTRWVSPALKNFLFOAKQIRRVSDVDMKYVDVSNQTSR 300
QY 241 PPDVAVSRVGGLEDOLSTRWVSPALKNFLFOAKQIRRVSDVDMKYVDVSNQTSR 300
DB 241 PPDVAVSRVGGLEDOLSTRWVSPALKNFLFOAKQIRRVSDVDMKYVDVSNQTSR 300
QY 301 LAGLPGATVYFVQVRCNPFGIYSKKAIGMSEMSHPTASTRSESRPGGVCPEPRGE 360
DB 301 LAGLPGATVYFVQVRCNPFGIYSKKAIGMSEMSHPTASTRSESRPGGVCPEPRGE 360
QY 361 PSSGPVRRRLKQFLGLKKAHAYCSNLSFRLYDQWRAMQSKRTNRQVLPATL 413
DB 361 PSSGPVRRRLKQFLGLKKAHAYCSNLSFRLYDQWRAMQSKRTNRQVLPATL 413

RESULT 3
ID W59804 standard; Protein; 425 AA.
AC W59804;
DE 26-OCT-1998 (first entry)
DE Nucleotide sequence of the murine U4 protein.
KW Murine; U4 protein; haematopoietin receptor superfamily;
KW cell proliferation; immune response; antibody; cell differentiation;
KW autoimmune disease; cancer; allergy.
OS Mus sp.
PN W09631811-A1.
PD 23-JUL-1998.
PF 15-JAN-1998; U00334.
PR 16-JAN-1997; US-784863.
PA (GENY) GENETICS INST INC.
PI Collins M, Donaldson DD, Neben T, Whitters M;
DR WPI: 98-414109/35.
DR N-PSDB: V41688.

PT New nucleic acid encoding U4 haematopoietin receptor superfamily
PT chain - potentially useful, e.g. for modulating cell proliferation
PT or immune response, for treating cancer and autoimmune disease
PS Claim 9; Pages 26-27; 38pp; English.
CC This is the amino acid sequence of the murine U4 protein from the
CC haematopoietin receptor superfamily, used in the method of the
CC invention for the modulation of cell proliferation, or the immune
CC response. Transformed mammalian cells are used to produce recombinant
CC U4 protein. The U4 protein is used to screen for specific binding
CC agents, raise antibodies. It is also used as reagents for assays and
CC as tissue markers for isolation of cognate ligands and receptors, and
CC in pharmaceutical compositions which may modulate cell proliferation,
CC cell differentiation, and the immune system (e.g. for treating immune
CC deficiency, inherited or the result of infection, autoimmune diseases,
CC cancer, and allergy).
SQ Sequence 425 AA;

Query Match 98.7%; Score 2222.5; DB 1; Length 425;
Best Local Similarity 98.6%; Pred. No. 1.6e-183;
Matches 408; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 1 MPAGRPVPAQASARRPPRLSSLSWSPLLLCVGVPRGSGGATAVISPDPTLLIGSSIQ 60
DB 1 MPAGRPVPAQASARRPPRLSSLSWSPLLLCVGVPRGSGGATAVISPDPTLLIGSSIQ 60
QY 61 ATCSIHGDTPGATAGLWTNLGRRLPSELRLNTSTLALANLNGSGDNLVCH 120
DB 61 ATCSIHGDTPGATAGLWTNLGRRLPSELRLNTSTLALANLNGSGDNLVCH 120
QY 121 ARDGSILAGSCLYVGLPEKPPENISCSWRNMKDLTCRMTPGAHGETFLHTNYSKYKLMW 180
DB 121 ARDGSILAGSCLYVGLPEKPPENISCSWRNMKDLTCRMTPGAHGETFLHTNYSKYKLMW 180
QY 121 ARDGSILAGSCLYVGLPEKPPENISCSWRNMKDLTCRMTPGAHGETFLHTNYSKYKLMW 180
DB 121 ARDGSILAGSCLYVGLPEKPPENISCSWRNMKDLTCRMTPGAHGETFLHTNYSKYKLMW 180
QY 181 YGQDNTCEHYHTVGHSHCHIPDLALFTPEYELWEATNRLGARSVDLTLVDLVYTTDP 240
DB 181 YGQDNTCEHYHTVGHSHCHIPDLALFTPEYELWEATNRLGARSVDLTLVDLVYTTDP 240
QY 241 PPDVAVSRVGGLEDOLSTRWVSPALKNFLFOAKQIRRVSDVDMKYVDVSNQTSR 300
DB 241 PPDVAVSRVGGLEDOLSTRWVSPALKNFLFOAKQIRRVSDVDMKYVDVSNQTSR 300
QY 241 PPDVAVSRVGGLEDOLSTRWVSPALKNFLFOAKQIRRVSDVDMKYVDVSNQTSR 300
DB 241 PPDVAVSRVGGLEDOLSTRWVSPALKNFLFOAKQIRRVSDVDMKYVDVSNQTSR 300
QY 301 LAGLPGATVYFVQVRCNPFGIYSKKAIGMSEMSHPTASTRSESRPGGVCPEPRGE 360
DB 301 LAGLPGATVYFVQVRCNPFGIYSKKAIGMSEMSHPTASTRSESRPGGVCPEPRGE 360
QY 361 PSSGPVRRRLKQFLGLKKAHAYCSNLSFRLYDQWRAMQSKRTNRQVLPATL 413
DB 361 PSSGPVRRRLKQFLGLKKAHAYCSNLSFRLYDQWRAMQSKRTNRQVLPATL 413

AC W70862;
DT 17-MAR-1999 (first entry)
DE Rat Zcyto5 protein.
KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
KW cardiac pathology; heart enlargement; Zcyto5 ligand.
OS Rattus sp.
PN M09849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jernberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
DR N-PSDB; V70896.
PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.,
PT down-regulating Zcyto5 natural ligands or detecting cardiostrophin-1
PT in blood
PS Claim 1; Page 75-76; 55pp; English.
CC The present sequence represents a protein designated Zcyto5, which is
CC a cytokinin-like receptor. Soluble Zcyto5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC thyroid, heart, and skeletal muscle for example to lessen the effect
CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
CC enlargement. Zcyto5 could be used to detect cardiostrophin-1 in the
CC blood, and to discover other possible Zcyto5 ligands. A probe
CC comprising Zcyto5 DNA or RNA can be used to determine the presence
CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify Zcyto5 and
CC therapeutically to modify Zcyto5 ligand effects.
SQ Sequence 425 AA;

Query Match 97.6%; Score 2197.5; DB 1; Length 425;
Best Local Similarity 97.6%; Pred. No. 2.3e-181;

Matches 404; Conservative 3; Mismatches 4; Indels 3; Gaps 1;

QY 1 MPAGRPVPAQASARRPRRLSSLSMPLLCVLYGVRGSGAHAVISPOPTLLIGSLQ 60
DB 1 MPAGRPVPAQASARRPRRLSSLSMPLLCVLYGVRGSGAHAVISPOPTLLIGSLH 60
QY 61 ATCSIHBDTGAATAGLWTLNGLRRLPELSRLINTSTLALANLNGSRQSGDNLYCH 120
DB 61 ATCSIHBDTGAATAGLWTLNGLRRLPELSRLINTSTLALANLNGSRQSGDNLYCH 120
QY 121 ARDGSILAGSCLVGLPPEKPFNISCSNMKDLTCMTGAGGFTLHTNYSLSKYLRLW 180
DB 121 ARDGSILAGSCLVGLPPEKPFNISCSNMKDLTCMTGAGGFTLHTNYSLSKYLRLW 180
QY 181 YGDNNTCEEHTVGPSCCHPKDLALFTPEIWEATNRLGARSVDLYLDVYVTTDP 240
DB 181 YGDNNTCEEHTVGPSCCHPKDLALFTPEIWEATNRLGARSVDLYLDVYVTTDP 240
QY 241 PPVHVSRVGLLEDQSLVRVSPALKDFLFOAKYQIRYVEDSVMKVYDVDSNQTSCR 300
DB 241 PPVHVSRVGLLEDQSLVRVSPALKDFLFOAKYQIRYVEDSVMKVYDVDSNQTSCR 300
QY 301 LAGLKGTIVFYVQVRCNPFGIYSKKAIGWSESHPTAASPSESRPGGVCCEPRGGE 360
DB 301 LAGLKGTIVFYVQVRCNPFGIYSKKAIGWSESHPTAASPSESRPGGVCCEPRGGE 360
QY 361 PSSGPRRELKQFLGWLKHAAYSNTSFLYDQWRAMQSKHTRNO---VLP 411
DB 361 PSSGPRRELKQFLGWLKHAAYSNTSFLYDQWRAMQSKHTRNO---VLP 411

RESULT 5
861
W70861 standard; Protein; 425 AA.

AC W70861;
DT 17-MAR-1999 (first entry)
DE Allelic variant of human Zcyto5.
KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
KW cardiac pathology; heart enlargement; Zcyto5 ligand; allelic variant.
OS Homo sapiens.
PN M09849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jernberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
DR N-PSDB; V70895.
PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.,
PT down-regulating Zcyto5 natural ligands or detecting cardiostrophin-1
PT in blood
PS Claim 1; Page 71-72; 55pp; English.
CC The present sequence represents an allelic variant of protein designated
CC Zcyto5, which is a cytokinin-like receptor. Soluble Zcyto5 may be
CC administered to down-regulate the effects of a growth and/or maintenance
CC factor in thyroid, heart, and skeletal muscle for example to lessen the
CC effect of cardiostrophin-1 on cardiac pathologies, so preventing heart
CC enlargement. Zcyto5 could be used to detect cardiostrophin-1 in the
CC blood, and to discover other possible Zcyto5 ligands. A probe
CC comprising Zcyto5 DNA or RNA can be used to determine the presence
CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify Zcyto5 and
CC therapeutically to modify Zcyto5 ligand effects.
SQ Sequence 425 AA;

Query Match 93.2%; Score 2098; DB 1; Length 425;
Best Local Similarity 91.1%; Pred. No. 8.4e-173;

Matches 391; Conservative 5; Mismatches 13; Indels 20; Gaps 3;

QY 1 MPAGRPVPAQASARRPRRLSSLSMPLLCVLYGVRGSGAHAVISPOPTLLIGSLQ 60
DB 1 MPAGRPVPAQASARRPRRLSSLSMPLLCVLYGVRGSGAHAVISPOPTLLIGSL 56
QY 61 ATCSIHBDTGAATAGLWTLNGLRRLPELSRLINTSTLALANLNGSRQSGDNLYCH 120
DB 57 ATCSYHBDTGAATAGLWTLNGLRRLPELSRYLNASTLALANLNGSRQSGDNLYCH 116
QY 121 ARDGSILAGSCLVGLPPEKPFNISCSNMKDLTCMTGAGGFTLHTNYSLSKYLRLW 180
DB 117 ARDGSILAGSCLVGLPPEKPFNISCSNMKDLTCMTGAGGFTLHTNYSLSKYLRLW 176
QY 181 YGDNNTCEEHTVGPSCCHPKDLALFTPEIWEATNRLGARSVDLYLDVYVTTDP 240
DB 177 YGDNNTCEEHTVGPSCCHPKDLALFTPEIWEATNRLGARSVDLYLDVYVTTDP 236
QY 241 PPVHVSRVGLLEDQSLVRVSPALKDFLFOAKYQIRYVEDSVMKVYDVDSNQTSCR 300
DB 237 PPVHVSRVGLLEDQSLVRVSPALKDFLFOAKYQIRYVEDSVMKVYDVDSNQTSCR 296
QY 301 LAGLKGTIVFYVQVRCNPFGIYSKKAIGWSESHPTAASPSESRPGGVCCEPRGGE 360
DB 297 LAGLKGTIVFYVQVRCNPFGIYSKKAIGWSESHPTAASPSESRPGGVCCEPRGGE 356
QY 361 PSSGPRRELKQFLGWLKHAAYSNTSFLYDQWRAMQSKHTRNO----- 408
DB 357 PSSGPRRELKQFLGWLKHAAYSNTSFLYDQWRAMQSKHTRNO----- 408
QY 408 ---VLP 413
DB 417 RREVLDPKL 425

RESULT 6
W70860 6
ID W70860 standard; Protein; 422 AA.
AC W70860;
DT 17-MAR-1999 (first entry)
DE Human zcyto5; cytokinin-like receptor; down-regulation; growth factor;
KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
KW cardiac pathology; heart enlargement; zcyto5 ligand.
OS Homo sapiens.
PN M09849307-A1.
PD 05-NOV-1998.
PE 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (Zymo) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
DR WPI; 99-034662/03.
DR N-PSDB; V70894.
PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
PT down-regulating zcyto5 natural ligands or detecting cardiotoxin-1
PS Claim 1: page 66-67; 55pp; English.
CC The present sequence represents a protein designated zcyto5, which is
CC a cytokinin-like receptor. Soluble zcyto5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC thyroid, heart, and skeletal muscle for example to lessen the effect
CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
CC enlargement. Zcyto5 could be used to detect cardiotoxin-1 in the
CC blood, and to discover other possible zcyto5 ligands. A probe
CC comprising zcyto5 DNA or RNA can be used to determine the presence
CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify zcyto5 and the
CC therapeutically to modify zcyto5 ligand effects.
SQ Sequence 422 AA;

Query Match 92.9%; Score 2092; DB 1; Length 422;
Best Local Similarity 93.5%; Pred. No. 2.7e-172;
Matches 387; Conservative 8; Mismatches 13; Indels 6; Gaps 3;
OY 1 MPAGRPVPAQASRRPRPRLSSILMSPLLCVGVPRGSGAHTAVISPDPTLLIGSSSQ 60
DB 1 MPAGRPVPAQASRRPRPRLSSILMSPLLCVGVPRGSGAHTAVISPDPTLLIGSSSQ 60
OY 61 ATCSIHGDTFGATFAGELVTLNGRRLLPSLRLNTSTLALANLNGSGDNLVCH 120
DB 58 ATCSIHGDTFGATFAGELVTLNGRRLLPSLRLNTSTLALANLNGSGDNLVCH 117
OY 121 ARDSILAGSCLVGLPPEKPNISCSNMKDLCTCMTPGAHGETFLHTNYSKYLKM 180
DB 118 ARDSILAGSCLVGLPPEKPNISCSNMKDLCTCMTPGAHGETFLHTNYSKYLKM 177
OY 181 YGQDNTCEHYHVGPHSCHIPKDLALFTPELWEATNRLSGARSDVLTLDVDTDP 240
DB 178 YGQDNTCEHYHVGPHSCHIPKDLALFTPELWEATNRLSGARSDVLTLDVDTDP 237
OY 241 PPDVAVSRVGLGLEDOLSTRWVSPALKDFLFOAKQIIRYVEDSDVMKVVDDVNSQSCR 300
DB 238 PPDVAVSRVGLGLEDOLSTRWVSPALKDFLFOAKQIIRYVEDSDVMKVVDDVNSQSCR 297
OY 301 LAGLPGTVYFVQVNCNFGIYGSKKAGIWSHPTAASIPRSRPPGGVCEPRGGE 360
DB 298 LAGLPGTVYFVQVNCNFGIYGSKKAGIWSHPTAASIPRSRPPGGVCEPRGGE 357
OY 361 PSSGVRRELKQFLGMLKKHAYCSNLSFRLYDQNRAMQKSHKTRNO---VLPA 411
DB 358 PSSGVRRELKQFLGMLKKHAYCSNLSFRLYDQNRAMQKSHKTRNO---VLPA 411

RESULT 7
W59805 7
ID W59805 standard; Protein; 408 AA.
AC W59805;
DT 26-OCT-1998 (first entry)
DE Amino acid sequence of the human U4 protein.
KW Human; U4 protein; haematopoietin receptor superfamily;
KW cell proliferation; immune response; antibody; cell differentiation;
KW auto-immune disease; cancer; allergy.
OS Homo sapiens.
PN M09831811-A1.
PD 23-JUL-1998.
PE 15-JAN-1998; U00334.
PR 16-JAN-1997; US-784863.
PA (GENE) GENETICS INST INC.
PI Collins M, Donaldson DD, Neben T, Whiters M;
DR WPI; 98-414109/35.
DR N-PSDB; V41689.
PT New nucleic acid encoding U4 haematopoietin receptor superfamily
PT chain - potentially useful, e.g. for modulating cell proliferation
PT or immune response, for treating cancer and auto-immune disease
PS Claim 9; pages 29-30; 38pp; English.
CC This is the amino acid sequence of the human U4 protein from the
CC haematopoietin receptor superfamily, used in the method of the
CC invention for the modulation of cell proliferation, or the immune
CC response. Transformed mammalian cells are used to produce recombinant
CC U4 protein. The U4 protein is used to screen for specific binding
CC agents, raise antibodies. It is also used as reagents for assays and
CC as tissue markers for isolation of cognate ligands and receptors, and
CC in pharmaceutical compositions which may modulate cell proliferation,
CC cell differentiation, and the immune system (e.g. for treating immune
CC deficiency, inherited or the result of infection, autoimmune diseases,
CC cancer, and allergy).
SQ Sequence 408 AA;

Query Match 90.4%; Score 2036; DB 1; Length 408;
Best Local Similarity 94.0%; Pred. No. 1.7e-167;
Matches 376; Conservative 7; Mismatches 11; Indels 6; Gaps 3;
OY 15 RPPRLSSILMSPLLCVGVPRGSGAHTAVISPDPTLLIGSSSQATCSIHGDTFGATA 74
DB 1 RPP-PLPDL-LLLCVGAAPRAGGATHTAVISPDPTLLIGSSSQATCSIHGDTFGATA 57
OY 75 EGLYTLNGRRLLPSLRLNTSTLALANLNGSGDNLVCHARDGSLIAGSCLV 134
DB 58 EGLYTLNGRRLLPSLRLNTSTLALANLNGSGDNLVCHARDGSLIAGSCLV 117
OY 135 GLPPEKPNISCSNMKDLCTCMTPGAHGETFLHTNYSKYLKMYGQDNTCEHYHVG 194
DB 118 GLPPEKPNISCSNMKDLCTCMTPGAHGETFLHTNYSKYLKMYGQDNTCEHYHVG 177
OY 195 PHSCHIPKDLALFTPELWEATNRLSGARSDVLTLDVDTDPDPPDVHVSRYGLED 254
DB 178 PHSCHIPKDLALFTPELWEATNRLSGARSDVLTLDVDTDPDPPDVHVSRYGLED 237
OY 255 QLSYRWVSPALKDFLFOAKQIIRYVEDSDVMKVVDDVNSQSCRGLKPGTYFVQV 314
DB 238 QLSYRWVSPALKDFLFOAKQIIRYVEDSDVMKVVDDVNSQSCRGLKPGTYFVQV 297
OY 315 RCNPFGIYGSKKAGIWSHPTAASIPRSRPPGGVCEPRGGEPSGVRRELKQFL 374
DB 298 RCNPFGIYGSKKAGIWSHPTAASIPRSRPPGGVCEPRGGEPSGVRRELKQFL 357
OY 375 GMLKKHAYCSNLSFRLYDQNRAMQKSHKTRNO---VLPA 411
DB 358 GMLKKHAYCSNLSFRLYDQNRAMQKSHKTRNO---VLPA 411
RESULT 8
W70841 8
ID W70841 standard; Protein; 365 AA.

AC W70841;
 DT 17-MAR-1999 (first entry)
 DE Human Zcyto5 variant.
 KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 KW cardiac pathology; heart enlargement; Zcyto5 ligand; variant.
 OS Homo sapiens.
 PN W09849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE.
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.
 PT down-regulating Zcyto5 natural ligands or detecting cardiostrophin-1
 PT in blood
 PS Claim 1: Page 83-84; 55pp; English.
 CC The present sequence represents a Zcyto5 variant protein. Zcyto5
 CC is a cytokinin-like receptor. Soluble Zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcyto5 could be used to detect cardiostrophin-1 in the
 CC blood, and to discover other possible Zcyto5 ligands. A probe
 CC comprising Zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcyto5 and the
 CC therapeutically to modify Zcyto5 ligand effects.
 SQ Sequence 385 AA.

Query Match 89.1%; Score 2006.5; DB 1; Length 385;
 Best Local Similarity 98.4%; Pred. No. 5.5e-165;
 Matches 368; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 41 AHTAVISPODPTLLIGSSLOATCSIHGDPGATAEGLYTLNGRRRLPSELRLNTSTA 100
 DB 1 AHTAVISPODPTLLIGSSLOATCSIHGDPGATAEGLYTLNGRRRLPSELRLNTSTA 60
 QY 101 LALANLNGSGROSGDNLVCHARDGSLIAGSCLYVGLPPEKPNISCSNMKDLTCRMP 160
 DB 61 LALANLNGSGROSGDNLVCHARDGSLIAGSCLYVGLPPEKPNISCSNMKDLTCRMP 120
 QY 161 GAHGETFLHTNLSLKYKLMWYGODNTCEHYHVGPHSCHIPDIALFTYEIWEATNRL 220
 DB 121 GAHGETFLHTNLSLKYKLMWYGODNTCEHYHVGPHSCHIPDIALFTYEIWEATNRL 180
 QY 221 GSARSVDLTLDVLTDPDPPDVHYSRVGLEDOLSVAVSPALKDLFOAKYQIRX 280
 DB 181 GSARSVDLTLDVLTDPDPPDVHYSRVGLEDOLSVAVSPALKDLFOAKYQIRX 240
 QY 281 VADSDVMKYVDVSNQTSQRLAGLPGTYFYQVRCNPFGIYSGKAGIWMSEMSHTAAS 340
 DB 241 VADSDVMKYVDVSNQTSQRLAGLPGTYFYQVRCNPFGIYSGKAGIWMSEMSHTAAS 300
 QY 341 TRSRPFGGVCPEPGEPSGPPVREBKQFLGWLKHAHCNSLSPFLYDQWRAMWOK 400
 DB 301 TRSRPFGGVCPEPGEPSGPPVREBKQFLGWLKHAHCNSLSPFLYDQWRAMWOK 360
 QY 401 SHKTRNQ--VLPAA 411
 DB 361 SHKTRNQDEGILPS 374

DT 17-MAR-1999 (first entry)
 DE Human Zcyto5 variant.
 KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 KW cardiac pathology; heart enlargement; Zcyto5 ligand; variant.
 OS Homo sapiens.
 PN W09849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE.
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.
 PT down-regulating Zcyto5 natural ligands or detecting cardiostrophin-1
 PT in blood
 PS Claim 1: Page 81-82; 55pp; English.
 CC The present sequence represents a Zcyto5 variant protein. Zcyto5
 CC is a cytokinin-like receptor. Soluble Zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcyto5 could be used to detect cardiostrophin-1 in the
 CC blood, and to discover other possible Zcyto5 ligands. A probe
 CC comprising Zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcyto5 and the
 CC therapeutically to modify Zcyto5 ligand effects.
 SQ Sequence 392 AA.

Query Match 88.0%; Score 1982; DB 1; Length 392;
 Best Local Similarity 92.9%; Pred. No. 7.3e-163;
 Matches 364; Conservative 5; Mismatches 7; Indels 16; Gaps 1;

QY 38 GGAHRAVISPODPTLLIGSSLOATCSIHGDPGATAEGLYTLNGRRRLPSELRLNTS 97
 DB 1 GGAHRAVISPODPTLLIGSSLOATCSIHGDPGATAEGLYTLNGRRRLPSELRLNTS 60
 QY 98 TALANLNGSGROSGDNLVCHARDGSLIAGSCLYVGLPPEKPNISCSNMKDLTCR 157
 DB 61 TALANLNGSGROSGDNLVCHARDGSLIAGSCLYVGLPPEKPNISCSNMKDLTCR 120
 QY 158 WTPGAHGETFLHTNLSLKYKLMWYGODNTCEHYHVGPHSCHIPDIALFTYEIWEAT 217
 DB 121 WTPGAHGETFLHTNLSLKYKLMWYGODNTCEHYHVGPHSCHIPDIALFTYEIWEAT 180
 QY 218 NTLGSARSVDLTLDVLTDPDPPDVHYSRVGLEDOLSVAVSPALKDLFOAKYQIR 277
 DB 181 NTLGSARSVDLTLDVLTDPDPPDVHYSRVGLEDOLSVAVSPALKDLFOAKYQIR 240
 QY 278 RYRVSDVMKYVDVSNQTSQRLAGLPGTYFYQVRCNPFGIYSGKAGIWMSEMSHT 337
 DB 241 RYRVSDVMKYVDVSNQTSQRLAGLPGTYFYQVRCNPFGIYSGKAGIWMSEMSHT 300
 QY 338 AASTRSPFGGVCPEPGEPSGPPVREBKQFLGWLKHAHCNSLSPFLYDQWRAMWOK 397
 DB 301 AASTRSPFGGVCPEPGEPSGPPVREBKQFLGWLKHAHCNSLSPFLYDQWRAMWOK 360
 QY 398 WOKSHKTRNQ-----VLPAA 413
 DB 361 WOKSHKTRNQHRTGSCPPADGARRVLPDXL 392

RESULT 9
 W70840
 W70840 standard; Protein; 392 AA.
 W70840;
 W70840;

RESULT 10
 W70839
 W70839 standard; Protein; 388 AA.
 AC W70839;
 DT 17-MAR-1999 (first entry)

DE Human zcyto5 variant.
 KM zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KM maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KM cardiac pathology; heart enlargement; zcyto5 ligand; variant.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc_difference 45 /note= "not specified"
 FN W09849307-A1.
 PD 05-NOV-1998.
 PE 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jernberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1; Page 80-81; 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcyto5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SQ Sequence 388 AA;

Query Match 87.5%; Score 1970.5; DB 1; Length 388;
 Best Local Similarity 95.2%; Pred. No. 7e-162;
 Matches 359; Conservative 8; Mismatches 7; Indels 3; Gaps 1;
 QY 38 GSGATAVISPODPTLLIGSSLOATCSIHGDPGATAGLYWTNGRLPSELRLNTS 97
 DB 1 GSGATAVISPODPTLLIGSSLOATCSIHGDPGATAGLYWTNGRLPSELRLNTS 60
 QY 98 LALANLNGSRQSGDNLVCHARDGSLAGSLVGLPEKPEFNISCSWNNKDLCTRT 157
 DB 61 LALANLNGSRQSGDNLVCHARDGSLAGSLVGLPEKPEFNISCSWNNKDLCTRT 120
 QY 158 WPPGAHGETFLHTNYSKTKRLMYGODNCEYHTVGPCHSIPKDLALFTPEIWEAT 217
 DB 121 WPPGAHGETFLHTNYSKTKRLMYGODNCEYHTVGPCHSIPKDLALFTPEIWEAT 180
 QY 218 NPLGARSVDLTLDLVVTTDPPDVHVSRYGLEDOLSVRWSPPLAKDFLQAKQIR 277
 DB 181 NPLGARSVDLTLDLVVTTDPPDVHVSRYGLEDOLSVRWSPPLAKDFLQAKQIR 240
 QY 278 RRVEDSVDMKVVVDVSNQTSCLAGLKPGLVYFVOVRCNPGFISGSKAGIWSMSHPT 337
 DB 241 RRVEDSVDMKVVVDVSNQTSCLAGLKPGLVYFVOVRCNPGFISGSKAGIWSMSHPT 300
 QY 338 AASTPRSEPPGGGVCERPGESSGPVRRLEKQFLGMLKHAHCSNLSFRLDQWAMNK 397
 DB 301 AASTPRSEPPGGGVCERPGESSGPVRRLEKQFLGMLKHAHCSNLSFRLDQWAMNK 360
 QY 398 MOKSHKTRNQ---VLPAL 411
 DB 361 MOKSHKTRNQDEGLIPS 377

RESULT 11
 W70850
 ID W70850 standard; Protein; 389 AA.

AC W70850:
 DT 17-MAR-1999 (first entry)
 DE Human zcyto5 variant.
 KM zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KM maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KM cardiac pathology; heart enlargement; zcyto5 ligand; variant.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc_difference 45 /note= "not specified"
 FN W09849307-A1.
 PD 05-NOV-1998.
 PE 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jernberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1; Page 95-96; 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcyto5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SQ Sequence 389 AA;

Query Match 87.4%; Score 1967; DB 1; Length 389;
 Best Local Similarity 93.1%; Pred. No. 1.4e-161;
 Matches 362; Conservative 4; Mismatches 7; Indels 16; Gaps 1;
 QY 41 AHTAVISPODPTLLIGSSLOATCSIHGDPGATAGLYWTNGRLPSELRLNTS 100
 DB 1 AHTAVISPODPTLLIGSSLOATCSIHGDPGATAGLYWTNGRLPSELRLNTS 60
 QY 101 LALANLNGSRQSGDNLVCHARDGSLAGSLVGLPEKPEFNISCSWNNKDLCTRT 160
 DB 61 LALANLNGSRQSGDNLVCHARDGSLAGSLVGLPEKPEFNISCSWNNKDLCTRT 120
 QY 161 GAGGETFLHTNYSKTKRLMYGODNCEYHTVGPCHSIPKDLALFTPEIWEAT 220
 DB 121 GAGGETFLHTNYSKTKRLMYGODNCEYHTVGPCHSIPKDLALFTPEIWEAT 180
 QY 221 GSARSDVLTLDLVVTTDPPDVHVSRYGLEDOLSVRWSPPLAKDFLQAKQIR 280
 DB 181 GSARSDVLTLDLVVTTDPPDVHVSRYGLEDOLSVRWSPPLAKDFLQAKQIR 240
 QY 281 VEDSVDMKVVVDVSNQTSCLAGLKPGLVYFVOVRCNPGFISGSKAGIWSMSHPT 340
 DB 241 VEDSVDMKVVVDVSNQTSCLAGLKPGLVYFVOVRCNPGFISGSKAGIWSMSHPT 300
 QY 341 TPRSRRPGGGVCERPGESSGPVRRLEKQFLGMLKHAHCSNLSFRLDQWAMNK 400
 DB 301 TPRSRRPGGGVCERPGESSGPVRRLEKQFLGMLKHAHCSNLSFRLDQWAMNK 360
 QY 401 SHKTRNQ-----VLPAL 413
 DB 361 SHKTRNQHRTGSCPRADGAREVLPDL 389

RESULT 12
 W70844
 ID W70844 standard; Protein; 389 AA.

DT 17-MAR-1999 (first entry)
 DE Human Zcyto5 variant.
 KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KW cardiac pathology; heart enlargement; Zcyto5 ligand; variant.
 OS Homo sapiens.
 PN W09849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; US-08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.
 PT down-regulating Zcyto5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1: Page 87-88; 55pp; English.
 CC The present sequence represents a Zcyto5 variant protein. Zcyto5
 CC is a cytokinin-like receptor. Soluble Zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcyto5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible Zcyto5 ligands. A probe
 CC comprising Zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcyto5 and
 CC therapeutically to modify Zcyto5 ligand effects.
 SQ Sequence 389 AA;

Query Match 87.3%; Score 1966; DB 1; Length 389;
 Best Local Similarity 92.8%; Pred. No. 1.7e-161;
 Matches 361; Conservative 5; Mismatches 7; Indels 16; Gaps 1;

QY 41 AHTAVISPODPTLLIGSSLOATCSIHGDTPGATAGLWTLNGRRLPSLSRLNTSTLA 100
 DB 1 AHTAVISPODPTLLIGSSLOATCSIHGDTPGATAGLWTLNGRRLPSLSRLNTSTLA 60

QY 101 LALANLNGSRGSGNVLCHARDGSIILAGSCLYVGLPEKPNISCSNMMDLTCRMT 160
 DB 61 LALANLNGSRGSGNVLCHARDGSIILAGSCLYVGLPEKPNISCSNMMDLTCRMT 120

QY 161 GAHGETFLHTNYSKYLKRWGQDNTCEHYHVGPHSCHIPRODLALFTPYELIWEATNRL 220
 DB 121 GAHGETFLHTNYSKYLKRWGQDNTCEHYHVGPHSCHIPRODLALFTPYELIWEATNRL 180

QY 221 GSARSDVLTLDVLTDDPPDVAVSRVGLLEDOLSVRWSPPALKDFLFOAKQIIRYR 280
 DB 181 GSARSDVLTLDVLTDDPPDVAVSRVGLLEDOLSVRWSPPALKDFLFOAKQIIRYR 240

QY 281 VEDSDVMKVVDDVSNQTSQCRLAGLPGTYFYQVRCNPFYIGSKKAGIWSMSHPTAAS 340
 DB 241 VEDSDVMKVVDDVSNQTSQCRLAGLPGTYFYQVRCNPFYIGSKKAGIWSMSHPTAAS 300

QY 341 TPRSRRPFGGVCBPRGEPSSGVRRELKQFLGMLKKHAYCSNLSFRLYDQWAMAK 400
 DB 301 TPRSRRPFGGVCBPRGEPSSGVRRELKQFLGMLKKHAYCSNLSFRLYDQWAMAK 360

QY 401 SHKTRNQ-----VLPAL 413
 DB 361 SHKTRNQHRTGSCPRADGARREVLDPDL 389

DE Human Zcyto5 variant.
 KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KW cardiac pathology; heart enlargement; Zcyto5 ligand; variant.
 OS Homo sapiens.
 PN W09849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; US-08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.
 PT down-regulating Zcyto5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1: Page 96-97; 55pp; English.
 CC The present sequence represents a Zcyto5 variant protein. Zcyto5
 CC is a cytokinin-like receptor. Soluble Zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcyto5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible Zcyto5 ligands. A probe
 CC comprising Zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcyto5 and
 CC therapeutically to modify Zcyto5 ligand effects.
 SQ Sequence 389 AA;

Query Match 87.3%; Score 1965; DB 1; Length 389;
 Best Local Similarity 92.5%; Pred. No. 2.1e-161;
 Matches 360; Conservative 6; Mismatches 7; Indels 16; Gaps 1;

QY 41 AHTAVISPODPTLLIGSSLOATCSIHGDTPGATAGLWTLNGRRLPSLSRLNTSTLA 100
 DB 1 AHTAVISPODPTLLIGSSLOATCSIHGDTPGATAGLWTLNGRRLPSLSRLNTSTLA 60

QY 101 LALANLNGSRGSGNVLCHARDGSIILAGSCLYVGLPEKPNISCSNMMDLTCRMT 160
 DB 61 LALANLNGSRGSGNVLCHARDGSIILAGSCLYVGLPEKPNISCSNMMDLTCRMT 120

QY 161 GAHGETFLHTNYSKYLKRWGQDNTCEHYHVGPHSCHIPRODLALFTPYELIWEATNRL 220
 DB 121 GAHGETFLHTNYSKYLKRWGQDNTCEHYHVGPHSCHIPRODLALFTPYELIWEATNRL 180

QY 221 GSARSDVLTLDVLTDDPPDVAVSRVGLLEDOLSVRWSPPALKDFLFOAKQIIRYR 280
 DB 181 GSARSDVLTLDVLTDDPPDVAVSRVGLLEDOLSVRWSPPALKDFLFOAKQIIRYR 240

QY 281 VEDSDVMKVVDDVSNQTSQCRLAGLPGTYFYQVRCNPFYIGSKKAGIWSMSHPTAAS 340
 DB 241 VEDSDVMKVVDDVSNQTSQCRLAGLPGTYFYQVRCNPFYIGSKKAGIWSMSHPTAAS 300

QY 341 TPRSRRPFGGVCBPRGEPSSGVRRELKQFLGMLKKHAYCSNLSFRLYDQWAMAK 400
 DB 301 TPRSRRPFGGVCBPRGEPSSGVRRELKQFLGMLKKHAYCSNLSFRLYDQWAMAK 360

QY 401 SHKTRNQ-----VLPAL 413
 DB 361 SHKTRNQHRTGSCPRADGARREVLDPDL 389

RESULT 13
 W70851
 ID W70851 standard; Protein; 389 AA.
 AC W70851;
 DT 17-MAR-1999 (first entry)

RESULT 14
 W70852
 ID W70852 standard; Protein; 389 AA.
 AC W70852;
 DT 17-MAR-1999 (first entry)
 DE Human Zcyto5 variant.

KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
KW cardiac pathology; heart enlargement; Zcyto5 ligand; variant.
OS Homo sapiens.
PN MO9849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; 008865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZIMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
DR WPI: 99-034662/03.
PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.
PT down-regulating Zcyto5 natural ligands or detecting cardiotrophin-1
PT in blood
PS Claim 1; Page 98-99; 55pp; English.
CC The present sequence represents a Zcyto5 variant protein. Zcyto5
CC is a cytokinin-like receptor. Soluble Zcyto5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC thyroid, heart, and skeletal muscle for example to lessen the effect
CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
CC enlargement. Zcyto5 could be used to detect cardiotrophin-1 in the
CC blood, and to discover other possible Zcyto5 ligands. A probe
CC comprising Zcyto5 DNA or RNA can be used to determine the presence
CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify Zcyto5 and
CC therapeutically to modify Zcyto5 ligand effects.
SQ Sequence 389 AA;

Query Match 87.3%; Score 1964; DB 1; Length 389;
Best Local Similarity 92.5%; Pred. No. 2.6e-161;
Matches 360; Conservative 6; Mismatches 7; Indels 16; Gaps 1;
QY 41 AHTAVISPODPTLLIGSSLOATCSIHGDPGATAGLWTLNGRRLPSELRLNTSTA 100
DB 1 AHTAVISPODPTLLIGSSLOATCSIHGDPGATAGLWTLNGRRLPSELRLNTSTA 60
QY 101 LALANLNGSRQSGDNLVCHARDGSLAGSCLVGLPEKPNISCSWNNMDDLTCRMT 160
DB 61 LALANLNGSRQSGDNLVCHARDGSLAGSCLVGLPEKPNISCSWNNMDDLTCRMT 120
QY 161 GAHGETFLHTNTSLKTKLRWYGODNTCEYHVGPHSCHIPDLALFTPEIWEATNRL 220
DB 121 GAHGETFLHTNTSLKTKLRWYGODNTCEYHVGPHSCHIPDLALFTPEIWEATNRL 180
QY 221 GSARSDVLTLDVLTDPDPPDVHVSRYGLEDLSRWSPPALKDLFOAKQIIR 280
DB 181 GSARSDVLTLDVLTDPDPPDVHVSRYGLEDLSRWSPPALKDLFOAKQIIR 240
QY 281 VEDSVDMKVVDDVSNQTSCLAGLKGTYVYFVQVNCNPGIYSGKAGIWMSEMSHTAAS 340
DB 241 VEDSVDMKVVDDVSNQTSCLAGLKGTYVYFVQVNCNPGIYSGKAGIWMSEMSHTAAS 300
QY 341 TPRESERPGGGVCPRGSGSPVRELKQFLGMLKKHAYCSNLSEFLYDQWAMMOK 400
DB 301 TPRESERPGGGVCPRGSGSPVRELKQFLGMLKKHAYCSNLSEFLYDQWAMMOK 360
QY 401 SHKTRNQ-----VLPKAL 413
DB 361 SHKTRNQHRTGSCPRADGARREVLDPKL 389

RESULT 15
W70846
ID W70846 standard; Protein: 389 AA.
AC W70846;
DT 17-MAR-1999 (first entry)
DE Human Zcyto5 variant.
KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;

KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
KW cardiac pathology; heart enlargement; Zcyto5 ligand; variant.
OS Homo sapiens.
PN MO9849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; 008865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZIMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
DR WPI: 99-034662/03.
PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.
PT down-regulating Zcyto5 natural ligands or detecting cardiotrophin-1
PT in blood
PS Claim 1; Page 89-90; 55pp; English.
CC The present sequence represents a Zcyto5 variant protein. Zcyto5
CC is a cytokinin-like receptor. Soluble Zcyto5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC thyroid, heart, and skeletal muscle for example to lessen the effect
CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
CC enlargement. Zcyto5 could be used to detect cardiotrophin-1 in the
CC blood, and to discover other possible Zcyto5 ligands. A probe
CC comprising Zcyto5 DNA or RNA can be used to determine the presence
CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify Zcyto5 and
CC therapeutically to modify Zcyto5 ligand effects.
SQ Sequence 389 AA;

Query Match 87.2%; Score 1963; DB 1; Length 389;
Best Local Similarity 92.5%; Pred. No. 3.1e-161;
Matches 360; Conservative 6; Mismatches 7; Indels 16; Gaps 1;
QY 41 AHTAVISPODPTLLIGSSLOATCSIHGDPGATAGLWTLNGRRLPSELRLNTSTA 100
DB 1 AHTAVISPODPTLLIGSSLOATCSIHGDPGATAGLWTLNGRRLPSELRLNTSTA 60
QY 101 LALANLNGSRQSGDNLVCHARDGSLAGSCLVGLPEKPNISCSWNNMDDLTCRMT 160
DB 61 LALANLNGSRQSGDNLVCHARDGSLAGSCLVGLPEKPNISCSWNNMDDLTCRMT 120
QY 161 GAHGETFLHTNTSLKTKLRWYGODNTCEYHVGPHSCHIPDLALFTPEIWEATNRL 220
DB 121 GAHGETFLHTNTSLKTKLRWYGODNTCEYHVGPHSCHIPDLALFTPEIWEATNRL 180
QY 221 GSARSDVLTLDVLTDPDPPDVHVSRYGLEDLSRWSPPALKDLFOAKQIIR 280
DB 181 GSARSDVLTLDVLTDPDPPDVHVSRYGLEDLSRWSPPALKDLFOAKQIIR 240
QY 281 VEDSVDMKVVDDVSNQTSCLAGLKGTYVYFVQVNCNPGIYSGKAGIWMSEMSHTAAS 340
DB 241 VEDSVDMKVVDDVSNQTSCLAGLKGTYVYFVQVNCNPGIYSGKAGIWMSEMSHTAAS 300
QY 341 TPRESERPGGGVCPRGSGSPVRELKQFLGMLKKHAYCSNLSEFLYDQWAMMOK 400
DB 301 TPRESERPGGGVCPRGSGSPVRELKQFLGMLKKHAYCSNLSEFLYDQWAMMOK 360
QY 401 SHKTRNQ-----VLPKAL 413
DB 361 SHKTRNQHRTGSCPRADGARREVLDPKL 389

Search completed: September 17, 1999, 03:08:12
Job time: 303 sec

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OM protein - protein search, using sw model

Run on: September 16, 1999, 19:07:29 ; Search time 68.96 Seconds

(without alignments)
4,462 Million cell updates/sec

Title: US-09-037-657-1

Sequence: 1 MSXWS 5

Scoring table: BLOSUM62

Searched: 201082 seqs, 61543640 residues

Database :

SPTREMBL.10:*
1: SP_archaea:*
2: SP_bacteria:*
3: SP_fungi:*
4: SP_human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_protist:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	30	96.8	2894	1	Q58791	Q58791 methanococ
2	30	96.8	367	1	O59408	O59408 pyrococcus
3	30	96.8	2529	2	O25579	O25579 helicobacte
4	30	96.8	394	2	O33205	O33205 mycobacteri
5	30	96.8	528	2	P70733	P70733 mycomonas c
6	30	96.8	2399	2	O92K59	O92K59 helicobacte
7	30	96.8	455	3	O08231	O08231 saccharomyc
8	30	96.8	437	3	O12007	O12007 saccharomyc
9	30	96.8	446	4	O43384	O43384 homo sapien
10	30	96.8	410	4	O14431	O14431 homo sapien
11	30	96.8	333	4	O16564	O16564 homo sapien
12	30	96.8	1522	4	O60242	O60242 homo sapien
13	30	96.8	984	4	O60297	O60297 homo sapien
14	30	96.8	1584	4	O16354	O16354 homo sapien
15	30	96.8	206	4	O16354	O16354 homo sapien
16	30	96.8	422	4	O16542	O16542 homo sapien
17	30	96.8	4123	4	O75851	O75851 homo sapien
18	30	96.8	52	4	O16340	O16340 homo sapien
19	30	96.8	820	4	O92489	O92489 homo sapien
20	30	96.8	328	4	O95061	O95061 homo sapien
21	30	96.8	72	5	O43983	O43983 cryptospori
22	30	96.8	291	5	O20991	O20991 caenorhabdi
23	30	96.8	947	5	O44171	O44171 caenorhabdi
24	30	96.8	769	5	O00816	O00816 toxoplasma
25	30	96.8	254	5	O19092	O19092 caenorhabdi
26	30	96.8	654	5	O19284	O19284 caenorhabdi
27	30	96.8	860	5	O22580	O22580 caenorhabdi
28	30	96.8	660	5	O23832	O23832 cryptospori
29	30	96.8	687	5	O23729	O23729 cryptospori

30	96.8	238	5	O76510	O76510 cryptospori
31	96.8	1207	5	O21535	O21535 caenorhabdi
32	96.8	1444	5	O17591	O17591 caenorhabdi
33	96.8	947	5	O26262	O26262 caenorhabdi
34	96.8	229	6	O27950	O27950 bos indicus
35	96.8	229	6	O28205	O28205 bos taurus
36	96.8	425	6	O02661	O02661 bos taurus
37	96.8	234	6	O97888	O97888 bos taurus
38	96.8	162	9	O38069	O38069 bacterioph
39	96.8	375	9	O92X59	O92X59 mycobacteri
40	96.8	316	11	O35545	O35545 iatus norv
41	96.8	147	11	O61427	O61427 mus musculu
42	96.8	898	11	O08721	O08721 iatus norv
43	96.8	1077	11	O62217	O62217 mus musculu
44	96.8	432	11	O64385	O64385 mus musculu
45	96.8	191	12	O65971	O65971 cucurbit ap

ALIGNMENTS

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RESULT 1
ID O58791 PRELIMINARY; PRT; 2894 AA.
AC O58791
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-JUN-1998 (TREMBLrel. 06, Last annotation update)
DE HYPOTHETICAL PROTEIN MJ1396.
GN MJ1396.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96337999.
RA BULL C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
RA SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCYNE J.D.,
RA KERVAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,
RA OVERBERG R., KIRNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODOK A.,
RA SCOTT J.L., GEOCHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,
RA UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,
RA COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BOROVOSKY M.,
RA KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RA jannaschii."
RL Science 273:1058-1073(1996).
CC -1- SIMILARITY: TO A.FULGIDUS AF2090-N AND IN THE C-TERMINAL, TO
CC AF2090-C.
CC EMBL; U67579; AAB99406.1; -.
DR Hypothetical protein.
KW SEQUENCE 2894 AA; 322361 MW; 4CF89EC9 CRC32;
SQ

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Query Match 96.8%; Score 30; DB 1; Length 2894;
Best Local Similarity 80.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MSXWS 5
Db 792 WSTWS 796

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RESULT 2
ID O59408 PRELIMINARY; PRT; 367 AA.
AC O59408
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)
DE 367AA LONG HYPOTHETICAL PROTEIN.
GN PH1708.
OS Pyrococcus horikoshii.

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OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-073
 RX MEDLINE; 98344137.
 RA KANARABAYASI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,
 YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOTAMA A., NAGAI Y.,
 RA SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMITA M., OHKUBO Y.,
 RA FUJAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,
 RA AOKI K., NAKAMURA Y., ROBE T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA H.,
 RA KIKUCHI H.,
 RT "Complete sequence and gene organization of the genome of a
 RT hyper-thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
 RL DNA Res. 5:55-76(1998).
 DR EMBL: AP000007; BAA30822.1;
 SQ SEQUENCE 367 AA; 41785 MW; B135C4EA CRC32;

Query Match 96.8%; Score 30; DB 1; Length 367;
 Best Local Similarity 80.0%; Pred. No. 3.3e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSXMS 5
 DB 262 WSXMS 266

RESULT 3
 ID 025579 PRELIMINARY; PRT; 2529 AA.
 AC 025579;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE TOXIN-LIKE OUTER MEMBRANE PROTEIN.
 GN HP0922.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-26695;
 RX MEDLINE; 97394467.
 RA TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G.,
 RA FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A.,
 RA NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S.,
 RA LOFTIS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODER A.,
 RA MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K.,
 RA BERG D.E., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M.,
 RA COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., MATTHEY L., WALLIN E.,
 RA HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
 RA VENTER J.C.,
 RT "The complete genome sequence of the gastric pathogen Helicobacter
 RT pylori."
 RL Nature 388:539-547(1997).
 DR EMBL: AE000602; AAD07969.1;
 DR TIGR: HP0922;
 KW Hypothetical protein.
 SQ SEQUENCE 2529 AA; 274561 MW; 31AAE6AC CRC32;

Query Match 96.8%; Score 30; DB 2; Length 2529;
 Best Local Similarity 80.0%; Pred. No. 1.9e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSXMS 5
 DB 87 WSXMS 91

RESULT 4
 ID 033205 PRELIMINARY; PRT; 394 AA.

AC 033205;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE HYPOTHETICAL 39.8 KD PROTEIN.
 GN MTC1125.28C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RA OLIVER K., HARRIS D.,
 RT Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
 RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RA PARKHILL J., BARRELL B.G., RAJANDREAN M.A.,
 RP Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RX MEDLINE; 96181548.
 RA PHILIPP W.J., POULET S., EIGLMETTER K., PASCOBELLA L.,
 RA BALSUBRAMANIAN V., HEIM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
 RA COLE S.T.,
 RT "An integrated map of the genome of the tubercle bacillus,
 RT Mycobacterium tuberculosis H37RV, and comparison with Mycobacterium
 RT leprae."
 RL Proc. Natl. Acad. Sci. U.S.A. 93:3132-3137(1996).
 DR EMBL: 298268; CAB10963.1;
 DR PFM: PF00823; PFE; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 394 AA; 39778 MW; 3F5F0DD5 CRC32;

Query Match 96.8%; Score 30; DB 2; Length 394;
 Best Local Similarity 80.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSXMS 5
 DB 300 WSXMS 304

RESULT 5
 ID P70733 PRELIMINARY; PRT; 528 AA.
 AC P70733;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
 DE ENDO-XYLANASE.
 GN XYN3.
 OS Aeromonas caviae.
 OC Bacteria; Proteobacteria; gamma subdivision; Aeromonas group;
 OC Aeromonas.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-W-61;
 RA OKAI N., NGUYEN D.V., NARAYAN R., MURAMOTO K., KANEKO J., TOMITA T.,
 RA KAMIO Y.,
 RT "Molecular cloning of new xylanase from Aeromonas caviae W-61."
 RT Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: D88553; BAA13641.1;
 KW Xylan degradation; Hydrolyase; Glycosidase.
 SQ SEQUENCE 528 AA; 58533 MW; 8D84F6AD CRC32;

Query Match 96.8%; Score 30; DB 2; Length 528;
 Best Local Similarity 80.0%; Pred. No. 4.6e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
1111
DB 517 MSTWS 521

RESULT 6

AC 09ZKS9 PRELIMINARY; PRT: 2399 AA.
AC 09ZKS9;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE PURTATIVE VACUOLATING CYTOTOXIN (VACA) PARALOG.
GN JHP0856.
OS Helicobacter pylori J99.
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-J99;
RA ALM R.A., LING L.-S.L., MOIR D.T., KING B.L., BROWN E.D., DOIG P.C.,
RA SMITH D.R., NOONAN B., GUID B.C., DEJONGE B.L., CARREL G.,
RA TUMMINO P.J., CARUSO A., URICA-NICHELSEN M., MILLS D.M., IVES C.,
RA GIBSON R., MERBERG D., MILLS S.D., JIANG Q., TAYLOR D.E., VOVIS G.F.,
RA TRIST T.J.;
RT "Genomic Sequence Comparison of Two Unrelated Isolates of the Human
RT Gastric Pathogen Helicobacter pylori."
RL Nature 397:176-180(1999).
RL EMBL; AE001515; AAD06432.1;
SQ SEQUENCE 2399 AA; 260015 MW; 9B40A7A6 CRC32;

Query Match 96.8%; Score 30; DB 2; Length 2399;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
1111
DB 86 WSSWS 90

RESULT 7

ID 008231 PRELIMINARY; PRT: 455 AA.
AC 008231;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBLrel. 01, Last annotation update)
DE CHROMOSOME XV READING FRAME ORF YOLO72M.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
RN (1)
RP SEQUENCE FROM N.A.
RA ALEXANDRAKI D., KATSIOLOU C., TZERMIA M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RA MIFS;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
SQ SEQUENCE 455 AA; 52678 MW; 15DC3CC3 CRC32;

Query Match 96.8%; Score 30; DB 3; Length 455;
Best Local Similarity 80.0%; Pred. No. 4e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
1111
DB 78 WSSWS 82

RESULT 8
012007 PRELIMINARY; PRT: 437 AA.
ID 012007;
AC 012007;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE)
DE (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE).
GN ENRL.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
RN (1)
RP SEQUENCE OF 1-331 FROM N.A.
RA DELIUS H., HEBLING U., HOFMANN B.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE OF 176-437 FROM N.A.
RA WABUTT R., WEDLER H.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN (3)
RP SEQUENCE FROM N.A.
RA DELIUS H., HEBLING U.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN (4)
RP SEQUENCE FROM N.A.
RA DUSTERHOEF A., FLOETH M., FRITZ M., HILBERT H., MOESTL D.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -1 CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE - PHOSPHOENOLPYRUVATE +
CC H(2)O.
CC -1 COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER (BY SIMILARITY).
CC -1 PATHWAY: GLYCOLYSIS.
CC -1 SUBUNIT: HOMODIMER (BY SIMILARITY).
DR EMBL; 275301; CAA99725.1; -;
DR EMBL; 273637; CAA98018.1; -;
DR EMBL; 275302; CAA99728.1; -;
DR PFW; PF00113; enolase; 1.
DR PROSITE; PS00164; ENOLASE; 1.
KM Lyase; Glycolysis; Magnesium.
FT ACT_SITE 344 344
FT METAL 356 356
SQ SEQUENCE 437 AA; 47327 MW; 1E54CA23 CRC32;

Query Match 96.8%; Score 30; DB 3; Length 437;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
1111
DB 304 WSSWS 308

RESULT 9

ID 043384 PRELIMINARY; PRT: 446 AA.
AC 043384;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE BAC CLONE GS164B05 FROM 7P21-P22, COMPLETE SEQUENCE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eubelata; Primates; Catarrhini; Hominoidea; Homo.
RN (1)
RP SEQUENCE FROM N.A.
RA ANDREWS S., HOLMES A., NGUYEN C.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RA WATERSTON R.;

RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC004160; AAC03417.1; -
 DR PFAM: PF00090; tsp_1; 3.
 FT NON_TER 1 1
 FT NON_TER 446 446
 SQ SEQUENCE 446 AA; 50444 MW; B793521E CRC32;

Query Match 96.8%; Score 30; DB 4; Length 446;
 Best Local Similarity 80.0%; Pred. No. 4e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
 Db 396 WSSWS 400

RESULT 10
 ID 014431 PRELIMINARY; PRT; 410 AA.
 AC 014431;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE GM-CSF RECEPTOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 91352066.
 RX CROSTIER K.E., WONG G.G., MATHYX-PEVOT B., NATAN D.G., SIEFF C.A.;
 RT "A functional isoform of the human granulocyte/macrophage
 RT colony-stimulating factor receptor has an unusual cytoplasmic
 RT domain."
 RL Proc. Natl. Acad. Sci. U.S.A. 88:7744-7748(1991).
 DR EMBL: M64445; AAA35908.1; -
 KW Transmembrane.
 SQ SEQUENCE 410 AA; 46901 MW; 30CE1609 CRC32;

Query Match 96.8%; Score 30; DB 4; Length 410;
 Best Local Similarity 80.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
 Db 306 WSSWS 310

RESULT 11
 ID 016564 PRELIMINARY; PRT; 333 AA.
 AC 016564;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE GM-CSF RECEPTOR PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 91376112.
 RX RAINES M.A., LIO U., QUAN S.G., JOE V., DIPERSIO J.F., GOLDE D.W.;
 RT "Identification and molecular cloning of a soluble human
 RT granulocyte-macrophage colony-stimulating factor receptor."
 RL Proc. Natl. Acad. Sci. U.S.A. 88:8203-8207(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RX MEDLINE; 91088339.
 RA ASHWORTH A., KRAFT A.;

RT "Cloning of a potentially soluble receptor for human GM-CSF."
 RL Nucleic Acids Res. 18:7178-7178(1990).
 DR EMBL: M73832; AAA5909.1; -
 DR EMBL: X54935; CAA38697.1; -
 KW Signal; Alternative splicing.
 FT SIGNAL 1 22
 FT CHAIN 23 333
 SQ SEQUENCE 333 AA; 38438 MW; 48178079 CRC32;

Query Match 96.8%; Score 30; DB 4; Length 333;
 Best Local Similarity 80.0%; Pred. No. 3e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
 Db 306 WSSWS 310

RESULT 12
 ID 060242 PRELIMINARY; PRT; 1522 AA.
 AC 060242;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DE BAI 3.
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE BAI 3.
 GN BAI 3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE; 98194217.
 RA SHIRATSUCHI T., NISHIMORI H., ICHISE H., NAKAMURA Y., TOKINO T.;
 RT "Cloning and characterization of BAI2 and BAI3, novel genes
 RT homologous to brain-specific angiogenesis inhibitor 1 (BAI1)."
 RL Cytogenet. Cell Genet. 79:103-108(1997).
 DR EMBL: AB005299; BAA25363.1; -
 DR PFAM: PF00090; tsp_1; 4.
 SQ SEQUENCE 1522 AA; 171490 MW; 740FCBCE CRC32;

Query Match 96.8%; Score 30; DB 4; Length 1522;
 Best Local Similarity 80.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSXWS 5
 Db 406 WSSWS 410

RESULT 13
 ID 060297 PRELIMINARY; PRT; 984 AA.
 AC 060297;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DE KINA0550 PROTEIN.
 GN KINA0550.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE; 98290545.
 RA NAGASE T., ISHIKAWA K., MIYAJIMA N., TANAKA A., KOTANI H., NOMURA N.,
 RA OHARA O.;
 RT "Prediction of the coding sequences of unidentified human genes. IX.
 RT The complete sequences of 100 new cDNA clones from brain which can

RT code for large proteins in vitro.
RL DNA Res. 5:31-39(1998).
DR EMBL; AB011122; BAA25476.1; -
PFAM; PF00090; tsp_1; 4
SO SEQUENCE 984 AA; 110897 MW; 39A158F8 CRC32;

Query Match

Best Local Similarity 96.8%; Score 30; DB 4; Length 984;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WSXWS 5
DB 406 WSSWS 410

RESULT 14

ID 014514 PRELIMINARY; PRT; 1584 AA.
AC 014514:
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE BAI 1.
GN BAI 1.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA NISHIMORI H., SHIRATSUCHI T., URANO T., KIMURA Y., KIYONO K.,
RA TATSUMI K., YOSHIDA S., ONO M., KIWANO M., NAKAMURA Y.;
RL Oncogene 0:0-0(1997).
DR EMBL; AB005297; BAA23647.1; -
DR PFAM; PF00090; tsp_1; 5.
SO SEQUENCE 1584 AA; 173531 MW; 235A5C42 CRC32;

Query Match

Best Local Similarity 96.8%; Score 30; DB 4; Length 1584;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WSXWS 5
DB 473 WSSWS 477

RESULT 15

ID 016354 PRELIMINARY; PRT; 206 AA.
AC 016354:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE PROLACTIN RECEPTOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE; 95286597.
RA FUH G., WELLS J.A.;
RT "Prolactin receptor antagonists that inhibit the growth of breast
cancer cell lines."
RL J. Biol. Chem. 270:13133-13137(1995).
DR EMBL; S78505; AAB34470.1; -
DR PFAM; PF00041; fn3; 2.
FT NON_TER 1
SO SEQUENCE 206 AA; 23950 MW; D7E57266 CRC32;

Query Match

96.8%; Score 30; DB 4; Length 206;

Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WSXWS 5
DB 191 WSSWS 195

Search completed: September 16, 1999, 20:40:03
Job time: 5594 sec

1	329	14.6	708	1	US-07-797-556-2	Sequence 2, Appl
2	329	14.6	708	3	PCT-US95-086530-2	Sequence 2, Appl
3	329	14.6	708	3	PCT-US95-086530-2	Sequence 2, Appl
4	254.5	11.3	836	1	US-07-923-976-4	Sequence 4, Appl
5	254.5	11.3	771	1	US-07-923-976-6	Sequence 6, Appl
6	254.5	11.3	863	1	US-07-923-976-8	Sequence 8, Appl
7	252.5	11.2	837	1	US-07-923-976-2	Sequence 2, Appl
8	252.5	9.8	372	1	US-07-865-878-4	Sequence 2, Appl
9	220.5	9.8	372	1	US-07-676-647-2	Sequence 2, Appl
10	220.5	9.8	372	1	US-08-449-329-2	Sequence 2, Appl
11	220.5	9.8	372	2	US-08-445-073-2	Sequence 2, Appl
12	220.5	9.8	372	3	PCT-US91-038996-2	Sequence 2, Appl
13	217.5	9.7	862	2	US-08-685-118-2	Sequence 2, Appl
14	217.5	9.7	862	2	US-08-915-495-2	Sequence 2, Appl
15	216.5	9.6	602	2	US-08-419-652-6	Sequence 6, Appl
16	206	9.2	572	2	US-08-419-652-5	Sequence 5, Appl
17	192.5	8.6	635	1	US-08-184-327A-4	Sequence 4, Appl
18	192.5	8.6	635	3	PCT-US95-00670-4	Sequence 4, Appl
19	192	8.5	633	1	US-08-230-859-17	Sequence 1, Appl
20	192	8.5	633	1	US-08-430-803-17	Sequence 1, Appl
21	192	8.5	633	3	PCT-US94-08860-17	Sequence 17, Appl
22	192	8.5	633	3	PCT-US95-01775-17	Sequence 17, Appl
23	192	8.5	633	3	PCT-US95-16626-7	Sequence 17, Appl
24	190	8.4	1001	1	US-07-797-556-6	Sequence 6, Appl
25	190	8.4	1001	1	US-07-943-843-2	Sequence 2, Appl
26	190	8.4	1097	1	US-07-943-843-6	Sequence 6, Appl
27	190	8.4	1001	2	US-08-347-003-2	Sequence 2, Appl
28	190	8.4	1097	2	US-08-347-003-6	Sequence 6, Appl
29	186	8.3	626	1	US-08-184-327A-2	Sequence 2, Appl
30	186	8.3	452	1	US-08-184-327A-8	Sequence 8, Appl
31	186	8.3	626	3	PCT-US95-00670-8	Sequence 2, Appl
32	185	8.3	482	3	PCT-US95-00670-8	Sequence 8, Appl
33	185	8.2	719	1	US-07-943-843-4	Sequence 4, Appl
34	185	8.2	719	2	US-08-347-003-4	Sequence 4, Appl
35	174.5	7.8	559	1	US-08-306-231-3	Sequence 3, Appl
36	174.5	7.8	960	1	US-08-355-888A-8	Sequence 8, Appl
37	174.5	7.8	960	2	US-08-693-697-8	Sequence 8, Appl
38	174.5	7.8	960	2	US-08-693-697-3	Sequence 3, Appl
39	174.5	7.8	898	2	US-08-693-697-36	Sequence 36, Appl

283 DSVDMKV---DDVSNQTSCLAGLKPGTVYFVQVRCNPFGIYGSKKAGIMSEWSHPTAA 339

DB 265 DASTSQIPPEDTASTRSSFTVODLKPFTEYFRIRC-----MKEDGGMDSMEASG 319
QY 340 STPRSERP 347
DB 320 IT-YEDRP 326

RESULT 2

US-08-308-881-2
; Sequence 2, Application US/08308881
; Patent No. 5783672
; GENERAL INFORMATION:
; APPLICANT: Mosley, Bruce
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Receptor for Oncostatin M
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,881
; FILING DATE: 12-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/249,553
; FILING DATE: 26-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2614-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 708 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-308-881-2

Query Match 14.6%; Score 329; DB 2; Length 708;
Best Local Similarity 28.6%; Pred. No. 1.2e-22;

Matches 88; Conservative 51; Mismatches 151; Indels 18; Gaps 8;

QY 46 ISPODPTLLIGSSLOATCSIHG---DIPGATAGELVTLNGRRLPSELSTLNTSLALA 102
DB 31 ISPESPVQLHSNFTAVCVLKEKCMDFHYNNANTIVKTNHFTIPREQYTIINRTASSVT 90
QY 103 LANNGSROOSGDNLVCHARDGSIILAGSLYGLPPEKPFNISCSWRNMKDLCTRWTPGA 162
DB 91 FTDIASINIQLCNIIILFQGLQEQNVYGIITISGLPEKRNLSICIYNECKKMCENDGGR 150
QY 163 HGEFTLHTNYSKTKKLMYGGDNTCEHYTVGPHSCHIRPDALFTPEYIWEATNRIGS 222
DB 151 --ETHLETNFTLSEWATKHFADCKAKRDT--PTSCYVDYSTVYFNIEVWEAENALGK 206
QY 223 ARSDVTLVLDVYVTPDPDVHVSRYGLEDOLSVRWSPPALKDFLPAKQIQRIVE 282
DB 207 VTSQHINFDVYKYPKPNHLSVINESEELSIKLTWTN-PSIKSYIT-LKTNIOYRTRK 264

QY 283 DSYDMKVV---DDVSNOTSRLAGLKPGTYVQVRCNPFQIYSGSKAGIWSMHPAA 339
DB 265 DASTSQIPPEDTASTRSSFTVODLKPFTEYFRIRC-----MKEDGGMDSMEASG 319
QY 340 STPRSERP 347
DB 320 IT-YEDRP 326

RESULT 3

PCT-US95-06530-2
; Sequence 2, Application PC/TUS9506530
; GENERAL INFORMATION:
; APPLICANT: Mosley, Bruce
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Receptor for Oncostatin M
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06530
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,881
; FILING DATE: 09-SEP-1994
; APPLICATION NUMBER: US 08/249,553
; FILING DATE: 26-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2614-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 708 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-06530-2

Query Match 14.6%; Score 329; DB 3; Length 708;
Best Local Similarity 28.6%; Pred. No. 1.2e-22;

Matches 88; Conservative 51; Mismatches 151; Indels 18; Gaps 8;

QY 46 ISPODPTLLIGSSLOATCSIHG---DIPGATAGELVTLNGRRLPSELSTLNTSLALA 102
DB 31 ISPESPVQLHSNFTAVCVLKEKCMDFHYNNANTIVKTNHFTIPREQYTIINRTASSVT 90
QY 103 LANNGSROOSGDNLVCHARDGSIILAGSLYGLPPEKPFNISCSWRNMKDLCTRWTPGA 162
DB 91 FTDIASINIQLCNIIILFQGLQEQNVYGIITISGLPEKRNLSICIYNECKKMCENDGGR 150
QY 163 HGEFTLHTNYSKTKKLMYGGDNTCEHYTVGPHSCHIRPDALFTPEYIWEATNRIGS 222
DB 151 --ETHLETNFTLSEWATKHFADCKAKRDT--PTSCYVDYSTVYFNIEVWEAENALGK 206
QY 223 ARSDVTLVLDVYVTPDPDVHVSRYGLEDOLSVRWSPPALKDFLPAKQIQRIVE 282

Db 207 VTSOHINFDVYKVPNPHNLVINSSELSIKLWTN-PSIKSVII-LKYNIOYRTK 264
QY 283 DSYDMKVV---DVSNOTSCLAGLKPQTVYVOVRCNPFGIYSKKGAGTSEMSHP1AA 339
Db 265 DASWWSIPEDPRTSTSSFTVODLKPFTEYVFRIC-----MKEDGKGYSDWSEANS 319
QY 340 STPRSREP 347
Db 320 IT-YEDRP 326

RESULT 4

US-07-923-976-4
Sequence 4, Application US/07923976
Patent No. 5574136
GENERAL INFORMATION:

APPLICANT: Nagata, Shigekazu
APPLICANT: Fukunaga, Rikio
TITLE OF INVENTION: DNA Encoding Granulocyte
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones, Tullar & Cooper, P.C.
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,976
FILING DATE: 19920922

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74539/1990
FILING DATE: 23-MAR-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 176629/1990
FILING DATE: 03-JUL-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP91/00375
FILING DATE: 22-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hellwege, James W.
REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 514853
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-415-1500
TELEFAX: 703-415-1508

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 836 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear

MOLECULE TYPE: protein
US-07-923-976-4

Query Match 11.3%; Score 254.5; DB 1; Length 836;
Best Local Similarity 28.9%; Pred. No. 1.5e-15;
Matches 97; Conservative 48; Mismatches 148; Indels 43; Gaps 16;

QY 21 SLSWSPLLCVLGVPRGSGAHTAVISPODPTLLIGSSLAQTSIHGDTGATAE-GLYW 79
Db 8 SLTWALLIILL-----PGSIECGHISVSAPIYHLDPTIASCTIKQNSHLDPEQILW 63
QY 80 TLNGRRLPELSLLN--TSTLALALANLNGSRQSGDNLVCHARDS---ILAGSLYV 134
Db 64 RLGAELQPGRGROORRLSDGTQESITILPHLNHTQA---FLSCCLNMGNSIQIILDQVELRA 119

QY 135 GLPPEKPEINIS-WSRNMKDLTCWTPGANGFTLHNTYSIK-YKLWYGO---DNTCEE 189
Db 120 GYPALPHNNISCLANLTTSSLICQWEP--ETHLPTSTLKSRSKGNCOQODSILDC 177
QY 190 YHTVPSCHIP-KDLLETPYEIWEATNRLSGARSVDLTLVDLYV-----TTDP 240
Db 178 VPKDGOSHCCIPRKHLHLLYQMGIMVQAEMLGTSMSPOLCLDNDVYKLEPPPLRTMDP 237
QY 241 PPDVYSRVGGLEDQLSVRWVSPALDFFLEQAKYQIRYVE-DSVDMKYVDVSNQT-S 298
Db 238 SPEAPPOAGCLQ-----LCW--EPMQPLHINQKCELRHKQREASAMALVGPLLEALQ 291
QY 299 CRLAGLKPGTYFYVOVRCNPFGIYSKKGAGTSEMS 334
Db 292 YELGGLPATATYTLQIRCIKRWPL-----PGHWSWDS 322

RESULT 5

US-07-923-976-6
Sequence 6, Application US/07923976
Patent No. 5574136
GENERAL INFORMATION:

APPLICANT: Nagata, Shigekazu
APPLICANT: Fukunaga, Rikio
TITLE OF INVENTION: DNA Encoding Granulocyte
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones, Tullar & Cooper, P.C.
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,976
FILING DATE: 19920922

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74539/1990
FILING DATE: 23-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 176629/1990
FILING DATE: 03-JUL-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP91/00375
FILING DATE: 22-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hellwege, James W.
REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 514853
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-415-1500
TELEFAX: 703-415-1508

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear

MOLECULE TYPE: protein
US-07-923-976-6

Query Match 11.3%; Score 254.5; DB 1; Length 771;
Best Local Similarity 28.9%; Pred. No. 1.3e-15;
Matches 97; Conservative 48; Mismatches 148; Indels 43; Gaps 16;

QY 21 SLSWSPLLCVLGVPRGSGAHTAVISPODPTLLIGSSLAQTSIHGDTGATAE-GLYW 79
Db 8 SLTWALLIILL-----PGSIECGHISVSAPIYHLDPTIASCTIKQNSHLDPEQILW 63
QY 80 TLNGRRLPELSLLN--TSTLALALANLNGSRQSGDNLVCHARDS---ILAGSLYV 134
Db 64 RLGAELQPGRGROORRLSDGTQESITILPHLNHTQA---FLSCCLNMGNSIQIILDQVELRA 119

Db 8 SLTMAALLILL----PGSLECGHISVSAPIVHLDPTIASCIIKONSHLDPEQIIM 63
 QY 80 TLNGRLPSELRLN--ISTALALANLNGSRQSGDNLYCHARGS---ILAGSCLYV 134
 Db 64 RGAELQPGGROQRSDGQESITTLPLNHTQA---FLSCCLMNGNSLQIIDQVELRA 119
 QY 135 GLPPEKPFNISC-WSRNMKDLTCRWTPGAHGEFTLNTYSLK-YKLRWGO---DNICEE 189
 Db 120 GYPPALPHNLSCLMNLITSSLCQMEPGP--ETHLPSTLTKFSKRGNCQTOGDSILDC 177
 QY 190 YHTVPHSCHIP-KDLAFETPEIWEATNRLGSARSVDLTLDVLYV-----TTDP 240
 Db 178 VPKDQSHCCIPRKHLLLYONNGIWOAENALGTSMSPOLCLDPMDVYKLEPMLRTMDP 237
 QY 241 PPDVHVSRYGLEDQLSYRWVSPALKDPLFOAKIQIRYVE-DSVDMKVVDDVSNQT-S 298
 Db 238 SPEAAPPOAGCLQ---LCW--EPWQPGIHNOKCELHKKPQGEASWALVGPLLEALQ 291
 QY 299 CRLAGLKPGTYEYVQVRCNPFYIGSKKAGISSEMS 334
 Db 292 YELCGLLPATATYTIQIRIRMPL-----PGHWSWMS 322

RESULT 6
 US-07-923-976-8
 ; Sequence 8, Application US/07923976
 ; Patent No. 5574136
 ; GENERAL INFORMATION:
 ; APPLICANT: Nagata, Shigekazu
 ; APPLICANT: Fukunaga, Rikio
 ; TITLE OF INVENTION: DNA Encoding Granulocyte
 ; TITLE OF INVENTION: Colony-Stimulating Factor Receptor
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jones, Tullat & Cooper, P.C.
 ; STREET: P.O. Box 2266 Eads Station
 ; CITY: Arlington
 ; STATE: Virginia
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/923, 976
 ; FILING DATE: 19920922
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 74539/1990
 ; FILING DATE: 23-MAR-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 176629/1990
 ; FILING DATE: 03-JUL-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/J991/00375
 ; FILING DATE: 22-MAR-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hellwege, James W.
 ; REGISTRATION NUMBER: 28,808
 ; TELECOMMUNICATION INFORMATION: 514853
 ; TELEPHONE: 703-415-1500
 ; TELEFAX: 703-415-1500
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 863 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-07-923-976-8

Query Match 11.3%; Score 254.5; DB 1; Length 863;
 Best Local Similarity 28.9%; Pred No. 1.5e-15;
 Matches 97; Conservative 48; Mismatches 148; Indels 43; Gaps 15;
 QY 21 SLSMPLICVLGVPRGGGARTAVISPODPTLLIGSSLOACNSIHDPGATAE-GLYV 79
 Db 8 SLTMAALLILL----PGSLECGHISVSAPIVHLDPTIASCIIKONSHLDPEQIIM 63
 QY 80 TLNGRLPSELRLN--ISTALALANLNGSRQSGDNLYCHARGS---ILAGSCLYV 134
 Db 64 RGAELQPGGROQRSDGQESITTLPLNHTQA---FLSCCLMNGNSLQIIDQVELRA 119
 QY 135 GLPPEKPFNISC-WSRNMKDLTCRWTPGAHGEFTLNTYSLK-YKLRWGO---DNICEE 189
 Db 120 GYPPALPHNLSCLMNLITSSLCQMEPGP--ETHLPSTLTKFSKRGNCQTOGDSILDC 177
 QY 190 YHTVPHSCHIP-KDLAFETPEIWEATNRLGSARSVDLTLDVLYV-----TTDP 240
 Db 178 VPKDQSHCCIPRKHLLLYONNGIWOAENALGTSMSPOLCLDPMDVYKLEPMLRTMDP 237
 QY 241 PPDVHVSRYGLEDQLSYRWVSPALKDPLFOAKIQIRYVE-DSVDMKVVDDVSNQT-S 298
 Db 238 SPEAAPPOAGCLQ---LCW--EPWQPGIHNOKCELHKKPQGEASWALVGPLLEALQ 291
 QY 299 CRLAGLKPGTYEYVQVRCNPFYIGSKKAGISSEMS 334
 Db 292 YELCGLLPATATYTIQIRIRMPL-----PGHWSWMS 322

RESULT 7
 US-07-923-976-2
 ; Sequence 2, Application US/07923976
 ; Patent No. 5574136
 ; GENERAL INFORMATION:
 ; APPLICANT: Nagata, Shigekazu
 ; APPLICANT: Fukunaga, Rikio
 ; TITLE OF INVENTION: DNA Encoding Granulocyte
 ; TITLE OF INVENTION: Colony-Stimulating Factor Receptor
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jones, Tullat & Cooper, P.C.
 ; STREET: P.O. Box 2266 Eads Station
 ; CITY: Arlington
 ; STATE: Virginia
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/923, 976
 ; FILING DATE: 19920922
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 74539/1990
 ; FILING DATE: 23-MAR-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 176629/1990
 ; FILING DATE: 03-JUL-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/J991/00375
 ; FILING DATE: 22-MAR-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hellwege, James W.
 ; REGISTRATION NUMBER: 28,808
 ; TELECOMMUNICATION INFORMATION: 514853
 ; TELEPHONE: 703-415-1500
 ; TELEFAX: 703-415-1500
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 837 amino acids

TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-923-976-2

Query Match 11.28; Score 252.5; DB 1; Length 837;
Best Local Similarity 27.8%; Pred. No. 2.3e-15;
Matches 107; Conservative 56; Mismatches 163; Indels 59; Gaps 20;

29 LCVLGVPRGSGAHTANISPODPLLLIGSSIQATCSIHGDPGATAG-LYTLNGRRL- 87
14 LITLLRLRSLSCGHITSP-PVYRLGDPVPLASCTISPNSKLDQOAKILMRLODEPIQ 71
87 PSELSRL--NTSTLALANLNGSRQSGDNLYCHARDGSIILAGSLYGLPEKPFNI 144
72 PGRQHHLPGQTGESLITLHLANT-QAFLECLVPMEDSVOLQOAEHLHAGYPPASSNL 130
145 SCMSR-NMKDLTRKWTGPGAGETFLHTNYSK-YKLR--WYGDNCEHYTVGPHSCH 199
131 SCIMHLTNSLVQMEGCP--ETHLPTSLKSPRSADQYQGDITPDCAKKRQNC 188
200 IP-KDLALFPEYIMWATNRLSARSVDVLTLDVLYTTDPP-----PDYHVSRYG 250
189 IPKKNLLIQYMAIWOAEKMLSSSPKLCLEPMDVYKLEPMLQALDYGDPVYSHQPG 248
251 GLEDQSVKVS-PPALKDPLFOAKQIRYRVE-DSYDMKYVDV-SNOTSCLRLAGLRG 307
249 CL-----WLSKRPKPSRYMEQECLEKRIQPOLKANMTLVHLPSKQOFLCGLHQA 301
308 TYEYVQRCNPFEGISYKSKAGIWSMS----HPT-AASTPRSERPGGVCPEPRGCEP 361
302 PYTTLQMRG-----IRSSLPEGFWSPPSGQLNPMTKAPRIHDT-----WCKKGLDP 350
362 SS-----GPRRELKQFLGML 377
351 GYVSVOLFKMPTPLQEDSGQIQGYL 375

RESULT 8

US-07-865-878A-4

Sequence 4, Application US/07865878A

Patent No. 5332672

GENERAL INFORMATION:

APPLICANT: Yancopoulos, George D. et al.

TITLE OF INVENTION: Cell Free Ciliary Neurotrophic
Factor/Receptor Complex

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSER: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/865, 878A

FILING DATE: 19911202

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/801/562

FILING DATE: 02-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Mistock, S. Leslie

REGISTRATION NUMBER: 18, 872

REFERENCE/DOCKET NUMBER: 6526-082

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 790-9090

TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 372 amino acids

TYPE: AMINO ACID

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-07-865-878A-4

Query Match 9.8%; Score 220.5; DB 1; Length 372;
Best Local Similarity 26.2%; Pred. No. 6.8e-13;
Matches 96; Conservative 42; Mismatches 149; Indels 79; Gaps 19;

41 AHTAVI-----SPDDPLL-----IGSSIQATCSIHGDPGATAGLYMTLNGRRLSELS 91
15 AAAYVYAGHSPQEAHPHYERLGSVTLPCGTANMDAAT-----WRNGTDLAPD-- 68
92 RLNTSTLALANLNGSRQSGDNLYCHARDGSIILAGS-CLYGLPEKPFNISCMSRN 150
68 -LNGSQLV-----LHGLEGHSGLYACFHRDSMHLRHQVILHVGLPPEPV-LSCRSNT 120
151 M-KDLQCRW-----TPGANGETFLHTNYSKYLKRWGQDNCEHYTVGPHSCHIRK 202
121 YPKGFTCSMHLPTPTIPTNTFNTVYLGSKIM-----VCEKDAL-KNRCHI-R 167
203 DLALFT--PYEIWEATNRLSARSVDVLTLDVLYTTDPPDVHVSRYGLEDQSVK 260
168 YMLFSTIKKVISIVSNALGH-NATAITDEFYKPPDPPEVAVARPPSNRRLEVTM 226
261 VSPPALKD-FLFOAKQIRYRVEDSVDMKYVDVSNQTSORLAGLPGTYEYVQVRCNPF 319
227 QTPSTWDPDSFPLKEFLRYRLILDQMHV-ELSDGTAHTIDAVAGREYIIQVAAK-- 284
320 GIGSKKAGIWSMS-----HPTAASPRSERPGGVCPEPRG 358
284 ----DNEIGTWSMVAHAHTPWTSEPRHLTTEQAAEYTTSTSLAPPPTTKIDP-- 338
359 GEPSSG 364
338 GELGSG 343

RESULT 9

US-07-676-647-2

Sequence 2, Application US/07676647

Patent No. 5426177

GENERAL INFORMATION:

APPLICANT: Davis, Samuel

APPLICANT: Squitto, Stephen P.

APPLICANT: Furl, Mark E.

APPLICANT: Yancopoulos, George D.

TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSER: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/676, 647

FILING DATE: 19910328

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Mistock, S. Leslie

REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 6526-048
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 8698864/9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 372 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-676-647-2

Query Match 9.8%; Score 220.5; DB 1; Length 372;
 Best Local Similarity 26.2%; Pred. No. 6.8e-13;
 Matches 96; Conservative 42; Mismatches 149; Indels 79; Gaps 19;

QY 41 AHFAVI-----SPDPTLL-----IGSSLQATCSIHGDTFGATAEGLYWTNGRLPSELS 91
 DB 15 AAAAVYAOHRSPQEAHPHYERLGSVDYLPCTANMDAAVT-----WRVNGTDLAPD-- 68
 QY 92 RLINTSTLALANLNGSRQSGDNLYCHARDGSIAGS-CLYVGLPPEKPPENISCSWSN 150
 DB 68 -LINGSQLY-----LHGLELGHSGLYACFHRDSWMLRHQVLLHVGLPPEPV-LSCRSM 120
 QY 151 M-KDLICRW-----TPGAGETFLHTNLSKYLKRWYGQNTCEHYHTVGPHSCHIRP 202
 DB 121 YPKGFYCSWMLPTPIYIPNTFNTVLHGSKIM-----VCEKDPAL-KNRCHI-R 167
 QY 203 DLALFT--PYEIVWEATNRLGSARSDVLTLDVAVTTDPPDVHRSRVGLEDQLSVNR 260
 DB 168 YMLFSTIKKVISIVSNALGH-NATATIDETITKPPDPENAVARPPSNRRLEVTW 226
 QY 261 VSPPALKD-FLFOAKQIQRVEDSVDMKVVDDVSNQTSCLAGLPGTVYEVQVNCNPF 319
 DB 227 QTPSTWPDPESPFLKFLRYRPLILDQMOHV-ELSDGTHTITDAAGKEIITQVAAK-- 284
 QY 320 GIYSKKGAIWSEMS-----HPTAASPPSERPPGGVCEPRG 358
 DB 284 ----DNEIGTWSMSVAHAATPTEERHLITTEAQAETTTSTSLAPPPTTKICDP-- 338
 QY 359 GEPSSG 364
 DB 338 GELGSG 343

RESULT 10
 US-08-449-329-2
 Sequence 2, Application US/08449329
 Patent No. 5648334
 GENERAL INFORMATION:
 APPLICANT: Davis, Samuel
 APPLICANT: Squinto, Stephen P.
 APPLICANT: Furth, Mark E.
 APPLICANT: Yancopoulos, George D.
 TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn, Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/449,329

FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/700,677
 FILING DATE: 15-MAY-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Mistrock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 6526-065
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 8698864/9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 372 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-449-329-2

Query Match 9.8%; Score 220.5; DB 1; Length 372;
 Best Local Similarity 26.2%; Pred. No. 6.8e-13;
 Matches 96; Conservative 42; Mismatches 149; Indels 79; Gaps 19;

QY 41 AHFAVI-----SPDPTLL-----IGSSLQATCSIHGDTFGATAEGLYWTNGRLPSELS 91
 DB 15 AAAAVYAOHRSPQEAHPHYERLGSVDYLPCTANMDAAVT-----WRVNGTDLAPD-- 68
 QY 92 RLINTSTLALANLNGSRQSGDNLYCHARDGSIAGS-CLYVGLPPEKPPENISCSWSN 150
 DB 68 -LINGSQLY-----LHGLELGHSGLYACFHRDSWMLRHQVLLHVGLPPEPV-LSCRSM 120
 QY 151 M-KDLICRW-----TPGAGETFLHTNLSKYLKRWYGQNTCEHYHTVGPHSCHIRP 202
 DB 121 YPKGFYCSWMLPTPIYIPNTFNTVLHGSKIM-----VCEKDPAL-KNRCHI-R 167
 QY 203 DLALFT--PYEIVWEATNRLGSARSDVLTLDVAVTTDPPDVHRSRVGLEDQLSVNR 260
 DB 168 YMLFSTIKKVISIVSNALGH-NATATIDETITKPPDPENAVARPPSNRRLEVTW 226
 QY 261 VSPPALKD-FLFOAKQIQRVEDSVDMKVVDDVSNQTSCLAGLPGTVYEVQVNCNPF 319
 DB 227 QTPSTWPDPESPFLKFLRYRPLILDQMOHV-ELSDGTHTITDAAGKEIITQVAAK-- 284
 QY 320 GIYSKKGAIWSEMS-----HPTAASPPSERPPGGVCEPRG 358
 DB 284 ----DNEIGTWSMSVAHAATPTEERHLITTEAQAETTTSTSLAPPPTTKICDP-- 338
 QY 359 GEPSSG 364
 DB 338 GELGSG 343

RESULT 11
 US-08-445-073-2
 Sequence 2, Application US/08445073
 Patent No. 5849897
 GENERAL INFORMATION:
 APPLICANT: Davis, Samuel
 APPLICANT: Squinto, Stephen P.
 APPLICANT: Furth, Mark E.
 APPLICANT: Yancopoulos, George D.
 TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,073
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,647
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-445-073-2

Query Match 9.8%; Score 220.5; DB 2; Length 372;
Best Local Similarity 26.2%; Pred. No. 6,8e-13;
Matches 96; Conservative 42; Mismatches 149; Indels 79; Gaps 19;

41 AHTAVI-----SPDDPTLL-----IGSSLAQATCSIHGDTPGATAEGLYWTNGRRLPSELS 91
15 AAAAVYVQRHSPOEAPHVQYERLGSVDTLPCGTAMDAVY-----WRVNGTDLAD-- 68
92 RLNTSTLALANLNGSRSGDNLVCHARDGSIAGS-CLYVGLPEPEKPFNISCMSRN 150
68 -LNGSGLV-----LHGELGHSGLYACFHRDSWHLRHOVLHVGLEPPREPV-LSCRSNT 120
151 M-KDLTCRW-----TPGAGETFLHTNYSIKYKLRWYGODNTCEEYHTVGPSCHIPK 202
121 YPKGFYSWMHLPPTYIPNTENVYVLGSKIM-----VCEKDPAL-KNRCHI-R 167
203 DLALFT--PEIWEATNRUGSARSVDLTLDVYTTDPPDVHVSRYGLEDOLSVRW 260
168 YMHLESTIKYKVSISVSNALGH-NATAITDEFIIVKPDPEENVVAPVSPNRRLEVTW 226
261 VSPPALMD-FLFOAKYQIRVEDSVDMKYVDVSNQTSCLAGLKPGTYFVQVRCNPF 319
227 QTPSTWDPDSFPLKFLRYRPLILDQMOHV-ELSDGTARTITDAYAKKEYIIOVAAK-- 284
320 GIYSKKAGIWMSEMS-----HPTASTPRSRERPGGVCGERG 358
284 ----DNELGWSMDSVAHAHPTWTEERHLLTEAOAAETTTSTTSLAPPPTTKICDP-- 338
359 GEPSSG 364
338 GELGSG 343

RESULT 12
PCT-US91-03896-2
Sequence 2, Application PC/TUS9103896
GENERAL INFORMATION:
APPLICANT: Davis, Samuel
APPLICANT: Squinto, Stephen P.
APPLICANT: Furch, Mark E.
APPLICANT: Yancopoulos, George D.
TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/03896
FILING DATE: 19910603
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-065-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US91-03896-2

Query Match 9.8%; Score 220.5; DB 3; Length 372;
Best Local Similarity 26.2%; Pred. No. 6,8e-13;
Matches 96; Conservative 42; Mismatches 149; Indels 79; Gaps 19;

41 AHTAVI-----SPDDPTLL-----IGSSLAQATCSIHGDTPGATAEGLYWTNGRRLPSELS 91
15 AAAAVYVQRHSPOEAPHVQYERLGSVDTLPCGTAMDAVY-----WRVNGTDLAD-- 68
92 RLNTSTLALANLNGSRSGDNLVCHARDGSIAGS-CLYVGLPEPEKPFNISCMSRN 150
68 -LNGSGLV-----LHGELGHSGLYACFHRDSWHLRHOVLHVGLEPPREPV-LSCRSNT 120
151 M-KDLTCRW-----TPGAGETFLHTNYSIKYKLRWYGODNTCEEYHTVGPSCHIPK 202
121 YPKGFYSWMHLPPTYIPNTENVYVLGSKIM-----VCEKDPAL-KNRCHI-R 167
203 DLALFT--PEIWEATNRUGSARSVDLTLDVYTTDPPDVHVSRYGLEDOLSVRW 260
168 YMHLESTIKYKVSISVSNALGH-NATAITDEFIIVKPDPEENVVAPVSPNRRLEVTW 226
261 VSPPALMD-FLFOAKYQIRVEDSVDMKYVDVSNQTSCLAGLKPGTYFVQVRCNPF 319
227 QTPSTWDPDSFPLKFLRYRPLILDQMOHV-ELSDGTARTITDAYAKKEYIIOVAAK-- 284
320 GIYSKKAGIWMSEMS-----HPTASTPRSRERPGGVCGERG 358
284 ----DNELGWSMDSVAHAHPTWTEERHLLTEAOAAETTTSTTSLAPPPTTKICDP-- 338
359 GEPSSG 364
338 GELGSG 343

RESULT 13
US-08-685-118-2
Sequence 2, Application US/08685118
Patent No. 5840530
GENERAL INFORMATION:
APPLICANT: Gudlet, Ulrich A
APPLICANT: Presky, David R
TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,118
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Robert A.
REGISTRATION NUMBER: 35,682
REFERENCE/DOCKET NUMBER: CD 9195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-2863
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 862 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-685-118-2

Query Match 9.7%; Score 217.5; DB 2; Length 862;
Best Local Similarity 25.6%; Pred. No. 4.5e-12;
Matches 84; Conservative 46; Mismatches 121; Indels 77; Gaps 14;
QY 53 LLIGSLATGCSIHGDTGATAGLYWTL-----NGRRRLPSELRL-L 94
DB 41 ILGSLVNTGSL-----KPRGCFHYSRRNKLILYFDRIRNFHGHSLNSQYTGJPL 94
QY 95 NSTLALANLNGSRQSGDNLYCHARDGSLAGSCLYGLPPEKPNISGWSRNMK-D 153
DB 95 GTTLFVCKLACINSEIQ-----ICGAELFVGAPBPQPNLSCIQAGEGT 140
QY 154 LTCRWTPGAHGETPLHNTSLKY-----KLRYGQ--DNTCEYHVG-----PHSCHI 200
DB 141 VACTWEMGR--DTHLYTEYTLQLSGPKNLTWOKCKDIYC-DYLDGGINLTPESPESNFT 197
QY 201 PKDALFTPEIWEATNRLSARSADVLTLDVYTTDPPDVHVSRYVGLDQLSVRW 260
DB 198 AK-----VTAVNSLGSSSSSLPSTFTFLDIYRPLPMDIRIKOKASVSCTLYW 246
QY 261 VSPALPKDFLOAKQOIRYVEDSVDMKVVDDVSNQTSCLAGLPGTVYFVQVRCNPG 320
DB 247 -----RDEGLVLLNRLRYRSPNSRLMNMVNTAKAGRHDLDLKPFTEYEPQI-SSKLH 299
QY 321 IYGSKKAGIWSWSHPTAASPRSRPG 348
DB 300 LY-----KGSWSDWSESLRAQTPEEPGTG 323

RESULT 14
US-08-915-495-2
Sequence 2, Application US/08915495
Patent No. 5832176
GENERAL INFORMATION:
APPLICANT: Gubler, Ulrich A
APPLICANT: Presky, David H
TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.

STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,495
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,118
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Robert A.
REGISTRATION NUMBER: 35,682
REFERENCE/DOCKET NUMBER: CD 9195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-2863
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 862 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-915-495-2

Query Match 9.7%; Score 217.5; DB 2; Length 862;
Best Local Similarity 25.6%; Pred. No. 4.5e-12;
Matches 84; Conservative 46; Mismatches 121; Indels 77; Gaps 14;
QY 53 LLIGSLATGCSIHGDTGATAGLYWTL-----NGRRRLPSELRL-L 94
DB 41 ILGSLVNTGSL-----KPRGCFHYSRRNKLILYFDRIRNFHGHSLNSQYTGJPL 94
QY 95 NSTLALANLNGSRQSGDNLYCHARDGSLAGSCLYGLPPEKPNISGWSRNMK-D 153
DB 95 GTTLFVCKLACINSEIQ-----ICGAELFVGAPBPQPNLSCIQAGEGT 140
QY 154 LTCRWTPGAHGETPLHNTSLKY-----KLRYGQ--DNTCEYHVG-----PHSCHI 200
DB 141 VACTWEMGR--DTHLYTEYTLQLSGPKNLTWOKCKDIYC-DYLDGGINLTPESPESNFT 197
QY 201 PKDALFTPEIWEATNRLSARSADVLTLDVYTTDPPDVHVSRYVGLDQLSVRW 260
DB 198 AK-----VTAVNSLGSSSSSLPSTFTFLDIYRPLPMDIRIKOKASVSCTLYW 246
QY 261 VSPALPKDFLOAKQOIRYVEDSVDMKVVDDVSNQTSCLAGLPGTVYFVQVRCNPG 320
DB 247 -----RDEGLVLLNRLRYRSPNSRLMNMVNTAKAGRHDLDLKPFTEYEPQI-SSKLH 299
QY 321 IYGSKKAGIWSWSHPTAASPRSRPG 348
DB 300 LY-----KGSWSDWSESLRAQTPEEPGTG 323

RESULT 15
US-08-419-652-6
Sequence 6, Application US/08419652
Patent No. 5831007
GENERAL INFORMATION:
APPLICANT: Chue, Anne O
APPLICANT: Gubler, Ulrich A
TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.

[illegible]

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:42:05 ; Search time 49.27 Seconds

(without alignments)
335,844 Million cell updates/sec

Title: US-09-037-657-13

Perfect score: 2251
Sequence: 1 MPAGRPVPAQASRRPRPL.....WRAMQKSHKTRNOYLPKAL 413

Scoring table: BLOSUM62

Searched: 122810 seqs, 40065486 residues

Database :

PIR_60: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	331	14.7	622	A40144	prolactin receptor
2	329	14.6	918	A36337	membrane glycoprot
3	324.5	14.4	206	A57018	prolactin receptor
4	319.5	14.2	917	I49699	glycoprotein 130 -
5	317.5	14.1	918	A44257	interleukin-6 sign
6	314	13.9	830	I50455	interleukin-6 sign
7	312	13.9	610	A34631	lactogen receptor
8	312	13.9	610	A36116	prolactin receptor
9	312	13.9	412	A41070	prolactin receptor
10	312	13.9	310	A29884	prolactin receptor
11	307.5	13.7	616	A30304	prolactin receptor
12	307.5	13.7	303	I77524	prolactin receptor
13	307.5	13.7	292	I77525	prolactin receptor
14	307.5	13.7	608	I53269	prolactin receptor
15	306	13.6	831	J01655	prolactin receptor
16	302.5	13.4	581	I45971	prolactin receptor
17	261.5	11.6	630	I51086	prolactin receptor
18	254.5	11.3	783	JH0329	granulocyte colony
19	254.5	11.3	771	B38252	granulocyte colony
20	254.5	11.3	863	C38252	granulocyte colony
21	252.5	11.2	837	A34898	granulocyte colony
22	234	10.4	372	I58141	granulocyte colony
23	220.5	9.8	372	I58141	ciliary neurotroph
24	209.5	9.3	422	I37891	ciliary neurotroph
25	208.5	9.3	432	I46343	interleukin-11 rec
26	208	9.2	362	S60614	interleukin-11 rec
27	203.5	9.0	460	JL0145	growth promoting a
28	200.5	8.9	468	A41242	interleukin-6 rece
29	199	8.8	156	A33868	prolactin receptor
30	194.5	8.6	440	JL0144	interleukin-6 rece
31	192.5	8.6	579	B45266	interleukin-6 rece
32	192.5	8.6	635	A45266	interleukin-6 rece
33	191.5	8.5	894	S68437	MPV-P protein prec
34	191.5	8.5	900	S68440	leptin receptor (V
35	191.5	8.5	805	S68441	leptin receptor (V
36	190	8.4	1097	S11308	leptin receptor (V
37	190	8.4	625	S35317	leukemia inhibitor
38	190	8.4	150	B34631	hematopoietic grow
39	188.5	8.4	894	JC4797	lactogen receptor
					leptin receptor pr

40 188.5 8.4 1162 2 PC4184 leptin receptor, O
41 188.5 8.4 805 3 JC4897 leptin receptor, O
42 186 8.3 626 2 S37622 proto-oncogene - m
43 185 8.2 1092 2 JX0312 differentiation-st
44 185 8.2 719 2 JC2181 differentiation-st
45 182 8.1 895 2 S74225 leptin receptor, l

ALIGNMENTS

RESULT 1

A40144
prolactin receptor long form precursor, hepatoma and breast cancer cells - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Sep-1998
C:Accession: A40144
R:Boutin, J.M.; Ederly, M.; Shirota, M.; Jolicoeur, C.; Lesneur, L.; Ali, S.; Gould
Mol. Endocrinol. 3, 1455-1461, 1989
N>Title: Identification of a cDNA encoding a long form of prolactin receptor in hu
A:Reference number: A40144; MUID:90114212
A:Accession: A40144
A:Molecule type: mRNA
A:Residues: 1-622 <BOD>
A:Cross-references: GB:M31661; NID:g190361; PID:g190362
C:Genetics:
A:Gene: GDB:PRLR
A:Cross-references: GDB:120315; OMIM:176761
A:Map position: 5p13.3-5p13.1
C:Keywords: glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-622/Product: prolactin receptor, long form #status predicted <MAT>
F:59,104,233/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match

Best Local Similarity 14.7%; Score 331; DB 2; Length 622;
Best Local Similarity 37.5%; Pred. No. 3.5e-19;
Matches 84; Conservative 27; Mismatches 95; Indels 18; Gaps 6;

QY 126 ILASGLVYG-LPPEKPFNISCMSRMKDLTCRMFGAGHGFLLHNTYKLRMYGOD 184
DB 15 LFLNCLNGQLPQKPELFCRSPKKEFTCMWRGTGG--LPNTYLTTHRGETLM 72
QY 185 NTCEHYHTVGPSPCHPNK-LALFTPEYETWEATNRLGARSVDLTLDVAVTTDPPD 243
DB 73 HECPDYITGGPNSCHGKQYTSMMRTYIMVNAATNGSSFDELYVDVYTIYQDPPE 132
QY 244 VAVSRVYGLLEDLSVRAW--SPALKDF--LFQAKYQIRYVEDSVDMKVVVDVSNOTS 298
DB 133 LAV-EVKQPEDRKPYLMIMSPPTLIDLTKGWFLLYEIRLPEKAEWE-IHFAQOOTE 190
QY 299 CRLAGIKPCTYFVYRCNPFYIGSKKAGIMSEWHPAAATP 342
DB 191 FFLSLHPQKYLVOVRKP-----DHGYSAWSPATFIQIP 227

RESULT 2

A36337
membrane glycoprotein gp130 precursor - human
C:Species: Homo sapiens (man)
C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-Sep-1998
C:Accession: A36337
R:Hihi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.
Cell 63, 1149-1157, 1990
A>Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
A:Reference number: A36337; MUID:91084844
A:Accession: A36337
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-918 <HIB>
A:Cross-references: GB:M57230; NID:g186353; PID:g186354
C:Genetics:
A:Gene: GDB:IL6ST; GP130

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: September 16, 1999, 20:42:05 ; Search time 49.27 seconds
(without alignments)
335.844 Million cell updates/sec

Title: US-09-037-657-13
Perfect score: 2251

Sequence: 1 MPAGRPQVVAQASARRPRPL.....WRAWQSKSTRNQVLPKAL 413

Scoring table: BLOSUM62

Searched: 122810 seqs, 40065486 residues

Database:

PIR_60:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	331	14.7	622	2	A40144	prolactin receptor
2	329	14.6	918	2	A36337	membrane glycoprotein
3	324.5	14.4	206	2	A57018	prolactin receptor
4	319.5	14.2	917	2	I49699	glycoprotein 130
5	317.5	14.1	918	2	A44257	interleukin-6 sign
6	314	13.9	830	2	I50455	prolactin receptor
7	312	13.9	610	2	A4631	prolactin receptor
8	312	13.9	412	2	A36116	prolactin receptor
9	312	13.9	610	2	A41070	prolactin receptor
10	312	13.9	310	2	A39884	prolactin receptor
11	307.5	13.7	616	2	A30304	prolactin receptor
12	307.5	13.7	303	2	I77524	prolactin receptor
13	307.5	13.7	292	2	I77525	prolactin receptor
14	307.5	13.7	608	2	I53269	prolactin receptor
15	306	13.6	831	2	J01655	prolactin receptor
16	302.5	13.4	581	2	I45971	prolactin receptor
17	281.5	11.6	630	2	I51086	prolactin receptor
18	284.5	11.3	783	2	JH0329	granulocyte colony
19	254.5	11.3	771	2	B38252	granulocyte colony
20	254.5	11.3	863	2	C38252	granulocyte colony
21	252.5	11.2	837	2	A34898	granulocyte colony
22	234	10.4	372	2	I58141	ciliary neurotroph
23	230.5	9.8	372	1	UHR0CN	ciliary neurotroph
24	209.5	9.3	422	2	I37891	interleukin-11 rec
25	208.5	9.3	432	2	I48343	interleukin-11 rec
26	208.5	9.2	362	2	S60614	interleukin-6 rece
27	203.5	9.0	460	2	JU0145	interleukin-6 rece
28	200.5	8.9	456	1	A11242	interleukin-6 rece
29	199	8.8	156	2	A32868	prolactin receptor
30	194.5	8.6	440	2	JU0144	prolactin receptor
31	192.5	8.6	579	2	B45266	leukemia inhibitor
32	192.5	8.6	635	2	A45266	leukemia inhibitor
33	191.5	8.5	894	2	S68437	leptin receptor (v
34	191.5	8.5	900	2	S68440	leptin receptor (v
35	191.5	8.5	805	2	S68441	leptin receptor (v
36	190	8.4	1097	2	I57308	leptin receptor (v
37	190	8.4	625	2	S35317	hematopoietic grow
38	190	8.4	150	2	B34631	lactogen receptor
39	188.5	8.4	894	2	JC4797	leptin receptor pr

40 188.5 8.4 1162 2 PC4184 leptin receptor, O
41 188.5 8.4 805 2 JC4897 leptin receptor, O
42 186 8.3 626 2 S37622 proto-oncogene - m
43 185 8.2 1092 2 JX0312 differentiation-st
44 185 8.2 719 2 JC2181 differentiation-st
45 182 8.1 895 2 S74225 leptin receptor, 1

ALIGNMENTS

RESULT 1
A40144
prolactin receptor long form precursor, hepatoma and breast cancer cells - human

C:Species: Homo sapiens (man)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Sep-1998

C:Accession: A40144
R:Buttin, J.M.; Edey, M.; Shiota, M.; Jolicoeur, C.; Lesueur, L.; All, S.; Gould, D

Mol. Endocrinol. 3, 1455-1461, 1989
A:Title: Identification of a cDNA encoding a long form of prolactin receptor in human

A:Reference number: A40144; MUID:90114212
A:Accession: A40144

A:Molecule type: mRNA
A:Residues: 1-622 <BOD>

A:Cross-references: GB:M31661; NID:G190361; PID:G190362
C:Genetics:

A:Gene: GDB:PRUR
A:Cross-references: GDB:120315; OMIM:176761

A:Map position: 5p13.3-5p13.1
C:Keywords: glycoprotein; transmembrane protein

F.1-24/Domains: signal sequence #status predicted <SIG>
F.25-622/Product: prolactin receptor, long form #status predicted <MAT>

F.59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.7%; Score 331; DB 2; Length 622;
Best Local Similarity 37.5%; Pred. No. 3.5e-15;
Matches 84; Conservative 27; Mismatches 95; Indels 18; Gaps 8;

QY 126 ILAAGCLVVG-LPEKPPNISCWSRNMDLCRTWPGAHGEFTLHTNYSLKXKLWVGQD 184
DB 15 LFLNCLINGQLPPCKPRFIFRCRSPNKEFTFCWMPGPDG--LPTNLSLYHREGETLM 72

QY 185 NTCEHYHTVGPCHSIPRD-LALFTPEIWEATNRUGASRDVLTLDVDTTPPPD 243
DB 73 HECPPYITGPNCSHFQYQYSMTYIMVYVATNMGSSSDLYDVYIYQPPPLE 132

QY 244 VHSVVGLEPOLSTRWV--SPALKDF--LFOAKIQRIRVEDSVDMKYVDVSNQTS 298
DB 133 LAV-EVKQPEDRKPYLWTKMSPPTLIDKTGMFTLLYEIRLKPKEKAEWE-IHFGQOTE 190

QY 299 CRLAGLKPGTYFVQVRCNPGIYGSKKAGISEMSHPTASTP 342
DB 191 FKILSLHFGQKTLVQVCKRP-----DHGIWSAMSPATFIQIP 227

RESULT 2
A36337
membrane glycoprotein gp130 precursor - human

C:Species: Homo sapiens (man)
C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-Sep-1998

C:Accession: A36337
R:HDH, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.

A:Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
A:Reference number: A36337; MUID:91084844

A:Accession: A36337
A:Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-918 <HIB>

A:Cross-references: GB:M57230; NID:G186353; PID:G186354
A:Gene: GDB:IL6ST; GP130

A:Cross-references: GDB:126725; OMIM:600694
 A:Map position: 5q11-5q11
 C:Keywords: glycoprotein; membrane protein

Query Match 14.6%; Score 329; DB 2; Length 918;

Best Local Similarity 28.6%; Pred. No. 8.6e-19;
 Matches 88; Conservative 51; Mismatches 151; Indels 18; Gaps 8;

QY 46 ISPDPTLLIGSSLGATCSHG---DTPGATAGLWTLNGRLSELRLNTSTLALA 102
 DB 31 ISPEFVQVQHSNFTAVCLAKKCDYFVNANVYVMTNHTTKEQDTIINRASSVT 90
 QY 103 LANLNGSRQSGDNLVCHARDGSIILAGSCLVGLPPEKFNISCSRMKDLTCRMTGCA 162
 DB 91 FTDIASLNTQILCNILTFEQLEQNYGIIISGLPPEKFNISCSRMKDLTCRMTGCA 150
 QY 163 HGETFLHTNYSKLYKLRWYQDNTCEHYHTVPHSCHIPKDLALTPPEIWEATNRLGS 222
 DB 151 --ETHELETNFKLSEWATKRFADCKAKRDT--PTSCYDYSYVYEVNIEVWEALNALGK 206
 QY 223 ARSDVLTLDVLTDPDPDVHVSRYGLEDQLSVRWSPALDKDFQAKYQIRRYV 282
 DB 207 VTSDHINPDVYKVPNPNNLSVINSELSILKLTWTN-PSISVLI-LKYNQYRFX 264
 QY 283 DSDVDRKVY---DDVSNQISCRLAGLKPGLVYFVQVRCNPFGIYSKAGINSESHPTAA 339
 DB 265 DASTSQIPEDTASTRSSEFTVQDLKPFTEYVERIR-----MKEDGYSWDSWSEASG 319
 QY 340 STPRSERP 347
 DB 320 IT-YEDRP 326

RESULT 3

Prolectin receptor - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-Jul-1996
 C:Accession: A57018
 R:Fun, G.; Wells, J.A.
 J. Biol. Chem. 270, 13133-13137, 1995
 A:Title: Prolectin receptor antagonists that inhibit the growth of breast cancer cell 11
 A:Reference number: A57018; MUID:95286597
 A:Accession: A57018
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-206 <RES>
 A:Cross-references: GB:S78505; NID:9999114; PID:9999115

Query Match 14.4%; Score 324.5; DB 2; Length 206;

Best Local Similarity 38.0%; Pred. No. 2.8e-19;
 Matches 81; Conservative 25; Mismatches 90; Indels 17; Gaps 7;

QY 136 LPPKPFNISCWSRMKDLTCRMTGAGETFLHTNYSKLYKLRWYQDNTCEHYHTVGP 195
 DB 2 LPPKPFNISCWSRMKDLTCRMTGAGETFLHTNYSKLYKLRWYQDNTCEHYHTVGP 59
 QY 136 HSCHPKD-LALFTPEIWEATNRLGSASDVLTLVDVLTDPDPDVHVSRYGLED 254
 DB 60 NSCHFGKQYTSMTWRTYIMVNTNONGSSELDVYDYYIQQPPELAV-EVKQPED 118
 QY 255 QLSVWV--SPALKDF---LQAKYQIRRYVEDSDVMDVVDVSNQISCRLAGLKPGLV 309
 DB 119 KRPYIMIKWSPPTLLDLKGTGWTLLYELRLKPEKAAEW-HPAQOQTEFKLISHPQK 177
 QY 310 YFVQVRCNPFGIYSKAGINSESHPTAASP 342
 DB 178 YLYVQRCRP-----DHGYWASMPATFIQIP 203

RESULT 4

149699
 glycoprotein 130 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 07-Feb-1997
 C:Accession: 149699; I48370
 R:Salto, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.
 J. Immunol. 148, 4066-4071, 1992
 A:Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, g
 A:Reference number: 148370; MUID:92291532
 A:Accession: 149699
 A:Status: translated from GB/EMBL/DBJ
 A:Residues: 1-917 <RES>
 A:Molecule type: mRNA
 A:Accession: 148370
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-917 <RES>
 A:Cross-references: EMBL:X62646; NID:9840816; PID:9840817
 C:Genetics:
 A:Gene: gp130
 C:Keywords: glycoprotein

Query Match 14.2%; Score 319.5; DB 2; Length 917;
 Best Local Similarity 29.6%; Pred. No. 5e-18;
 Matches 92; Conservative 50; Mismatches 146; Indels 23; Gaps 10;

QY 46 ISPDPTLLIGSSLGATCSHG---DTPGATAGLWTLNGRLSELRLNTSTLALA 102
 DB 31 IYPEFVQVQHSNFTAVCLAKKCDYFVNANVYVMTNHTTKEQDTIINRASSVT 90
 QY 103 LANLNGSRQSGDNLVCHARDGSIILAGSCLVGLPPEKFNISCSRMKDLTCRMTGCA 162
 DB 91 FTDIASLNTQILCNILTFEQLEQNYGIIISGLPPEKFNISCSRMKDLTCRMTGCA 150
 QY 163 HGETFLHTNYSKLYKLRWYQDNTCEHYHTVPHSCHIPKDLALTPPEIWEATNRLGS 222
 DB 151 --ETHELETNFKLSEWATKRFADCKAKRDT--PTSCYDYSYVYEVNIEVWEALNALGK 203
 QY 223 ARSDVLTLDVLTDPDPDVHVSRYGLEDQLSVRWSPALDKDFQAKYQIRRYV 281
 DB 204 KYSSSINFDVYKVPNPNNLSVINSELSILKLTWTN-PSISVLI-LKYNQYRFX 261
 QY 283 DSDVDRKVY---DDVSNQISCRLAGLKPGLVYFVQVRCNPFGIYSKAGINSESHPTA 338
 DB 262 KDASTWQVPLEDTPMSPRTSTVQDLKPFTEYVERIR-----SIRDGK-GYWSWSEAS 316
 QY 339 AST--PRSERP 347
 DB 317 GTYEDRPSRP 327

RESULT 5

A44257
 Interleukin-6 signal transducing molecule gp130 - rat

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
 C:Accession: A44257
 R:Wang, Y.; Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M.
 Genomics 14, 666-672, 1992
 A:Title: Molecular cloning and characterization of the rat liver IL-6 signal transdu
 A:Reference number: A44257; MUID:93053397
 A:Accession: A44257
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-918 <RAN>
 A:Experimental source: liver
 A:Note: sequence extracted from NCBI backbone (NCBIP:118488)
 C:Keywords: transmembrane protein

Query Match 14.1%; Score 317.5; DB 2; Length 918;

Best Local Similarity 29.8%; Pred. No. 7.3e-18;
Matches 92; Conservative 51; Mismatches 145; Indels 21; Gaps 10;

QY 46 ISPPDPTLLIGSSIAQTCISIHG---DTPGATAGLWTLNGLRPLBELSLTLTSLTALA 102
Db 31 IYEPFVVGROGNSFTRATCYLKEKCLQVYSNATYIYWKTNHVAVPEQVIVIRNTASSVY 90
QY 103 LANWNSRQOOSDNLVCHARDGSIAGSLIYVGLPPEKPFNISCGRNMKDLTCRTTPGA 162
Db 91 FPDVFOVWOLTCNLISFQIQONVYGITLSGYPPDITNLSCITNEGRNMLCQDPER 150
QY 163 HGEPLHTNYSILKYLRWGGOP--NCEETHTVGPCHPLPKDLALFTPEIWEATNRLG 221
Db 151 --ETLENTYTLKSE--WATEKFPDCKTKH--GTSSCKMGTYPIYVNIWEVWEALNAG 204
QY 222 SARSDVLTLDVLTDPDPPVHYSRVGGLEDOLSVRVSPPALKDFLFOAKYQIRYRV 281
Db 205 NVSSPPIFDPVDKPKPSPHLSVTNSEELSLIKLAVNSGL--DSLIRLKSIDQYRT 262
QY 282 EDSVDWKVY---DDVSNQTSCLAGLKPQVYFVQRCNPFGIYSGKAGIWEWSHPTA 338
Db 263 KDASTWIOVPLEDETVSPRTSFTVQDLKPFTEVFRIR----SIKNGK-GIYSDWSE-EA 316
QY 339 ASTRSRSEP 347
Db 317 SGTYEDRP 325

RESULT 6
150455

prolactin receptor - pigeon
C/Species: Columba livia (domestic pigeon)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Sep-1996

A/Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor.
A/Reference number: 150455; MOID:94283267
A/Accession: 150455
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-830 <CH>
A/Cross-references: EMBL:U07694; NID:9466381; PID:9466382

Query Match 13.9%; Score 314; DB 2; Length 830;
Best Local Similarity 37.1%; Pred. No. 1.2e-17;

Matches 76; Conservative 29; Mismatches 82; Indels 18; Gaps 8;
Y 137 PPEKPFNISCGRNMKDLTCRTTPGAHGETFLH-TNYSLKYLKRWGGODTCEHYHVG 195
Db 231 PPEKPTIICRSPEKETFTCWWRGSDG---HPTNYTLISKEGEERYTECPDYKTAGP 287
Y 196 HSCHT-PRDLALFTPEIWEATNRLGASRSDVLTLDVLTDPDPPV--HYSRVGGL 252
Db 288 NSCYDCKHTISMTIYNITVKAINEIGSNVSDPLYVDVYITGDTDPVNTLELKTIVN 347
Y 253 EDQLSVRWSPALDFF--LFOAKYQIRYVEDSDVKYVDVDSYQTSCLAGLKPQV 309
Db 348 KRYLVLTW-SPPPLADVNSGWLTLDELRLKPEEAEMEETI-FVGGQTHYKMFSLNPKK 405
Y 310 YFVQVRCNPFGIYSGKAGIWEWS 334
Db 406 YIVQIHCKP-----DHGNSWSEMS 424

RESULT 7
34631

actogen receptor 1 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 13-Jul-1990 #sequence_revision 09-Oct-1992 #text_change 10-Sep-1997
A/Accession: A34631
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-610 <SH>
A/Cross-references: EMBL:U07694; NID:9466381; PID:9466382

Biochem. Biophys. Res. Commun. 168, 415-422, 1990
A/Title: Isolation and characterization of two novel rat ovarian lactogen receptor cD
A/Reference number: A34631; MOID:90241201
A/Accession: A34631
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-610 <SH>
A/Cross-references: GB:M34083; NID:9205122; PID:9205123
A/Note: the authors translated the codon GAG for residue 533 as Gly

Query Match 13.9%; Score 312; DB 2; Length 610;
Best Local Similarity 35.4%; Pred. No. 1.2e-17;
Matches 80; Conservative 35; Mismatches 85; Indels 26; Gaps 10;

QY 125 SIAGSCLVGLPPEKPFNISCGRNMKDLTCRTTPGAHGETFLHNTSLKYKLRWGGOD 184
Db 15 SILKQGS-----PPKPEIHKCRSPDKETFTCWWRGSDG--LPTNLSLYSKR--GEK 65
QY 185 NT--CEEHTVGPCHPLPKDLALFTPEIWEATNRLGASRSDVLTLDVLTDPDPP 241
Db 66 TTYECPDYKTSQPNCSFESKQYTSIMKIYITVNTNMGSSSDPLYVDVYIYEPEPP 125
QY 242 PDVHSRVGLEDOLSVRWV--SPPALDFF--LFOAKYQIRYVEDSDVKYVDVDSNQ 296
Db 126 RNLTL-EVKQLDKKTYLWVKMSPTLIDVATGTFMEIRLKEEAEME-ITFTGHQ 183
QY 297 TSCRLAGLKPQVYFVQRCNPFGIYSGKAGIWEWSHPTAATP 342
Db 184 TQFVFDLYPGQKLYVQRCRP-----DHGYSRMSQESSVEMP 222

RESULT 8
A36116

prolactin receptor 2 precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 10-Sep-1997
A/Accession: A36116
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-610 <SH>
A/Cross-references: GB:M57668; NID:9206366; PID:9206367; GB:M60728

Query Match 13.9%; Score 312; DB 2; Length 610;
Best Local Similarity 35.4%; Pred. No. 1.2e-17;

Matches 80; Conservative 35; Mismatches 85; Indels 26; Gaps 10;
QY 125 SIAGSCLVGLPPEKPFNISCGRNMKDLTCRTTPGAHGETFLHNTSLKYKLRWGGOD 184
Db 15 SILKQGS-----PPKPEIHKCRSPDKETFTCWWRGSDG--LPTNLSLYSKR--GEK 65
QY 185 NT--CEEHTVGPCHPLPKDLALFTPEIWEATNRLGASRSDVLTLDVLTDPDPP 241
Db 66 TTYECPDYKTSQPNCSFESKQYTSIMKIYITVNTNMGSSSDPLYVDVYIYEPEPP 125
QY 242 PDVHSRVGLEDOLSVRWV--SPPALDFF--LFOAKYQIRYVEDSDVKYVDVDSNQ 296
Db 126 RNLTL-EVKQLDKKTYLWVKMSPTLIDVATGTFMEIRLKEEAEME-ITFTGHQ 183
QY 297 TSCRLAGLKPQVYFVQRCNPFGIYSGKAGIWEWSHPTAATP 342
Db 184 TQFVFDLYPGQKLYVQRCRP-----DHGYSRMSQESSVEMP 222

RESULT 9
A41070

prolactin receptor ND2 precursor - rat

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 10-Sep-1997
 C:Accession: A41070; I55417
 R:All, S.; Pellegrini, I.; Kelly, P.A.
 J. Biol. Chem. 266, 20110-20117, 1991
 A:Title: A prolactin-dependent immune cell line (NB2) expresses a mutant form of prolactin
 A:Reference number: A41070; MUID:92041834
 A:Accession: A41070
 A:Molecule type: mRNA
 A:Residues: 1-412 <ALI>
 A:Cross-references: GB:M74152; NID:g206389; PID:g206390
 R:O'Neil, K.D.; Yu-Lee, L.Y.
 J. Biol. Chem. 269, 26076-26082, 1994
 A:Title: Differential signal transduction of the short, NB2, and long prolactin receptor
 A:Reference number: I55417; MUID:95014432
 A:Accession: I55417
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-412 <RES>
 A:Cross-references: EMBL:U07567; NID:g641963; PID:g641964
 A:Experimental source: NB2-11C cell line
 C:Keywords: transmembrane protein

Query Match 13.98; Score 312; DB 2; Length 412;
 Best Local Similarity 35.48; Pred. No. 7.2e-18;
 Matches 80; Conservative 35; Mismatches 85; Indels 26; Gaps 10;

125 SILGSCLYVGLPEKPNISCSRNKMDLTCRWTPGAHGFTLHTNYSLKRLRWGOD 184
 15 SLKSGS-----PPKPEIHKCRSPDKETFTCMNPGDGG--LPTNLSLTSE--GEK 65
 185 NT--CEEHYTVGPHSCHLPND-LALFTPEIWEATNRLGSARSDVLTLDVLTDP 241
 66 TTTCPPDKTSGPNSCFSSKQYTSIMKYLITVATNQMSSSDPLDYVTIYEPEPP 125
 242 PDVHVSRYGLEDOLSRWV--SPPALKDF--LFOAKYQIRYVEDSVDMKVVDSNQ 296
 126 RNLLT-EVKOLKDKRTILVMKSPPTITDVTGFTMEYERLKEPEAEWE--IHTGHO 183
 297 TSCRGLKPGTYVFOVRCNPFGIYSGKRAIWESEHPTASTP 342
 184 TQFVFDLYGQKYLIVQTRCKP-----DHGYSRMSQSSVEMP 222

RESULT 10
 A29884
 prolactin receptor precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 20-Mar-1998
 C:Accession: A29884
 R:Boutin, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Ederly, M.; Shlrota, M.; Banville
 Cell 53, 69-77, 1988
 A:Title: Cloning and expression of the rat prolactin receptor, a member of the growth hc
 A:Reference number: A29884; MUID:88165035
 A:Accession: A29884
 A:Molecule type: mRNA
 A:Residues: 1-310 <BOU>
 A:Cross-references: GB:M19304; NID:g206364; PID:g206365
 C:Keywords: transmembrane protein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-310/Product: prolactin receptor #status predicted <MAT>

Query Match 13.98; Score 312; DB 2; Length 310;
 Best Local Similarity 35.48; Pred. No. 5e-18;
 Matches 80; Conservative 35; Mismatches 85; Indels 26; Gaps 10;

125 SILGSCLYVGLPEKPNISCSRNKMDLTCRWTPGAHGFTLHTNYSLKRLRWGOD 184
 15 SLKSGS-----PPKPEIHKCRSPDKETFTCMNPGDGG--LPTNLSLTSE--GEK 65
 185 NT--CEEHYTVGPHSCHLPND-LALFTPEIWEATNRLGSARSDVLTLDVLTDP 241

DB 66 TTTCPPDKTSGPNSCFSSKQYTSIMKYLITVATNQMSSSDPLDYVTIYEPEPP 125
 242 PDVHVSRYGLEDOLSRWV--SPPALKDF--LFOAKYQIRYVEDSVDMKVVDSNQ 296
 126 RNLLT-EVKOLKDKRTILVMKSPPTITDVTGFTMEYERLKEPEAEWE--IHTGHO 183
 297 TSCRGLKPGTYVFOVRCNPFGIYSGKRAIWESEHPTASTP 342
 184 TQFVFDLYGQKYLIVQTRCKP-----DHGYSRMSQSSVEMP 222

RESULT 11
 A30304

prolactin receptor 2 precursor - rabbit
 N:Alternate names: prolactin receptor, mammary gland
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Mar-1998
 C:Accession: A30304; A60380
 R:Ederly, M.; Jolicoeur, C.; Levi-Meyueis, C.; Dusanter-Fourt, I.; Petridou, B.; Bout
 Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116, 1989
 A:Title: Identification and sequence analysis of a second form of prolactin receptor
 A:Reference number: A30304; MUID:89184578
 A:Accession: A30304
 A:Molecule type: mRNA
 A:Residues: 1-616 <EDE>
 A:Cross-references: GB:J04510; NID:g165669; PID:g165670
 R:Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I.
 Int. J. Biochem. 22, 1089-1095, 1990
 A:Title: Purification and partial sequence of the rabbit mammary gland prolactin rece
 A:Reference number: A60380; MUID:91146782
 A:Accession: A60380

A:Molecule type: protein
 A:Residues: 41-58, 'x', 60-66-90-93, 'x', 95-96, 'x', 98-103, 'x', 105, 'NK', 108, 150-154, 'XX',
 A>Note: the amino end of the mature protein was blocked
 C:Keywords: blocked amino end; glycoprotein; transmembrane protein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-616/Product: prolactin receptor 2 #status predicted <MAT>
 F:235-258/Domain: transmembrane #status predicted <TM>
 F:59,104,132,347,389,411/Binding site: carbohydrate (Asn) (covalent) #status predicte

Query Match 13.7%; Score 307.5; DB 2; Length 616;
 Best Local Similarity 36.3%; Pred. No. 2.8e-17;
 Matches 77; Conservative 28; Mismatches 90; Indels 17; Gaps 7;

137 PPKFPNISCWSRNKMDLTCRWTPGAHGFTLHTNYSLKRLRWGODNTCEEHYTVGP 196
 27 PPKFPFIFKCRSEKETFTCMNPGDGG--LPTNLTLLYHKGEFTTHCCPDKITGGPN 84
 197 SCHI-PRDIALFTPEIWEATNRLGSARSDVLTLDVLTDPDPDVHVSRYGLEDQ 255
 85 SCFSSKHSIMYITVATNQMSSSDPLDYVTIYEPEPPVNLTL-EVKHPEDR 143
 256 LSVRWVS--SPPALKDF--LFOAKYQIRYVEDSVDMKVVDSNOTSCLAGLKPGTYV 310
 144 KPLVMKMLPELTIVDRSGMLTLQVEIRLKEPEAEWE--IHTGQGTQFNLISLYGQKY 202
 311 FVOVRCNPFGIYSGKRAIWESEHPTASTP 342
 203 LVQVRCNP-----DHGYSRMSQSSVEMP 222

RESULT 12

177524
 prolactin receptor precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 02-Aug-1996
 C:Accession: I77524
 R:Davis, J.A.; Linzer, D.I.H.
 Mol. Endocrinol. 3, 674-680, 1989
 A:Title: Expression of multiple forms of the prolactin receptor in mouse liver.
 A:Reference number: I57699; MUID:89261824

A:Accession: 177524
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-303 <RES>
 A:Cross-references: GB:M22958; NID:g200479; PID:g200480

Query Match 13.7%; Score 307.5; DB 2; Length 303;
 Best Local Similarity 32.6%; Pred. No. 1,1e-17;
 Matches 85; Conservative 37; Mismatches 92; Indels 47; Gaps 11;

90 LSRLNTSTLALANLNSRQSGDNLVCHARDSTIAGSCLYGLPEKPFNISCMSR 149
 1 MSSALAYMLYLISILNG--QS-----PPKPEIHRCRSP 34
 150 NMKDLTCRMTPGANGHGFELHTNYSLKYLRYGODNT--CEEHYVGPNSCHIPKD-LAL 206
 35 DKETFTCMWNPBGSDG--LPTNYSLTYSKE--GEKNYTECPDYKTSGPSNCFSPSKQYTSI 90
 207 FTPEIWEATNRLGASRSDVLTLDVYTTDPPDVHVSRYGLEDOLSVRWVS--PP 264
 91 WKIYITVNAATNEMGSSDPLVYDVYIYEPEPRNLT--EVKQLDKKTYLLWVWLP 149
 265 ALKDF---LEQAKQIRRYVEDSDVKVVDVSNQTSCLAGLKPFTYFVQVRCNPFGI 321
 150 TITDVTKGTFMEYEIRLKESEADEWE-IHFTGHQTFKVFYDLPGQKYLVOQTRCKP--- 206
 322 YGSKKAGINSEMSHPTAASP 342
 206 ----DHGYWSRMOEKSEIEIP 222

RESULT 13
 177525
 Prolactin receptor precursor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Aug-1996 #sequence-revision 02-Aug-1996 #text-change 02-Aug-1996
 C:Accession: 177525
 R:Davis, J.A.; Linzer, D.I.H.
 M:J. Endocrinol. 3, 674-680, 1989
 A:Title: Expression of multiple forms of the prolactin receptor in mouse liver.
 A:Reference number: 157699; MUID:89261824
 A:Accession: 177525
 A:Molecule type: mRNA
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Residues: 1-292 <RES>
 A:Cross-references: GB:M22959; NID:g200481; PID:g200482

Query Match 13.7%; Score 307.5; DB 2; Length 292;
 Best Local Similarity 32.6%; Pred. No. 1,1e-17;
 Matches 85; Conservative 37; Mismatches 92; Indels 47; Gaps 11;

90 LSRLNTSTLALANLNSRQSGDNLVCHARDSTIAGSCLYGLPEKPFNISCMSR 149
 1 MSSALAYMLYLISILNG--QS-----PPKPEIHRCRSP 34
 150 NMKDLTCRMTPGANGHGFELHTNYSLKYLRYGODNT--CEEHYVGPNSCHIPKD-LAL 206
 35 DKETFTCMWNPBGSDG--LPTNYSLTYSKE--GEKNYTECPDYKTSGPSNCFSPSKQYTSI 90
 207 FTPEIWEATNRLGASRSDVLTLDVYTTDPPDVHVSRYGLEDOLSVRWVS--PP 264
 91 WKIYITVNAATNEMGSSDPLVYDVYIYEPEPRNLT--EVKQLDKKTYLLWVWLP 149
 265 ALKDF---LEQAKQIRRYVEDSDVKVVDVSNQTSCLAGLKPFTYFVQVRCNPFGI 321
 150 TITDVTKGTFMEYEIRLKESEADEWE-IHFTGHQTFKVFYDLPGQKYLVOQTRCKP--- 206
 322 YGSKKAGINSEMSHPTAASP 342
 206 ----DHGYWSRMOEKSEIEIP 222

RESULT 14

Prolactin receptor, long form - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Aug-1996 #sequence-revision 02-Aug-1996 #text-change 29-Jan-1999
 C:Accession: 153269; J06671; S34356
 R:Clarke, D.L.; Linzer, D.I.H.
 Endocrinology 133, 224-232, 1993

A:Title: Changes in prolactin receptor expression during pregnancy in the mouse ovary
 A:Reference number: 153269; MUID:93307149
 A:Accession: 153269

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-608 <RES>
 A:Cross-references: GB:L14811; NID:g293769; PID:g293770
 R:Moore, R.C.; Oka, T.
 Gene 134, 263-265, 1993
 A:Title: Cloning and sequencing of the cDNA encoding the murine mammary gland long-form
 A:Reference number: J06671; MUID:94085788
 A:Accession: J06671
 A:Molecule type: mRNA
 A:Residues: 1-608 <MOO>
 A:Cross-references: GB:L13593; NID:g347398; PID:g347842
 R:Edery, M.; Pezet, A.; Nandi, S.; Kelly, P.A.
 Submitted to the EMBL Data Library, June 1993
 A:Description: Isolation and nucleotide sequence of a mouse cDNA prolactin receptor.
 A:Reference number: S34356
 A:Accession: S34356
 A:Molecule type: mRNA
 A:Residues: 1-557, 559-608 <EDE>
 A:Cross-references: EMBL:X13372; NID:g312696; PID:g312697
 C:Comment: Prolactin receptor have long form and short form which are resulted from a
 C:Comment: This long form receptor is capable of transducing a signal to milk protein
 C:Keywords: receptor; transmembrane protein
 F:230-253/Domin: transmembrane #status predicted <TM>

Query Match 13.7%; Score 307.5; DB 2; Length 608;
 Best Local Similarity 32.6%; Pred. No. 2,8e-17;
 Matches 85; Conservative 37; Mismatches 92; Indels 47; Gaps 11;

90 LSRLNTSTLALANLNSRQSGDNLVCHARDSTIAGSCLYGLPEKPFNISCMSR 149
 1 MSSALAYMLYLISILNG--QS-----PPKPEIHRCRSP 34
 150 NMKDLTCRMTPGANGHGFELHTNYSLKYLRYGODNT--CEEHYVGPNSCHIPKD-LAL 206
 35 DKETFTCMWNPBGSDG--LPTNYSLTYSKE--GEKNYTECPDYKTSGPSNCFSPSKQYTSI 90
 207 FTPEIWEATNRLGASRSDVLTLDVYTTDPPDVHVSRYGLEDOLSVRWVS--PP 264
 91 WKIYITVNAATNEMGSSDPLVYDVYIYEPEPRNLT--EVKQLDKKTYLLWVWLP 149
 265 ALKDF---LEQAKQIRRYVEDSDVKVVDVSNQTSCLAGLKPFTYFVQVRCNPFGI 321
 150 TITDVTKGTFMEYEIRLKESEADEWE-IHFTGHQTFKVFYDLPGQKYLVOQTRCKP--- 206
 322 YGSKKAGINSEMSHPTAASP 342
 206 ----DHGYWSRMOEKSEIEIP 222

RESULT 15

J01655
 Prolactin receptor precursor - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 30-Sep-1993 #sequence-revision 30-Sep-1993 #text-change 10-Sep-1997
 C:Accession: J01655
 R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
 Biochem. Biophys. Res. Commun. 188, 490-496, 1992
 A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA
 A:Reference number: J01655; MUID:93075121

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OM protein - protein search, using sw model

Run on: September 17, 1999, 03:10:11 ; Search time 35.09 Seconds

(without alignments)
332,710 Million cell updates/sec

Title: US-09-037-657-13

Sequence: 1 MPAGRGPVQASARRPPRL.....WRAMQSHKTRNYPRL 413

Scoring table: BLOSUM62

Searched: 77977 seqs, 28268293 residues

Database: Swissprot_37:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	331	14.7	622	1	PLRL_HUMAN
2	329	14.6	918	1	IL6B_HUMAN
3	319.5	14.2	917	1	IL6B_MOUSE
4	317.5	14.1	938	1	IL6B_RAT
5	314	13.9	830	1	IL6B_MOUSE
6	312	13.9	610	1	IL6B_MOUSE
7	307.5	13.7	608	1	IL6B_MOUSE
8	307.5	13.7	616	1	IL6B_MOUSE
9	306	13.6	831	1	IL6B_MOUSE
10	305	13.5	831	1	IL6B_MOUSE
11	303	13.5	831	1	IL6B_MOUSE
12	302.5	13.4	581	1	IL6B_MOUSE
13	261.5	11.6	630	1	IL6B_MOUSE
14	254.5	11.3	836	1	IL6B_MOUSE
15	252.5	11.2	837	1	IL6B_MOUSE
16	234	10.4	372	1	IL6B_MOUSE
17	222.5	9.9	372	1	IL6B_MOUSE
18	222.5	9.2	372	1	IL6B_MOUSE
19	203.5	8.9	460	1	IL6B_MOUSE
20	200.5	8.9	468	1	IL6B_MOUSE
21	196.5	8.7	462	1	IL6B_MOUSE
22	192.5	8.6	635	1	IL6B_MOUSE
23	191.5	8.5	1162	1	IL6B_MOUSE
24	190	8.4	1097	1	IL6B_MOUSE
25	190	8.4	625	1	IL6B_MOUSE
26	185	8.2	1092	1	IL6B_MOUSE
27	175	7.8	427	1	IL6B_MOUSE
28	174.5	7.8	1165	1	IL6B_MOUSE
29	170	7.6	888	1	IL6B_MOUSE
30	164.5	7.3	638	1	IL6B_MOUSE
31	158.5	7.0	508	1	IL6B_MOUSE
32	157	7.0	507	1	IL6B_MOUSE
33	156.5	7.0	507	1	IL6B_MOUSE
34	155	6.9	507	1	IL6B_MOUSE
35	151	6.7	638	1	IL6B_MOUSE
36	147	6.5	1040	1	IL6B_MOUSE
37	146.5	6.5	424	1	IL6B_MOUSE
38	145	6.4	634	1	IL6B_MOUSE
39	143.5	6.4	380	1	IL6B_MOUSE
40	143	6.4	638	1	IL6B_MOUSE
41	142	6.3	897	1	IL6B_MOUSE
42	140.5	6.2	850	1	IL6B_MOUSE
43	140.5	6.2	297	1	IL6B_MOUSE

ALIGNMENTS

44 139.5 6.2 608 1 GHR_CHICK
45 136.5 6.1 1036 1 AXOL_CHICK
002092 gallus gall
P28685 gallus gall

RESULT	ID	Query Match	Length	ID	Description
1	PLRL_HUMAN	14.7	622	1	PLRL_HUMAN
2	PLRL_HUMAN	14.6	918	1	IL6B_HUMAN
3	PLRL_HUMAN	14.2	917	1	IL6B_MOUSE
4	PLRL_HUMAN	14.1	938	1	IL6B_RAT
5	PLRL_HUMAN	13.9	830	1	IL6B_MOUSE
6	PLRL_HUMAN	13.9	610	1	IL6B_MOUSE
7	PLRL_HUMAN	13.7	608	1	IL6B_MOUSE
8	PLRL_HUMAN	13.7	616	1	IL6B_MOUSE
9	PLRL_HUMAN	13.6	831	1	IL6B_MOUSE
10	PLRL_HUMAN	13.5	831	1	IL6B_MOUSE
11	PLRL_HUMAN	13.5	831	1	IL6B_MOUSE
12	PLRL_HUMAN	13.4	581	1	IL6B_MOUSE
13	PLRL_HUMAN	11.6	630	1	IL6B_MOUSE
14	PLRL_HUMAN	11.3	836	1	IL6B_MOUSE
15	PLRL_HUMAN	11.2	837	1	IL6B_MOUSE
16	PLRL_HUMAN	10.4	372	1	IL6B_MOUSE
17	PLRL_HUMAN	9.9	372	1	IL6B_MOUSE
18	PLRL_HUMAN	9.2	372	1	IL6B_MOUSE
19	PLRL_HUMAN	8.9	460	1	IL6B_MOUSE
20	PLRL_HUMAN	8.9	468	1	IL6B_MOUSE
21	PLRL_HUMAN	8.7	462	1	IL6B_MOUSE
22	PLRL_HUMAN	8.6	635	1	IL6B_MOUSE
23	PLRL_HUMAN	8.5	1162	1	IL6B_MOUSE
24	PLRL_HUMAN	8.4	1097	1	IL6B_MOUSE
25	PLRL_HUMAN	8.4	625	1	IL6B_MOUSE
26	PLRL_HUMAN	8.2	1092	1	IL6B_MOUSE
27	PLRL_HUMAN	7.8	427	1	IL6B_MOUSE
28	PLRL_HUMAN	7.8	1165	1	IL6B_MOUSE
29	PLRL_HUMAN	7.6	888	1	IL6B_MOUSE
30	PLRL_HUMAN	7.3	638	1	IL6B_MOUSE
31	PLRL_HUMAN	7.0	508	1	IL6B_MOUSE
32	PLRL_HUMAN	7.0	507	1	IL6B_MOUSE
33	PLRL_HUMAN	7.0	507	1	IL6B_MOUSE
34	PLRL_HUMAN	6.9	507	1	IL6B_MOUSE
35	PLRL_HUMAN	6.7	638	1	IL6B_MOUSE
36	PLRL_HUMAN	6.5	1040	1	IL6B_MOUSE
37	PLRL_HUMAN	6.5	424	1	IL6B_MOUSE
38	PLRL_HUMAN	6.4	634	1	IL6B_MOUSE
39	PLRL_HUMAN	6.4	380	1	IL6B_MOUSE
40	PLRL_HUMAN	6.4	638	1	IL6B_MOUSE
41	PLRL_HUMAN	6.3	897	1	IL6B_MOUSE
42	PLRL_HUMAN	6.2	850	1	IL6B_MOUSE
43	PLRL_HUMAN	6.2	297	1	IL6B_MOUSE

Query Match 14.7% Score 331; DB 1; Length 622;
Best Local Similarity 37.5%; Pred. No. 1.2e-19;
Matches 84; Conservative 27; Mismatches 95; Indels 18; Gaps 8;

DR	PDB: 1BOU; 26-AUG-98.	
DR	PMID: 500694; -	
DR	PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.	
DR	PRIM: PF00041; fn3; 3.	
KW	RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL; REPEAT; 3D-STRUCTURE.	
KW	SIGNAL	1 22
FT	CHAIN	23 918
FT	DOMAIN	23 619
FT	TRANSMEM	620 641
FT	DOMAIN	642 918
FT	DOMAIN	26 120
FT	DOMAIN	124 222
FT	DOMAIN	223 324
FT	DOMAIN	325 423
FT	DOMAIN	424 517
FT	DOMAIN	518 613
FT	DOMAIN	725 755
FT	DISULFID	134 144
FT	DISULFID	172 182
FT	CARBOHYD	43 43
FT	CARBOHYD	83 83
FT	CARBOHYD	131 131
FT	CARBOHYD	137 137
FT	CARBOHYD	227 227
FT	CARBOHYD	379 379
FT	CARBOHYD	383 383
FT	CARBOHYD	390 390
FT	CARBOHYD	553 553
FT	CARBOHYD	564 564
DO	SEQUENCE	918 AA; 103522 MW; 7C0C6F05 CRC32;

IL6_MOUSE	RESULT	3
ID	IL6_MOUSE	STANDARD;
AC	C00560;	PT; 917 AA.
DT	01-FEB-1995	(REL. 31, CREATED)
DT	01-FEB-1995	(REL. 31, LAST SEQUENCE UPDATE)
DT	15-DEC-1998	(REL. 37, LAST ANNOTATION UPDATE)
DE	INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN-6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN I30) (GP130).	
GN	IL6ST.	
OS	MUS MUSCULUS (MOUSE).	

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIROGNATHI; MORIDAE; MORINAE; MUS.
 [1]
 SEQUENCE FROM N.A.
 RC STRAIN-ICR; TISSUE-MACROPHAGE;
 RX MEDLINE; 92291532.
 RA SAITO M., YOSHIDA K., HIBI M., TAGA T., KISHIMOTO T.;
 RT Molecular cloning of a murine IL-6 receptor-associated signal
 transducer, gp130, and its regulated expression in vivo.
 J. IMMUNOL. 148:4066-4071(1992).
 CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
 IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
 SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
 RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
 AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
 EMBRYONIC DEVELOPMENT.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- TISSUE SPECIFICITY: FOUND IN TISSUES SUCH AS BRAIN, HEART, THYMUS,
 SPLEEN, KIDNEY, LUNG AND LIVER. FOUND IN ALL THE CELL LINES TESTED
 EXCEPT BAF-B03. EXPRESSION NOT RESTRICTED TO IL-6-RESPONSIVE
 CELLS.
 CC -1- DEVELOPMENTAL STAGE: IN EMBRYONIC STEM CELLS IT IS FOUND FROM DAY
 6 OF GESTATION. IT REACHES A PEAK ON DAY 8 AND GRADUALLY DECLINES
 DURING THE REST OF EMBRYOGENESIS.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 CC EMBL; X62646; G840817;
 CC MGD; M83336; G193592;
 CC PROSITE; P500340; RECEPTOR_CYTOKINES_2; 1.
 CC PFM; P500041; fn3; 3.
 CC HSSP; P40189; 1BOU.
 CC RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
 CC REPEAT.
 CC SIGNAL.
 CC CHAIN.
 CC DOMAIN 1 23 917 22 POTENTIAL.
 CC DOMAIN 23 617 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
 CC TRANSMEM 618 639 EXTRACELLULAR (POTENTIAL).
 CC DOMAIN 640 917 POTENTIAL.
 CC DOMAIN 26 120 CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 124 220 IG-LIKE C2-TYPE DOMAIN.
 CC DOMAIN 221 322 FIBRONECTIN TYPE-III.
 CC DOMAIN 323 420 FIBRONECTIN TYPE-III.
 CC DOMAIN 422 515 FIBRONECTIN TYPE-III.
 CC DOMAIN 516 611 FIBRONECTIN TYPE-III.
 CC DOMAIN 723 741 SER-RICH.
 CC DISULFID 134 144 BY SIMILARITY.
 CC DISULFID 172 180 POTENTIAL.
 CC CARBOHYD 43 43 POTENTIAL.
 CC CARBOHYD 61 61 POTENTIAL.
 CC CARBOHYD 83 83 POTENTIAL.
 CC CARBOHYD 131 131 POTENTIAL.
 CC CARBOHYD 157 157 POTENTIAL.
 CC CARBOHYD 225 225 POTENTIAL.
 CC CARBOHYD 388 388 POTENTIAL.
 CC CARBOHYD 476 476 POTENTIAL.
 CC CARBOHYD 551 551 POTENTIAL.
 CC SEQUENCE 917 AA; 102452 MW; ASDCD259 CRC32;
 Query Match 14.2%; Score 319.5; DB 1; Length 917;

Best Local Similarity 29.6%; Pred. No. 1.8e-18;
 Matches 92; Conservative 50; Mismatches 146; Indels 23; Gaps 10;
 CC QY 46 ISPODPTLLIGSSLOATCSING---DTPGATAEGLYTWLNGRRRLPSELSRLNTSTALA 102
 CC DB 31 IYEPFVYVQSGNSFTALCYLKEACLOHYNNASIVYKTNHAAVPRQVYVINTTSVT 90
 CC QY 103 LANNGSGSGDNVCHANDGSLAAGSCLYVLPPEKPNISGSMNMDLCRTWPGA 162
 CC DB 91 FTDVYLVSVOLTCNLTSEFGIEQNVYGVTMISGPPDKPNTLCIVNEGNMLQOMPGR 150
 CC QY 163 HGEFTLNTSLKTKLWYOD -NICEHYTVGSHCHIKDLALFTPIEIVWATNRLG 221
 CC DB 151 -ETLETNTLSE--WAEKEPPDCSKHGT---SCWVSYMPYVNIIEVWEAENALG 203
 CC QY 222 SARSDVLTLLDVTTDPPDDVSVRGLEDQLSVRWSPALNKLFLQAKYQYRVR 281
 CC DB 204 KYSESEINFPVDKVKRTPYNNSTYSELSLKLKSWSGL--GGLDLDSDIQYRT 261
 CC QY 282 EDSYDKVY--DVSNOTICRLAGLPGTYFVQVNCNPFQIGSKRKGIMSWSHPTA 338
 CC DB 262 KDSYTWQVLEDTMSPTSFYQDLKPFYEVFRIR---SIKSGK-GYMSDWEENAS 316
 CC QY 339 AST--PRESEP 347
 CC DB 317 GTTYEDPSRP 327
 CC RESULT 4
 CC IL6B_RAT STANDARD; PRT; 918 AA.
 CC ID IL6B_RAT
 CC AC P40190;
 CC DT 01-FEB-1995 (REL. 31, CREATED)
 CC DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 CC DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 CC DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
 CC DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).
 CC GN IL6ST.
 CC OS RATTUS NORVEGICUS (RAT).
 CC OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC OC RODENTIA; SCIROGNATHI; MORIDAE; MORINAE; RATTUS.
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC TISSUE-LIVER;
 CC RX MEDLINE; 93052397.
 CC RA WANG Y., NESBITT J.E., FUENTES N.L., FULLER G.M.;
 CC RT Molecular cloning and characterization of the rat liver IL-6 signal
 CC RT transducing molecule, gp130.
 CC RT GENOMICS 14:666-672(1992).
 CC CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
 CC IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
 CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
 CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
 CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
 CC EMBRYONIC DEVELOPMENT (BY SIMILARITY).
 CC CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC CC -1- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS
 CC AND ENDOTHELIAL CELLS.
 CC CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE IG-LIKE DOMAIN.
 CC CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; M92340; -; NOT_ANNOTATED_CDS.

DR PIR: A44257; A44257.
 DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR PFAM; PF00041; fn3; 3.
 DR HSSP; P40189; 180U.
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
 REPEAT.
 FT SIGNAL 1 22
 FT CHAIN 23 918
 FT DOMAIN 23 618
 FT TRANSMEM 619 640
 FT DOMAIN 641 918
 FT DOMAIN 26 120
 FT DOMAIN 124 221
 FT DOMAIN 222 323
 FT DOMAIN 324 422
 FT DOMAIN 423 516
 FT DOMAIN 517 612
 FT DOMAIN 724 754
 FT DISULFID 134 144
 FT DISULFID 172 181
 FT CARBOHYD 43 43
 FT CARBOHYD 61 61
 FT CARBOHYD 83 83
 FT CARBOHYD 131 131
 FT CARBOHYD 137 157
 FT CARBOHYD 205 205
 FT CARBOHYD 226 226
 FT CARBOHYD 382 382
 FT CARBOHYD 389 389
 FT CARBOHYD 477 477
 FT CARBOHYD 552 552
 SQ SEQUENCE 918 AA; 102450 MW; BEDECD0 CRC32;

Query Match 14.1%; Score 317.5; DB 1; Length 918;
 Best Local Similarity 29.8%; Pred. No. 2,6e-18;

Matches 92; Conservative 51; Mismatches 145; Indels 21; Gaps 10;

QY 46 ISPOPTLLIGSSLOATCSING---DTPGATAGLWTLNGRLRPSLSESLRLNTSTIALA 102
 DB 31 IYEPFVVGSGSNFATCLKREKCLQVSVNATYIWKNNHVAVREQVTVINRTASSVT 90
 QY 103 LANLNGSRQSGDNLYCHARDGSLAGSCLYVGLPEPKFNISCSRNKDKLTCTWTPGA 162
 DB 91 FTDVVFQNLTCNLTISFGQIBQNYGIRILSGYPPDPTNLSCLYNEGKNLQDLPGR 150
 QY 163 HGETLHTYSLKYLKRWGOD--NCEHYHTGPHSCHLPKDLAFTPEIYVETATNRLG 221
 DB 151 --ETYLEYVTLKSE--WATERKFPDCRKH--GTSSCMAGYTPPIYFVNLEVVAEMLAG 204
 QY 222 SARSDVLTLDVAVVTTDPPDVHVSRYGLEDQLSVRVSPALKDFFLOAKYQIRYV 281
 DB 205 NVSSSEINPDYKXKPSPHLSVTNSBELSILKLANVNSGL--DSLRLKSDIQRT 262
 QY 282 EDSDVMKVV---DVSNOTSCLAGIKPQTVYFVYRCNPFQIYSGKAGIWSHPTGA 338
 DB 263 KDASTWIOVPLEDTVSPRSTFVODLKPTETVEYFRLR---SIKENGR-GYSDMSSE-EA 316
 QY 339 ASTPRSERP 347
 DB 317 SGTIEDRP 325

RESULT 5

PRLR COLLI STANDARD: PRT: 830 AA.

AC 090374;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
 OS PRLR.
 OS COLUMBA LIVIA (DOMESTIC PIGEON).

CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
 CC NEOGNATHAE; COLUMBIFORMES; COLUMBIDAE; COLUMBA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-CROPSAC;
 RX MEDLINE; 94283267.
 RA CHEN X., HORSEMAN N.D.;
 RT "Cloning, expression, and mutational analysis of the pigeon prolactin receptor".
 RL ENDOCRINOLOGY 135:269-276(1994).
 RT -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -----
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 CC -----

DR EMBL; U07694; G466382;
 DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 2.
 DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 2.
 DR PFAM; PF00041; fn3; 4.
 DR HSSP; P16471; 1BP3.
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
 FT SIGNAL 1 23
 FT CHAIN 24 830
 FT DOMAIN 24 439
 FT TRANSMEM 440 460
 FT DOMAIN 461 830
 FT DOMAIN 25 122
 FT DOMAIN 123 226
 FT DOMAIN 229 326
 FT DOMAIN 327 429
 FT DISULFID 36 46
 FT DISULFID 75 86
 FT CARBOHYD 59 59
 FT CARBOHYD 91 91
 FT CARBOHYD 100 100
 FT CARBOHYD 112 112
 FT CARBOHYD 132 132
 FT CARBOHYD 263 263
 FT CARBOHYD 304 304
 FT CARBOHYD 316 316
 FT CARBOHYD 336 336
 SQ SEQUENCE 830 AA; 94507 MW; 5EPAD51 CRC32;

Query Match 13.9%; Score 314; DB 1; Length 830;
 Best Local Similarity 37.1%; Pred. No. 4.4e-18;
 Matches 76; Conservative 29; Mismatches 82; Indels 18; Gaps 8;

QY 137 PPEKPFNISCWRNKKDLTCRTPGAHGETFLH--TNYSLKYLKRWYGDNTCEETHVGP 195
 DB 231 PPEKPTIIRKSPPEKETFTCWKKPSSDGG---HPTNYTLKSKSEGEERYECPDYKTAGP 287
 QY 196 HSCHT--PRDLAFTPEIYVETATNRLGARSQVLTLDVAVTTPDPPDV--HVSRYGGL 252
 DB 288 NSCFDKKHTSWITNYITVATNLTGNSVSDPLVDTYIVQDPPVNVLELTKTVNR 347
 QY 253 EDQLSVRVNSPALKDF---LFOAKYQIRYVEDSDVMKVVDDVSNQTSCLAGIKPQTV 309
 DB 348 KPYVLVLTN--SPPPLADVNSGTLTLDYELRLRPEAEEMETI--FVGQOYHYMFLSLNPKK 405
 QY 310 YFVYVRCNPFQIYSGKAGIWSHPTGA 334
 DB 406 YIVQIHCKP-----DHHGSWSHWS 424

RESULT 6

PRIR_RAT ID STANDARD: PRT: 610 AA.

PRIR_RAT ID STANDARD: PRT: 610 AA.

05710: 063451: 062832: 064274: 064479:

01-NOV-1988 (REL. 09, CREATED)

01-NOV-1987 (REL. 35, LAST SEQUENCE UPDATE)

01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

PROLACTIN RECEPTOR PRECURSOR (PRL-R) (LACTOGEN RECEPTOR).

RATUS NORVEGICUS (RAT).

EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:

RODENTIA: SCIUROGNATHI: MORIDAE: MORINAE: RATIUS.

SEQUENCE FROM N.A.

SHIROTA M., BANVILLE D., ALI S., JOLICOEUR C., BOUTIN J.M.,

EDERY M., DJIANE J., KELLY P.A.:

"Expression of two forms of prolactin receptor in rat ovary and

liver."

MOL. ENDOCRINOL. 4:1136-1143(1990).

(2)

SEQUENCE FROM N.A. (LONG FORM AND SHORT FORM).

STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY;

MEDLINE: 90241201.

ZHANG R., BUCCKO E., TSAI-MORRIS C.H., HU Z.Z., DUFAU M.L.:

"Isolation and characterization of two novel rat ovarian lactogen

receptor cDNA species."

BIOCHEM. BIOPHYS. RES. COMMUN. 168:415-422(1990).

(3)

SEQUENCE OF 281-610 FROM N.A.

BANVILLE D., STOCO R., MURPHY K.K., BOLE Y., KELLY P.A.:

SUBMITTED (MAR-1996) TO EMBL/GENBANK/DBJ DATA BANKS.

(4)

SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (MEDIUM FORM).

TISSUE-LIVER;

MEDLINE: 88165059.

BOUTIN J.-M., JOLICOEUR C., OKAMURA H., GAGNON J., EDERY M.,

SHIROTA M., BANVILLE D., DUSANTER-FOURTE I., DJIANE J., KELLY P.A.:

"Cloning and expression of the rat prolactin receptor, a member of

the growth hormone/prolactin receptor gene family."

CELL. 53:69-77(1988).

(5)

SEQUENCE FROM N.A. (FORM NB2).

TISSUE-LYMPHOMA;

MEDLINE: 92041834.

ALI S., PELLIGRINI I., KELLY P.A.:

"A prolactin-dependent immune cell line (Nb2) expresses a mutant form

of prolactin receptor."

J. BIOL. CHEM. 266:20110-20117(1991).

(6)

SEQUENCE FROM N.A. (FORM NB2).

MEDLINE: 95014432.

O'NEAL K.D., YU-LEE L.Y.:

"Differential signal transduction of the short, Nb2, and long

prolactin receptors. Activation of interferon regulatory factor-1 and

cell proliferation."

J. BIOL. CHEM. 269:26076-26082(1994).

(7)

EDUCATION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE

PROLACTIN.

-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-1- ALTERNATIVE PRODUCTS: DIFFERENT FORMS ARE PRODUCED BY ALTERNATIVE

SPLICING OF THE PRLR GENE.

-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

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CC

EMBL: M57668: G206367: -

DR EMBL: M34083: G205123: -

DR EMBL: L48060: G1019651: -

DR EMBL: U34730: G1238859: -

DR EMBL: M19304: G206365: -

DR EMBL: M74152: G206390: -

DR EMBL: U07567: G641864: -

DR PIR: A29884: A29884: -

DR POSITE: P500241: RECEPTOR_CYTOKINES_1: 1.

DR POSITE: P500340: RECEPTOR_CYTOKINES_2: 1.

DR PFAM: PF00041: fn3: 2.

DR HSP: P16471: 1BP3

KW RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL, REPEAT;

KW ALTERNATIVE SPLICING.

FT SIGNAL 1 19

FT CHAIN 20 610

FT DOMAIN 20 229

FT TRANSMEM 230 253

FT DOMAIN 254 610

FT DOMAIN 20 117

FT DOMAIN 119 222

FT DISULFID 31 41

FT DISULFID 70 81

FT CARBOHYD 54 54

FT CARBOHYD 99 99

FT CARBOHYD 127 127

FT VARSPLIC 131 150

FT VARSPLIC 151 610

FT VARSPLIC 281 310

FT VARSPLIC 311 610

FT VARSPLIC 342 539

FT CONFLICT 236 236

FT CONFLICT 345 345

FT CONFLICT 465 465

FT CONFLICT 466 466

FT CONFLICT 469 469

FT CONFLICT 541 541

FT CONFLICT 555 555

SO SEQUENCE 610 AA: 68599 MW: C579BC43 CRC32;

POTENTIAL.

EVOLKDKTYLWVKSPPT -> DYRMEVSCQENALPKSA

KLN (IN SHORT FORM).

MISSING (IN SHORT FORM).

KKSEELSLALACQDPPTSDDEDLVEFL ->

TGSPSKRYDLVLAIPGGFKQKLDNAGELDY (IN

MEDIUM FORM).

MISSING (IN MEDIUM FORM).

MISSING (IN FORM NB2).

V -> V (IN REF. 2).

G -> V (IN REF. 2).

E -> K (IN REF. 1).

Q -> E (IN REF. 1).

A -> G (IN REF. 2).

T -> M (IN REF. 2).

Q -> K (IN REF. 1).

Query Match 13.9%; Score 312; DB 1; Length 610;

Best Local Similarity 35.4%; Pred. No. 4.3e-18;

Matches 80; Conservative 35; Mismatches 85; Indels 26; Gaps 10;

QY 125 SIAGSCLVGLPPEKPFNISCWSRMKDLCTCRWPGAGGEFLHTNYSLKTKLRWYGD 184

DB 15 SILKGS-----PPGKPELHKCRSPKKEFTCWANPGIDGG--LPTNLSLTYSKE--GSK 65

QY 185 NT--CEEYTVGPHSCHPRD-LAETPYEIVWEATNIRGSASDYLITDVLVYTTDP 241

DB 66 TYEECPDYKTSGFNSCFSEFKQYTSIKWYIITVNAITNGMSSSDPLVYVYIEPPEP 125

QY 242 PNYHNSRVGGLDQLSVKRV--SPRLADF---LQAKIQIRYEDSVYDKRVVDVSNQ 296

DB 126 RWLTL-EYQALDKKTYLWVWVSPPTIIDVKTGTFMEIEILKPEEAEME--IHTGHQ 183

QY 297 TSCRLAGLKPGTVYVQVQNCNPFGLYGSKAGIWEWSHPTAASP 342

DB 184 TQFKYFDLYPGOKYIVQRCRP-----DHGIYRWQSSSEVEMP 222

RESULT 7

PRIR_MOUSE ID STANDARD: PRT: 608 AA.

AC 008501: 062099: P15213: P15212:

DT 01-APR-1980 (REL. 14, CREATED)

DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)

DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
 GN PRL.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 RN KODENTIA; SCIODONTIA; MORIDAE; MORINAE; MUS.
 (1)
 RP SEQUENCE FROM N.A. (FORM PRL-R3).
 RC STRAIN-3H; TISSUE-MAMMARY GLAND;
 RX MEDLINE: 94085788.
 RA MOORE R.C., OKA T.;
 RT Cloning and sequencing of the cDNA encoding the murine mammary gland
 RT long-form prolactin receptor.";
 RL GENE 134:263-265(1993).
 (2)
 RN SEQUENCE FROM N.A. (FORM PRL-R3).
 RP STRAIN-SWISS WEBSTER; TISSUE-LIVER.
 RX MEDLINE: 93307149.
 RA CLARKE D.L., LINZER D.I.H.;
 RT "Changes in prolactin receptor expression during pregnancy in the
 RT mouse ovary.";
 RL ENDOCRINOLOGY 133:224-232(1993).
 (3)
 RN SEQUENCE FROM N.A. (FORM PRL-R3).
 RA SASAKI M.;
 RT SUBMITTED (JUL-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
 (4)
 RN SEQUENCE FROM N.A. (FORM PRL-R3).
 RP STRAIN-BALB/C; TISSUE-MAMMARY GLAND;
 RA EDERY M., PEZET A., NANDI S., KELLY P.A.;
 RT SUBMITTED (JUN-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
 (5)
 RP SEQUENCE FROM N.A. (FORMS PRL-R2 AND PRL-R1).
 RC STRAIN-SWISS WEBSTER; TISSUE-LIVER;
 RX MEDLINE: 89261824.
 RA DAVIS J.A., LINZER D.I.H.;
 RT Expression of multiple forms of the prolactin receptor in mouse
 RT liver.";
 RL MOL. ENDOCRINOLOGY 3:674-680(1989).
 (1)
 CC FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN. AS WELL AS PLACENTAL LACTOGEN I AND II.
 (1)
 CC SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 (1)
 CC ALTERNATIVE PRODUCTS: THREE FORMS, PRL-R1, PRL-R2 AND PRL-R3
 CC (SHOWN HERE) ARE PRODUCED BY ALTERNATIVE SPLICING OF THE PRLR
 CC GENE.
 (1)
 CC SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 (1)
 CC SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 (1)
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 CC or send an email to license@isb-sib.ch).
 (1)
 CC EMBL: L13593; G347842;
 DR EMBL: L14811; G293770;
 DR EMBL: D10214; G220576;
 DR EMBL: X73372; G312697;
 DR EMBL: M22959; G200482;
 DR EMBL: M22958; G200480;
 DR PIR: J10671; J10671.
 DR MGI: 97763; PRLR.
 DR PROSITE: PS00341; RECEPTOR_CYTOKINES_1;
 DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; FALSE_NEG.
 DR PIR: P00041; fn3; 2.
 DR HSSP: P16471; 1BP3.
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT;
 FT ALTERNATIVE SPLICING.
 FT CHAIN 1 19 POTENTIAL.
 FT DOMAIN 20 608 PROLACTIN RECEPTOR.
 FT TRANSMEM 230 253 EXTRACELLULAR (BY SIMILARITY).
 CC BY SIMILARITY.

FT DOMAIN 254 608 CYTOPLASMIC (BY SIMILARITY).
 FT DOMAIN 20 117 FIBRONECTIN TYPE-III.
 FT DOMAIN 119 222 FIBRONECTIN TYPE-III.
 FT DISULFID 31 41 BY SIMILARITY.
 FT DISULFID 70 81 BY SIMILARITY.
 FT CARBOHYD 54 54 POTENTIAL.
 FT CARBOHYD 99 99 POTENTIAL.
 FT CARBOHYD 127 127 POTENTIAL.
 FT VARSPLIC 281 292 MISSING (IN PRL-R2).
 FT VARSPLIC 293 608 MISSING (IN PRL-R1).
 FT VARSPLIC 281 303 MISSING (IN PRL-R1).
 FT VARSPLIC 304 608 MISSING (IN REF. 2).
 FT CONFLICT 558 558 L->F (IN REF. 2).
 FT SEQUENCE 608 AA; 68240 MW; AA601E67 CRC32;
 SQ
 Query Match 13.7%; Score 307.5; DB 1; Length 608;
 Best Local Similarity 32.6%; Pred. No. 1e-17;
 Matches 85; Conservative 37; Mismatches 92; Indels 47; Gaps 11;
 QY 90 LSRLLNTSTLALALNNGSSROSGDNLVCHARDSTLAGSCLVGLPEKPFNISCWR 149
 DB 1 MSSALAYMLVLSISLNG--QS-----PGKPEIHCRCSP 34
 QY 150 NKKDLTCRWTPGAGHETPLNTYSLKXKRWYGODNT--CEEXHYVGRPHSCHRPD-LAL 206
 DB 35 DETETTCWNPSSDGG--LPTNYSLSYKRE--GEKNTYECPKYKSGPSCFESQYTSI 90
 QY 207 FPEYIWEATNRLSANSADVLTLDVYTTDPDPDVHVSAGLEDDLSVRWVS--PP 264
 DB 91 WIIYIITVATNEMSSSTSDPLVYDYVYVEEPPRNLT-LVKKLKKDKKTLTKWKLPP 149
 QY 265 AKDP---LFOAKYQIRRRVEDSVDMKVVDVSNQTSCHLAKGKGYVGVRCNPFGI 321
 DB 150 RTIDVKTGFTWEYRIIRLKESEADEWE-LHFGHOTQFVFLYPGOKYLVOTRCKP--- 206
 QY 322 YSKKAGTSMSESHPTASTP 342
 DB 206 ---DHGWSRWGQKSEIETP 222
 RESULT 8
 PRLR_RABIT STANDARD; PRT; 616 AA.
 AC P14787;
 DT 01-APR-1990 (REL. 14, CREATED)
 DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
 GN PRLR.
 OS ORCTOLAGUS CUNICULUS (RABBIT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC LAGOMORPHA; LEPORIDAE; ORCTOLAGUS.
 (1)
 RN SEQUENCE FROM N.A.
 RP TISSUE-MAMMARY GLAND;
 RX MEDLINE: 89184578.
 RA EDERY M., JOLICOEUR C., LEVI-MEYRUEIS C., DUSANTER-FOUR I.,
 RA PETRIDOU B., BOUYIN J.M., LESOURE L., KELLY P.A., DJIANE J.;
 RT "Identification and sequence analysis of a second form of prolactin
 RT receptor by molecular cloning of complementary DNA from rabbit
 RT mammary gland.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 86:2112-2116(1989).
 (2)
 RN 3D-STRUCTURE MODELLING OF 30-228.
 RP MEDLINE: 97248733.
 RA HALABY D., THOREAU E., DJIANE J., MORROW J.P.;
 RT "Homology modelling of rabbit prolactin hormone complexed with its
 RT receptor.";
 RL PROTEINS 27:459-468(1997).
 CC FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: J04510; G165670; -
 CC PIR: A30304; A30304.
 CC DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
 CC DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 CC DR PFM: PFO0041; fn3; 2.
 CC DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT; 3D-STRUCTURE.
 CC FT SIGNAL 1 24
 CC FT CHAIN 1 24
 CC FT FT 25 616
 CC FT FT 25 234
 CC FT FT 25 258
 CC FT FT 259 616
 CC FT FT 25 122
 CC FT FT 124 227
 CC FT FT 36 46
 CC FT FT 75 86
 CC FT FT 59 59
 CC FT FT 104 104
 CC FT FT 132 132
 CC FT SEQUENCE 616 AA; 68840 MW; FB6170B1 CRC32;
 CC -----
 CC Query Match 13.7%; Score 307.5; DB 1; Length 616;
 CC Best Local Similarity 36.3%; Pred. No. 1e-17; Indels 17; Gaps 7;
 CC Matches 77; Conservative 28; Mismatches 90;
 CC Y 137 PEKPPNISCWSNMKDLTCRWTPGAHGETFLHTNYSLKRLMYGQDNCEHYHYP 196
 CC Y 27 PEKPEIFRCRSEPEKFTFCWMPRGADG--LPTNTLYTHKGERITHCPRDKTGSPN 84
 CC Y 197 SCGHI-PKDLALFTPYEIMVETNRLGSASDVLTLDVLDVTTDPPDVHVSRYGLEDQ 255
 CC Y 85 SCYFSKHTSTYITITVATNOMGSVSDPRYVDVTVIYEPDPVNNLT-EVKRDEDR 143
 CC Y 256 LSVRWVS--PALKDF---LFOAKYQIRYVEDSVDMKYVDVSNQTSCLAGLKGTYV 310
 CC Y 144 KPLVWKMPLPLVDVRSGLTLQYETRLKPEKAAEME-TTFAGQOTOFKILSLYPGQKY 202
 CC Y 311 FVOVRCNPFGIYSGKAGIWMSESHPTASTP 342
 CC Y 203 LVQVRCKP-----DHGFWMSVMSPESSIOIP 227
 CC -----
 CC RESULT 9
 CC PIR: CHICK STANDARD: PRT: 831 AA.
 CC D 004594;
 CC T 01-JUN-1994 (REL. 29, CREATED)
 CC T 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
 CC T 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 CC P PROLACTIN RECEPTOR PRECURSOR (PRL-R) (CDRLP).
 CC P PRLR.
 CC P GALLUS GALLUS (CHICKEN).
 CC P EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: ARCHOSAURIA: AVES:
 CC P NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
 CC P [1]
 CC P SEQUENCE FROM N.A.
 CC P STRAIN-WHITE LECHORN; TISSUE-KIDNEY;
 CC P MEDLINE: 93075121.
 CC P TANAKA M., MAEDA K., OKUBO T., NAKASHIMA K.;
 CC P "Double antenna structure of chicken prolactin receptor deduced from

FT the cDNA sequence."
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 168:490-496(1992).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: D13154; G222849; -
 CC PIR: J01655; J01655.
 CC DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 2.
 CC DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 2.
 CC DR PFM: PFO0041; fn3; 4.
 CC DR HSP: P16471; 1BP3.
 CC DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
 CC FT SIGNAL 1 23
 CC FT CHAIN 1 23
 CC FT FT 24 831
 CC FT FT 24 438
 CC FT FT 439 459
 CC FT FT 460 831
 CC FT FT 25 122
 CC FT FT 123 225
 CC FT FT 228 325
 CC FT FT 326 428
 CC FT FT 36 46
 CC FT FT 75 86
 CC FT FT 59 59
 CC FT FT 91 91
 CC FT FT 100 100
 CC FT FT 112 112
 CC FT FT 132 132
 CC FT FT 262 262
 CC FT FT 303 303
 CC FT FT 315 315
 CC FT FT 335 335
 CC FT SEQUENCE 831 AA; 94102 MW; B977BF07 CRC32;
 CC -----
 CC Query Match 13.6%; Score 306; DB 1; Length 831;
 CC Best Local Similarity 35.0%; Pred. No. 2e-17; Indels 18; Gaps 8;
 CC Matches 76; Conservative 27; Mismatches 96;
 CC Y 137 PEKPPNISCWSNMKDLTCRWTPGAHGETFLH-TNYSLKRLMYGQDNCEHYHYP 195
 CC Y 230 PEKPEIFRCRSEPEKFTFCWMPRGDGG--HPTNTLYLTSKEEEOYECDPYTAGP 286
 CC Y 196 HSCHI-PKDLALFTPYEIMVETNRLGSASDVLTLDVLDVTTDPPDVHVSRYGLEDQ 252
 CC Y 287 NSCYFDKHTSTYITITVATNOMGSVSDPRYVDVTVIYQPPVANNVLELKKPINR 346
 CC Y 253 EQQLSVRWVSPALKDF---LFOAKYQIRYVEDSVDMKYVDVSNQTSCLAGLKGPTV 309
 CC Y 347 KPLVLTW-SPPPLADVRSGLTLQYETRLKPEEKEEWETI-FVQGOQYQKMFSLNPKK 404
 CC Y 310 FVOVRCNPFGIYSGKAGIWMSESHPTASTPSSR 346
 CC Y 405 YIIQIHCKP-----DHGMSSEMSSENYIOPNDR 435
 CC -----
 CC RESULT 10
 CC PIR: MELGA STANDARD: PRT: 831 AA.
 CC ID 091094; 091091; 091092;
 CC AC 091094; 091091; 091092;
 CC DT 01-NOV-1997 (REL. 35, CREATED)
 CC DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

QY 253 EDQSLVWVSPSPAKDF----LQAKYIIRYVEQSVMKVVDVDSNQSCHLAKIPQTV 309
 DB 347 KPYMLM-W-SPPPLADVRSGMLTIDYELRLKPEGEHEM-Y-FVGGQGYQYMFSLNPKX 404
 QY 310 YFVQVRCNPEGIYSKKAIGVSEWSHPTASTPSER 346
 DB 405 YVIOHCKP-----DHGGSWSESSSENYIEIPNDFR 435
 RESULT 11
 PRIR CEREL STANDARD; PRT; 561 AA.
 AC Q28235;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
 GN PRLR.
 OS CERVUS ELAPHUS (RED DEER).
 OC EURIOACOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC ARTIODACTYLA; RUMINANTIA; PECORA; CERVIDAE; CERVIDAE; CERVINAE;
 OC CERVUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER;
 RX MEDLINE; 96030711.
 RA CLARKE L.A., EDERY M., LOUDON A.S., RANDALL V.A., POSTEL-VINAY M.C.,
 RA KELLY P.A., JABBOUR H.N.,
 RT "Expression of the prolactin receptor gene during the breeding and
 RT non-breeding seasons in red deer (Cervus elaphus): evidence for the
 RT expression of two forms in the testis".
 RL J. ENDOCRINOL. 146:313-321(1995).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -----
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 CC or send an email to license@isb.slb.ch).
 CC -----
 DR EMBL; X94953; E218406; -
 DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
 DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR PFM; PFO0041; fn3; 2.
 DR HSSP; P14787; IAN3.
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
 FT SIGNAL 1 24
 FT CHAIN 25 581
 FT DOMAIN 25 234
 FT TRANSMEM 235 558
 FT DOMAIN 25 581
 FT DOMAIN 123 227
 FT DISULFID 36 46
 FT DISULFID 75 86
 FT CARBOHYD 59 59
 FT CARBOHYD 132 132
 FT CARBOHYD 233 233
 SEQUENCE 561 AA; 65159 MW; 721F0366 CRC32;
 Query Match 13.5%; Score 303; DB 1; Length 581;
 Best Local Similarity 33.6%; Pred. No. 2.2e-17;
 Matches 76; Conservative 36; Mismatches 92; Indels 22; Gaps 8;
 123 DGSIIAGSLYGLDPEKPFNISCWSRNKKDITCMTDGAHGCTFLHNTYSLIKYLRNYG 182

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Db 18 NSLNGOS-----PRKRIKCRSPGKETFTCMWEPGSDG--LPTNTLYHHEGET 70
OY 183 QONTCEYHFTVGPSPHSCHI-PKDLALFTPYEIVEATNRLGASARDVLTLDLVYTTDP 241
Db 71 LIHECPDYKGTGPNCTYFSKHTSIKIKIYITVNAINMGVSSSDPLYDYVYIPEPP 130
OY 242 PDVHVSRRVGGLEDQLSVRVVS--PPALKDF--LFOAKQIIRYRVEDSVDMKVVDSVNO 296
Db 131 ANLTLT-ELKHPRDRPRYLTIKWFPPILLTDVKSQWFMIOYEIRLKPETADWE-IHFAAQ 188
OY 297 TSCRLAGLKPGTVFYVQVRCNPGIISGSKKAGIWSMSHPTAASP 342
Db 189 TOLKIFSLYFGOKIYVQVCKP-----DHGIWSEMSPESSIQIP 227

RESULT 12
PRLR BOVIN STANDARD. PRT: 581 AA.
AC 028172:
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
PRLR.
OS BOS TAURUS (BOVINE).
OC EDUARIOTA; METAQOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVIDEA; BOVINAE; BOS.
RN [1]
RP SEQUENCE FROM N. A.
RX TISSUE-ENDOMETRIUM;
RX MEDLINE; 93246019.
RA SCOTT P., KESSLER M.A., SCHULER L.A.;
RT "Molecular cloning of the bovine prolactin receptor and distribution
of prolactin and growth hormone receptor transcripts in fetal and
uterio-placental tissues."
RL MOL. CELL. ENDOCRINOL. 89:47-58(1992).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
PROLACTIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC
CC EMBL; L02549; G13618;
CC PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
CC PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
CC PFM: PFM0041; fn3; 2.
CC HSP: P14787; IAN3.
CC KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
CC FT SIGNAL 1 24 POTENTIAL.
CC FT CHAIN 25 581 PROLACTIN RECEPTOR.
CC FT DOMAIN 25 234 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 235 258 POTENTIAL.
CC FT DOMAIN 259 581 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 25 122 FIBRONECTIN TYPE-III.
CC FT DOMAIN 123 227 FIBRONECTIN TYPE-III.
CC FT DISULFID 36 46 BY SIMILARITY.
CC FT DISULFID 75 86 BY SIMILARITY.
CC FT CARBOHYD 59 59 POTENTIAL.
CC FT CARBOHYD 132 132 POTENTIAL.
CC SO SEQUENCE 581 AA; 65153 MW; COECAOA2 CRC32;

Query Match 13.48; Score 302.5; DB 1; Length 581;
Best Local Similarity 31.98; Pred. No. 2,4e-17;
Matches 83; Conservative 38; Mismatches 92; Indels 47; Gaps 10;

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OY 91 SRLNTSLALANINGSGROGNDLVCHARGDILASCLYGLPPKPNISWMSN 150
Db 7 SRVFTLLFLVSLNG--QS-----PPEKPKLYKCRSPG 40
OY 151 MKDLNCRMTFGARGFTFLNTSLKYLKRMYGODNTCEEHTVGPSPHSCHI-PKDLALFTP 209
Db 41 KEFTICWMEPGADG--LPTNTLYHHEGETLIHECPDYKGTGPNCTYFSKHTSIKIKI 98
OY 210 YEIWEATNRLGASARDVLTLDLVYTTDPPDVHVSRRVGGLEDQLSVRV--SPPALK 267
Db 99 YITVNAINMGVSSSDPLYVYTYIPEPPANLTL-ELKHPRDRKPYLTIKMSHPTMT 157
OY 268 D-----FLFOAKQIIRYRVEDSVDMKVVDSVNOISCRLAGLKPGTVFYVQVRCNPGIY 322
Db 158 DVKSGWFTIO--YEIRLKEKATDWE-THFTLKQOLKIFNLPGOKIYVQVCKRP----- 211
OY 323 GSKKAGIWSMSHPTAASP 342
Db 211 ---DHGIWSEMSPESSIQIP 227

RESULT 13
PRLR ORENI STANDARD. PRT: 630 AA.
AC 091513:
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
PRLR.
OS OROCHOMYS NITOTICUS (NILE TILAPIA) (TILAPIA NITOTICA).
OC EDUARIOTA; METAQOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
OC TELEOSTEI; EUTELEOSTEI; ACANTHOPTERYGII; PERCOMORPHA; PERCIFORMES;
OC LABROIDEI; CICHLIDAE; TILAPIA.
RN [1]
RP SEQUENCE FROM N. A.
RX TISSUE-KIDNEY;
RX MEDLINE; 95320210.
RA SANDRA O., SOHM F., DE LUZE A., PRUNET P., EDERY M., KELLY P.A.;
RT "Expression cloning of a cDNA encoding a fish prolactin receptor."
RL PROC. NATL. ACAD. SCI. U.S.A. 92:6037-6041(1995).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
PROLACTIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC
CC EMBL; L34783; G903847;
CC PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
CC PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
CC PFM: PFM0041; fn3; 2.
CC HSP: P16471; IAP3.
CC KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
CC FT SIGNAL 1 23 BY SIMILARITY.
CC FT CHAIN 24 630 PROLACTIN RECEPTOR.
CC FT DOMAIN 24 234 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 235 258 POTENTIAL.
CC FT DOMAIN 259 630 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 124 228 FIBRONECTIN TYPE-III.
CC FT DISULFID 37 47 BY SIMILARITY.
CC FT DISULFID 76 87 BY SIMILARITY.
CC FT CARBOHYD 92 92 POTENTIAL.
CC FT CARBOHYD 101 101 POTENTIAL.

```

RT		moltf of the granulocyte colony-stimulating factor receptor and its interaction with ligand."
RL	NAT.	STRUCT. BIOL. 4:498-503(1997).
RN	[6]	
RP	3D-STRUCTURE MODELLING OF	125-331.
RX	MEDLINE:	98037802.
RA	LAYTON J.E., IARIA J., SMITH D.K., TREUTLEIN H.R.;	
RR	"Identification of a ligand-binding site on the granulocyte colony-	
RT	stimulating factor receptor by molecular modeling and mutagenesis";	
RL	J. BIOC. CHEM. 272:29735-29741(1997).	
CC	-1- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR (G-CSF). IN ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION EVENTS AT THE CELL SURFACE.	
CC	-1- SUBUNIT: DIMER (PROBABLY).	
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE GCSFR-2 FORM, WHICH LACKS THE TRANSMEMBRANE DOMAIN, MAY REPRESENT A SOLUBLE FORM OF THE RECEPTOR.	
CC	-1- TISSUE SPECIFICITY: ONE OR SEVERAL FORMS HAVE BEEN FOUND IN MELOEOWEN LEUKEMIA CELL LINE KG-1, LEUKEMIA U937 CELL LINE, IN BOONE MARROW CELLS, PLACENTA, AND PERIPHERAL BLOOD GRANULOCYTES.	
CC	THE GCSFR-2 FORM HAS BEEN FOUND ONLY IN LEUKEMIA U937 CELLS. THE GCSFR-3 FORM IS HIGHLY EXPRESSED IN PLACENTA.	
CC	-1- ALTERNATIVE PRODUCTS: AT LEAST FOUR FORMS, GCSFR-1 (SHOWN UNDER), GCSFR-2, GCSFR-3 AND GCSFR-4/D7, ARE PROBABLY PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY DIFFER IN THEIR C-TERMINAL PORTION.	
CC	-1- DISEASE: DEFECTS IN GCSFR ARE A CAUSE OF KOSTMANN SYNDROME; ALSO KNOWN AS SEVERE CONGENITAL NEUTROPENIA (SCN).	
CC	-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE IG-LIKE DOMAIN.	
CC	-1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.	
CC	-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.	
CC	-1- DATABASE: NAME-PROV: NOTE-CD GUIDE CD114 ENTRY: WWW-http://www.ncbi.nlm.nih.gov/prov/cd/cd114.htm"	
CC		
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DR	EMBL: X55721; G31697; .	
DR	EMBL: X55720; G31699; .	
DR	EMBL: S71484; G240884; .	
DR	EMBL: M59816; G183047; .	
DR	EMBL: M59819; G485364; .	
DR	EMBL: M59820; G183049; .	
DR	PIR: JHO329; JHO329.	
DR	PIR: JHO330; JHO330.	
DR	PIR: A38252; A38252.	
DR	PDB: 1A27; 28-JAN-98.	
DR	MIW: 138971; .	
DR	MIW: 202700; .	
DR	PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.	
DR	PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.	
KM	PRAM: PR00041; fn3: 3.	
KM	RECEPTOR_TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL; REPEAT; ALTERNATIVE SPLICING; 3D-STRUCTURE.	
KW	SIGNAL	1 24
FT	CHAIN	25 836
FT	DOMAIN	25 627
FT	TRANSSEM	628 650
FT	DOMAIN	651 836
FT	DOMAIN	25 117
FT	DOMAIN	121 227
FT	DOMAIN	228 332
FT	DOMAIN	333 428
FT	DOMAIN	429 525
FT	DOMAIN	526 621
FT	DISULTID	131 142
FT	GRANULOCYTE COLONY STIMULATING FACTOR RECEPTOR EXTRACELLULAR (POTENTIAL) CYTOPLASMIC (POTENTIAL) IG-LIKE C2-TYPE DOMAIN. FIBRONECTIN TYPE-II. FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III. BY SIMILARITY.	

Query Match 11.3%, Score 254.5, DB 1, Length 836;
Best Local Similarity 28.9%, Pred. NO. 3.3e-13;
Matches 97; Conservative 48; Mismatches 146; Indels 43; Gaps 16

Query Match	Best Local Similarity	Score 252.5; DB 1; Length 837; Pred. No. 4.8e-13;
RA	FUKUNAGA R., ISHIANA-IKEDA E., SETO Y., NAGATA S.; "Expression cloning of a receptor for murine granulocyte colony- stimulating factor"; CELL 61:341-350(1990).	
RT	[2]	
RL	STRUCTURE BY NMR OF 225-333. MEDLINE: 97331327.	
RP	YAMASAKI K., NAITO S., AMAGUCHI H., OHKUBO T., OTA Y.; "Solution structure of an extracellular domain containing the WSWWS motif of the granulocyte colony-stimulating factor receptor and its interaction with ligand"; NAT. STRUCT. BIOL. 4:498-504(1997).	
RA	-1- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR. IN ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION EVENTS AT THE CELL SURFACE.	
CC	-1- SUBUNIT: DIMER (PROBABLE).	
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.	
CC	-1- TISSUE SPECIFICITY: FOUND IN BONE MARROW.	
CC	-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE IG-LIKE DOMAIN.	
CC	-1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.	
CC	-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.	
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CC	EMBL: M58288. G193455; .	
CC	PIR: A34898; A34898.	
CC	PDB: 1GCF; 22-OCT-97.	
CC	PDB: 1GTO; 22-OCT-97.	
CC	MGI: 88533; CSEGR.	
CC	PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.	
CC	PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.	
CC	PFAM: PF00041; fn3.3	
CC	RECEPTOR_TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL; REEEA; 3D-STRUCTURE.	
CC	CHAIN	
CC	1	
CC	26	
CC	837	
CC	25	POTENTIAL.
CC	1	GRANULOCYTE COLONY STIMULATING FACTOR
CC	26	RECEPTOR.
CC	626	POTENTIAL.
CC	630	EXTRACELLULAR (POTENTIAL).
CC	651	CYTOPLASMIC (POTENTIAL).
CC	837	IG-LIKE C2-TYPE DOMAIN.
CC	26	IG-LIKE C2-TYPE DOMAIN.
CC	118	FIBRONECTIN TYPE-III.
CC	122	FIBRONECTIN TYPE-III.
CC	228	FIBRONECTIN TYPE-III.
CC	229	FIBRONECTIN TYPE-III.
CC	334	FIBRONECTIN TYPE-III.
CC	431	FIBRONECTIN TYPE-III.
CC	432	FIBRONECTIN TYPE-III.
CC	528	FIBRONECTIN TYPE-III.
CC	529	FIBRONECTIN TYPE-III.
CC	624	FIBRONECTIN TYPE-III.
CC	132	BY SIMILARITY.
CC	143	BY SIMILARITY.
CC	249	BY SIMILARITY.
CC	296	BY SIMILARITY.
CC	310	BY SIMILARITY.
CC	51	POTENTIAL.
CC	94	POTENTIAL.
CC	129	POTENTIAL.
CC	186	POTENTIAL.
CC	186	POTENTIAL.
CC	279	POTENTIAL.
CC	392	POTENTIAL.
CC	392	POTENTIAL.
CC	408	POTENTIAL.
CC	474	POTENTIAL.
CC	474	POTENTIAL.
CC	487	POTENTIAL.
CC	487	POTENTIAL.
CC	582	POTENTIAL.
CC	582	POTENTIAL.
CC	613	POTENTIAL.
CC	613	POTENTIAL.
CC	837 AA;	93406 MW; D55F84D4 CRC32;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:40:03 ; Search time 68.96 seconds
(Without alignments)
368.584 Million cell updates/sec

Title: US-09-037-657-13

Perfect score: 2251

Sequence: 1 MPAGRPBPVAVASARRPPRL.....WRAMQKSHKTRNQYLPAKL 413

Scoring table: BLOSUM62

Searched: 201082 segs, 61543640 residues

Database : SPTREMBL_10:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_protent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2096	93.1	422	4	075462	075462 homo sapien
2	355.5	15.8	881	13	057519	057519 xenopus lae
3	324.5	14.4	206	4	016354	016354 homo sapien
4	306	13.6	581	6	046561	046561 ovis aries
5	302.5	13.4	296	6	018880	018880 bos taurus
6	268.5	11.9	346	13	093404	093404 oreochromis
7	234.5	10.4	217	6	046385	046385 mustela vis
8	230.5	10.2	128	6	018985	018985 cervus elap
9	226.5	10.1	335	6	018985	018985 cervus elap
10	226	10.0	372	11	088507	088507 mus musculu
11	217.5	9.7	862	4	099665	099665 homo sapien
12	215.5	9.6	874	11	097378	097378 mus musculu
13	209.5	9.3	422	4	016542	016542 homo sapien
14	208.5	9.3	432	11	064385	064385 mus musculu
15	201	8.9	440	11	070225	070225 mus musculu
16	194.5	8.6	440	11	000343	000343 mus musculu
17	193.5	8.6	710	13	057520	057520 xenopus lae
18	187.5	8.3	1165	6	002671	002671 sus scrofa
19	182	8.1	895	11	062960	062960 ratius norv
20	177	7.9	316	11	035545	035545 ratius norv
21	174.5	7.8	958	4	092920	092920 homo sapien
22	174.5	7.8	1165	4	092921	092921 homo sapien
23	174.5	7.8	958	4	013592	013592 homo sapien
24	174.5	7.8	906	4	013593	013593 homo sapien
25	174.5	7.8	896	4	013594	013594 homo sapien
26	174.5	7.8	896	4	092919	092919 homo sapien
27	163	7.2	1093	11	070535	070535 ratius norv
28	162	7.2	427	4	095646	095646 homo sapien
29	159.5	7.1	383	11	088786	088786 mus musculu

30	156.5	7.0	971	11	070458	070458 mus musculu
31	156.5	7.0	970	11	088821	088821 mus musculu
32	153.5	6.8	229	6	027950	027950 bos indicus
33	153.5	6.8	229	6	028206	028206 bos taurus
34	153.5	6.8	228	11	035228	035228 mus musculu
35	149.5	6.6	229	4	075269	075269 homo sapien
36	149	6.6	1896	4	060468	060468 homo sapien
37	149	6.6	1571	4	060468	060468 homo sapien
38	143	6.4	279	11	064236	064236 ratius norv
39	142.5	6.3	86	6	018853	018853 mustela put
40	141.5	6.3	229	4	014213	014213 homo sapien
41	139.5	6.2	890	11	092140	092140 cavia porce
42	136.5	6.1	634	6	046600	046600 bos taurus
43	136.5	6.1	269	6	079195	079195 macaca mlla
44	133	5.9	396	4	014631	014631 homo sapien
45	133	5.9	420	4	014633	014633 homo sapien

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	422 AA.
ID	075462			
AC	075462			
DT	01-NOV-1998 (TREMBLrel. 08, Created)			
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)			
DT	01-MAY-1999 (TREMBLrel. 10, Last annotation update)			
DE	CYTOKINE-LIKE FACTOR-1 PRECURSOR.			
GN	CLF-1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
RN	[1]			
RA	SEQUENCE FROM N.A.			
RA	ELSON G.C.A., GRABER P., LOSBERGER P., HERREN S., GREUTNER D.,			
RA	MEMOUD L.N., WELLS T.N.C., KOSCO-VILBOIS M.H., GAUCHAT J.F.,			
RT	"CLF-1, a Novel Soluble Protein Shares Homology With Members of the			
RT	Cytokine Type-1 Receptor Family."			
RL	J. Immunol. 0:0-0(1998).			
DR	EMBL; AF059293; AAC28335.1; -			
DR	PFAM; PF00041; fn3; 2.			
KW	Signal.			
FT	SIGNAL.			
FT	CHAIN			
FT	SEQUENCE			
FT	38	422	POTENTIAL.	
FT	422 AA; 46301 MW; 8779BC9 CRC32;			

Query Match 93.1%; Score 2096; DB 4; Length 422;
Best Local Similarity 93.7%; Pred. No. 9.2e-177;
Matches 388; Conservative 7; Mismatches 13; Indels 6; Gaps 3;

QY	1	MPAGRPBPVAVASARRPPRLSPILLVLPVPGGSAHRAVISPODPTLLIGSSIQ	60
DB	1	MPAGRPBPVAVASARRPPRLSPILLVLPVPGGSAHRAVISPODPTLLIGSSIQ	57
QY	61	ATCSIHDPGATAGLTYLTLNGRLPSELRLNTSTLALANLNGSROOGDNVYCH	120
DB	58	ATGVHDPGATAGLTYLTLNGRLPSELRLNTSTLALANLNGSROOGDNVYCH	117
QY	121	ARDGSIAGSCLVGLPPEKPFNISCWSRMKDLTCRWTPGAGETFLHTNSLKYLRM	180
DB	118	ARDGSIAGSCLVGLPPEKPFNISCWSRMKDLTCRWTPGAGETFLHTNSLKYLRM	177
QY	181	YGDNCCCEHYHVGPHSCHLPKDLAFTPEIVENANRLGARSVDLIDVYTTDP	240
DB	178	YGDNCCCEHYHVGPHSCHLPKDLAFTPEIVENANRLGARSVDLIDVYTTDP	237
QY	241	PPVHVSRYVGLDQSLVSRVSPALKDFFQAKYQIRYRVESVYMKVVDVSNQTSR	300
DB	238	PPVHVSRYVGLDQSLVSRVSPALKDFFQAKYQIRYRVESVYMKVVDVSNQTSR	297
QY	301	LAQKAGTYVYFVQVRCNPFQIGSKRAGIMSEWSHPTAATPSRSPRPGGVCBGRCE	360

QY 334 SHPTASTP 342
DB 171 SPKRSTQIP 179

RESULT 8

ID 018985 PRELIMINARY; PRT; 198 AA.

AC 018985;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, last annotation update)
DE SOLUBLE PROLACTIN RECEPTOR.
OS Cereus elaphus nelsoni (American elk).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
OC Cervinae; Cervus.
RN (1)
RP SEQUENCE FROM N.A.
RA JABBOUR H.N.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y14753; CAA/5048.1;
DR PFAM; PF00041; fn3; 1.
SQ SEQUENCE 198 AA; 22652 MW; COABAB0 CRC32;

Query Match 10.2%; Score 230.5; DB 6; Length 198;
Best Local Similarity 33.7%; Pred. No. 6, 4e-13;
Matches 62; Conservative 31; Mismatches 76; Indels 15; Gaps 7;

QY 123 DGSILGSCLYGLVLPPEKPEPNISCMRNMDLCRMTPGAHGTFHTNLSLYKLRWYG 182
DB 18 NASLNGOS-----PEKPKIKRSGSGKETTQWEPGSDG--LPTNTLLYHKEGT 70
QY 183 QDNTECEHYTHVGHSHI-PKDLALFTPEIWEATNRLGSARSVDYLLDVTVDTP 241
DB 71 LHECPDKYKGTGNTCFKSKHKSIMKIYITVNAINQMVSSSDPLYVTVIYEPEP 130
QY 242 PDVHVSNGVGLDQGLSVRWYS--PPALKD--LFOAKYQIRRVEDSVDAKVVYDVSK 236
DB 131 ANLTL-ELKHPEDRKPYLMIKWPPTLLDVKSGWFMQYRILKPEYATDWE-HDDLHP 188
QY 297 TSCR 300
DB 189 TSSR 192

RESULT 9

ID P79203 PRELIMINARY; PRT; 335 AA.

AC P79203;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, last annotation update)
DE PROLACTIN RECEPTOR (FRAGMENT).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae; Bovidae;
OC Caprinae; Ovis.
RN (1)
RP SEQUENCE FROM N.A.
RA STRAIN-M2/80; TISSUE-ANTERIOR PITUITARY;
RA TORTOISE D.T.; BROOKS J.; INGELTON P.; MCNEILLY A.S.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y10578; CAA/1597.1;
DR PFAM; PF00041; fn3; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 335 AA; 38326 MW; 88A05AB1 CRC32;

Query Match 10.1%; Score 226.5; DB 6; Length 335;

Best Local Similarity 31.4%; Pred. No. 2, 8e-12;
Matches 58; Conservative 28; Mismatches 68; Indels 31; Gaps 7;

QY 164 GETFLHTNLSLYKLRWYGODNTCEHYTHVGHSHIPKD-LALTPYIWEATNRLGS 222
DB 8 GETFL-----ECPDKYKGTGNTCFKSKHKSIMKIYITVNAINQMV 51
QY 223 ARSDVLLDVLVDVTTDPPDVHVSNGVGLDQGLSVRWY--SPALKDF--LFOAKYQI 277
DB 52 SSSDPLYDVTVIYEPEPVNLT-ELKHPEDRKPYLMIKWPPTLLDVKSGWFMQYRIL 110
QY 278 RRVEDSVDAKVVYDVSKNOTSCLAGLRGTYYFYQVRCNPGIYSGKAGIWSWSHPT 337
DB 111 RLKPEKATDWE-THRAPKLTLQKIFNLYGQKYLVOIRCKP-----DHGYWSEWSPES 162
QY 338 AASTP 342
DB 163 FTQIP 167

RESULT 10

ID 088507 PRELIMINARY; PRT; 372 AA.

AC 088507;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, last annotation update)
DE CILIARY NEUROTROPHIC FACTOR RECEPTOR ALPHA PRECURSOR.
GN CNTR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN (1)
RP SEQUENCE FROM N.A.
KC TISSUE-BRAIN, SKELETAL MUSCLE;
RA MAEDA M., YAGUCHI N., HANYU C., NAKATA Y., ONODA N., TULIN E.E.,
RA KOJIMA T., HASEGAWA M., KIKUCHI Y., NOMURA H.;
RT "Mouse homolog of human ciliary neurotrophic factor receptor.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF068615; AAC25711.1;
DR PFAM; PF00041; fn3; 1.
DR PFAM; PF00047; fn3; 1.
FT SIGNAL.
FT SIGNAL.
FT CHAIN 1 20 POTENTIAL.
FT CHAIN 21 336 CILIARY NEUROTROPHIC FACTOR RECEPTOR
FT CHAIN ALPHA.
SQ SEQUENCE 372 AA; 40831 MW; 9A40FE12 CRC32;

Query Match 10.0%; Score 226; DB 11; Length 372;
Best Local Similarity 26.0%; Pred. No. 3, 6e-12;
Matches 97; Conservative 45; Mismatches 157; Indels 74; Gaps 18;

QY 30 CYLGVPRGSGANTAVISPDPTLLIGSSLOATCSHGDPGATAE--GLYTLNGRL 86
DB 9 CCAVLAATAAAAYVTKHSPDEAPHYOYERLGAADVTL---PCGTASDAVAVTRVNGTDL 64
QY 87 PSELSLNTSTALALANLNGRSGDNLVCHADGSLAS-CUYGLPPEKPNIS 145
DB 65 APD--LLNGSOLILRSLGSHGLYA---CFHDSWRLRQVLHVLHGLPPREY-LS 115
QY 146 CWRNN-KDLTCRW-----TPGAGETFLHTNLSLYKLRWYGODNTCEHYTHVGH 197
DB 116 CRSNTPKGYGCSWHLPTPIYINTNLYLHRSKIM-----VEKDPAL-KNR 163
QY 198 CHIPKDLALET--PYEIWEATNRLGSARSVDYLLDVLVDVTTDPPDVHVSNGVGLDQ 255
DB 164 CHI-RYMLHLESTIKYKVSISVNALGH-NTTATTFDEFTIVKDPDENVAVARVPSPNR 221
QY 256 LSVRWSPPLKD-FLEPAKQYQIRRVEDSVDAKVVYDVSKNOTSCLAGLRGTYYFYQV 314
DB 222 LEVTWQTPSTWPDSPSPPLFLRLYRPLLDQOHV-ELSDGTAHTTDAVAKKEYIIIV 280

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OY 315 RCNPGICGSKKAGIWSMS-----HPTAASPPRSRPPGCGV 353
DB 281 AAK-----DNEIGTWSMSVAHAHATPWTPEERHLTTEAOAETTSTSTSSLAAPPITKI 334
OY 354 CEP-----RGEPSS 362
DB 335 CDPGELSGSGGGS 347

RESULT 11
OY 099665 PRELIMINARY: PRT: 862 AA.
ID 099665:
DB 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DE 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE IL-12 RECEPTOR BETA2.
Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN (1)
RP SEQUENCE FROM N.A.
RA PRESKY D.H., YANG H., MINETTI L.J., CHUA A.O., NABAVI N., WOU C.Y.,
GATELY M.K., GUBLER U.,
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U64198; AAB36675.1;
PFAM: PF00041; fn3: 3.
SQ SEQUENCE 862 AA; 97134 MW; 5FE4FBDS CRC32;

Query Match
Best Local Similarity 9.78; Score 217.5; DB 4; Length 862;
Matches 84; Conservative 46; Mismatches 121; Indels 77; Gaps 14;

OY 53 LIGSSIAQTCSHGTPGATAGLYWTL-----NGRRLPELSRL-L 94
DB 41 ILIGSVNTTCSL-----KPRGCFHYSRNRKLLYKFRIRNFHGHSLNQVTLPL 94
OY 95 NSTTALALANLNGSRQSGDNLVCHARDGSLAGSLYGLPPEKPNISCSHRNK-D 133
DB 95 GTTLFYCKLACINSIDIQ-----ICGAEIFGVAPEOPONSCIOKEGOGT 140
OY 154 LECRTPGAGHETFLHTNTSLKY---KLRWYQ--DNCEEHYTVG-----PHSCHI 200
DB 141 VACITWGRK--DTHTLEYTLQSLGPKNLWQKQDIYC-DLDDGINTLPPSPESNFT 197
OY 201 PRDLALFTYELTWEATNLGSRASVYLDVYTTDPPDPVHVSRYGGLDQLSVRW 260
DB 198 AK-----VTAVNSLIGSSSLPSTFFELDIYRPLPMDIRIKFKASVSRGTLW 246
OY 261 VSPALKDFLFOAKYQIRYVEDSVDMKYVDVDSNOTSCLAGLAKGYTFVQVRCNPG 320
DB 247 -----RBDGLVLLNRKLRPSNRSLMNNVNTKAKGRDLDLCKFTEFEFOI-SSKLH 299
OY 321 IYSGKAGIWSMSHPTASTPRSERPG 348
DB 300 LY-----KGSMSDMSLSLRAGTBEERTG 323

RESULT 12
OY 099665 PRELIMINARY: PRT: 874 AA.
ID 099665:
DB 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DE 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE INTERLEUKIN 12 RECEPTOR, BETA 2 (IL-12 RECEPTOR BETA2).
Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN (1)
RP SEQUENCE FROM N.A.

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RA PRESKY D.H., YANG H., MINETTI L.J., CHUA A.O., NABAVI N., WOU C.Y.,
GATELY M.K., GUBLER U.,
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U64199; AAB36676.1;
DR MGD: MG1:1270861; IL12RB2.
DR PFAM: PF00041; fn3: 4.
SQ SEQUENCE 874 AA; 98196 MW; 9B90EB47 CRC32;

Query Match
Best Local Similarity 9.68; Score 215.5; DB 11; Length 874;
Matches 96; Conservative 59; Mismatches 145; Indels 79; Gaps 19;

OY 9 VAGSARPPREFSLMSPLLL-----CVLGPFGSGAHTAVISPODPTLIGSSSQAT 62
DB 1 MAQVRECSLALFLFMILLKANIDVCKG-----TVYQPA-PVLPSSANIS 50
OY 63 CSIH-----GDTPATN-----BELYTLNGRL-----PELSRLINTST-LALAL 103
DB 51 CSLNPKGCSHYPSSNELLILKFVNDVLENLHGKRVHDHGHSTGQVNTLSIGMTLFV 110
OY 104 ANLNGSRQSGDNL-VCHARDGSLAGSLYGLPPEKPNISCSHRNK-DLTCRWTPG 161
DB 111 CKLNGSNSQKKPPYPC-----GVELSVGAPEPPONISCVGEGENGTVACSVNSG 161
OY 162 AHGETFLHTNYSIKYKLRWYGDN-TCE-EYHTVGPSC-----HIPDLAFTPYEI 212
DB 162 K--VYTLKNTYTLQLS-----GPNNLGQKCFSDNRCNRLDLGILNSPLDL-ESRFIV 214
OY 213 WPEATNLGASABSDVLTLDVYTTDPPDPVHVSRYGGLDQLSVRWVSPALKDFLQ 272
DB 215 RVAILNDLGNSSLPHTFFELDIYRPLPMDIRINFLNAGSGSGLTQW-----EDEGV 268
OY 273 AKQIRYVEDSVDMKYVDVDSNOTSCLAGLAKGYTFVQVRCNPGIYGR---KAGI 329
DB 269 VNLQIKQPLNSTSMNNVNTKAKRTDLDLDPFTEFEFOI-----SSKLHSGS 320
OY 330 WSEMSHPTASTPRSERPG 348
DB 321 WSNWSESLRTRTPEERTG 339

RESULT 13
OY 016542 PRELIMINARY: PRT: 422 AA.
ID 016542:
DB 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE INTERLEUKIN-11 RECEPTOR.
Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN (1)
RP SEQUENCE FROM N.A.
RA CHEREL M., SOREL M., LEBEAU B., DOBOIS S., MOREAU J.F., BATAILLE R.,
MEDLINE: 95399754.
RX MEDLINE: 95399754.
RA CHEREL M., SOREL M., LEBEAU B., DOBOIS S., MOREAU J.F., BATAILLE R.,
MINIVIELLE S., JACQUES Y.,
RT "Molecular cloning of two isoforms of a receptor for the human
hematopoietic cytokine interleukin-11."
RL Blood 86:2534-2540(1995).
RN (2)
RP SEQUENCE FROM N.A.
RA VAN LEUVEN F., STAS L., HILLIER C., MIYAKE Y., GOSSIER A.,
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
RN (3)
RP SEQUENCE OF 3-390 FROM N.A.
RA TISSUE-PLACENTA;
RC CHEREL M., SOREL M., DOBOIS S., LEBEAU B., MOREAU J., JACQUES Y.,
RA MINIVIELLE S.,
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U32324; AAB36492.1;

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DR EMBL: Z38102; CAA86524.1; -
DR EMBL: U32323; AAB3491.1; -
DR EMBL: Z46593; CAA86570.1; -
DR PFAM: PFO0047; fn3. 2.
DR PFAM: PFO0047; 1g. 1.
SQ SEQUENCE 422 AA; 45522 MM; 29011292 CRC32
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Query Match	9.38;	Score 209.5;	DB 4;	Length 422;
Best Local Similarity	23.98;	Pred. No. 1.2e-10;		
Matches 89;	Conservative 53;	Mismatches 138;	Indels 93;	Gaps 18;

QY	43	TAVISPODPTLLI	-----GSSLQATCSIHGDTPGATA-EGLYTLNG--RRLPS	88
Db	17	TALVYASASPCQAMGPBGVOYCGGRSVKLC	-----PGYTAGDPVSWTRDGPCKLLG	70
QY	89	ELSLRLTSTLATALANLINGSROOSGDNLYCHARDGSIILAGSCLYGLPPEKPFNISCWS	148	
Db	71	PDGSLGHELVLAQNDSTDEGT	-----YICQLDGLAGVWTLQGLYPPARPV-VSCQA	122
QY	149	RNMADLCRMTPGAHGETFLHTNYSLKXKLRWQDNTCEYHFWGHSHCHIPRD	204	
Db	123	ADVENFSCSTSPSG--ISGLPTRLTYSRKTYLVLGADSORRSPSTGWPCC--PDDPLGAA	178	
QY	204	-----LALFPYIWEATNRGLSASDVLTDLYDVTYTTDPPDVHVSNGSLEJOLS	257	
Db	179	RCVHGAELFMSQIYINTEVNPGL-ASTRLDVSLOSILRPDPGGLRVESVPEYPRRLR	237	
QY	258	VRWVSP---PALMKDFLQAKYQIYRVEDSVDMKVVNDVSNQTSCLRGLK	307	
Db	238	ASWYTPYPSWPOQPHFL--KFRLOYRAGHNMSTVP	266	
QY	308	TVTYVOYRCNDFGIYGSKKAGISWEMSHPTASTPRSERPPGGVCEPGEBSGPVR	367	
Db	287	LPHAVRYARSARDF-----LDAGTWSTWS-PEA	321	
QY	368	RELKQFLGWLKXH	380	
Db	322	KEIP--AWGQLH	331	
RESULT	14			
ID	064385	PRELIMINARY	PRY	432 AA.
DT	064385			
DC	01-JAN-1998	(TREMblrel. 05, Created)		
DT	01-JAN-1998	(TREMblrel. 05, Last sequence update)		
DT	01-NOV-1998	(TREMblrel. 08, Last annotation update)		
DE	INTEREDUKIN-11 RECEPTOR ALPHA CHAIN 1 PRECURSOR (NRL) (ETL2)			
DE	(IL-11RALPHA) (IL11RA1).			
GN	IL11RA1 OR IL11RA OR ETL2 OR ETL2/IL11 REC.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-C57BL/6 X CBA; TISSUE-LIVER;			
RC	MEDLINE; 95045367.			
RA	HILTON D.J., HILTON A.A., RACEYIC A., RAKAR S., HARRISON-SMITH M.,			
RA	GOUGH N.M., BEGLEY C.G., METCALF D., NICOLA N.A., WILLSON T.A.;			
RT	"Cloning of a murine IL-11 receptor alpha-chain; requirement for			
RT	gp130 for high affinity binding and signal transduction."			
EX	EMBO J. 13:4765-4775(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BALB/C, AND C57BL/6; TISSUE-EMBRYO;			
RA	NEUHARS H., BETENNAUSEN B., BILINSKI P., SIMON-CHAZOTTES D.,			
RA	GUENET J.L., GOSSLER A.;			
RL	Dev. Biol. 166:521-542(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BALB/C, AND C57BL/6;			
RA	GOSSLER A.;			

ID	Query Match	Best Local Similarity	Matches	94; Conservative	51; Mismatches	136; Indels	113; Gaps	20;
15	RESULT	9.38; Score 208.5; DB 11; Length 432;						
70225		Best Local Similarity 23.9%; Pred. No. 1.5e-10;						
P70225		Matches 94; Conservative 51; Mismatches 136; Indels 113; Gaps 20;						
1	Submitted (Feb-1995) to the EMBL/GenBank/DBJ databases.							
141	SEQUENCE FROM N.A.							
RA	BILINSKI P., HALI M.A., NEUHAUS H., GISEL C., HEATH J.R.,							
RA	GOSLER A.;							
RT	"Two differentially expressed interleukin-11 receptor genes in the							
RT	mouse genome.";							
RT	Riochem. J. 320:359-363(1996).							
CC	- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11.							
CC	BINDS TO IL-11 WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A							
CC	SIGNAL.							
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.							
CC	- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.							
CC	- TISSUE SPECIFICITY: WIDELY EXPRESSED.							
CC	- SIMILARITY: BELONGS TO THE IMMUGLOBULIN SUPERFAMILY.							
CC	CONTAINS ONE IG-LIKE DOMAIN.							
DR	- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.							
DR	EMBL; J74953; CAA532908.1; -							
DR	EMBL; U14412; AAA53248.1; -							
DR	EMBL; X94163; CAA63873.1; -							
DR	EMBL; X94163; CAA63873.1; JOINED.							
DR	MED; MGI:107426; IL11R1.							
DR	PFAM; PF00041; fn3. 2.							
DR	PFAM; PF00047; Ig. 1.							
KM	Receptor; Transmembrane; Glycoprotein; Immunoglobulin fold; Signal.							
FT	SIGNAL	1	23	POTENTIAL.				
FT	CHAIN	24	432	INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 1.				
FT	DOMAIN	24	367	EXTRACELLULAR (POTENTIAL).				
FT	TRANSEM	368	393	POTENTIAL.				
FT	DOMAIN	394	432	CYTOPLASMIC (POTENTIAL).				
FT	DOMAIN	41	102	IG-LIKE C2-TYPE DOMAIN.				
FT	CARBOHYD	127	127	POTENTIAL.				
FT	CARBOHYD	194	194	POTENTIAL.				
SO	SEQUENCE	432 AA;	46655 MW;	F55B3060 CRC32;				
7	GPAVQASRRPRRLPSLSMLSPILLICVLVGRPGSGAHNAVIRPODPTLLIGSSLSATCSIH							
31	GPPGVQYGGPGR-----PVMLCCPGVSAG-----							
67	GDTGATGAEGLYMTLNGRRLPELSRLIN--TSTLA--LALANLNGSRQSGDNLVCHAR							
55	--TP-----VSWRRDGD-----SRLLGDSGLGRLVLAQVDSPE---GIYVCTL							
123	DGSLIAGSCLVGLRPEKPFENISGWSRMKDLTCRWTPGAHGFTLHINYSLLKRYLWYG							
98	DGVSGGWTTLLTGPPPARP--EVSCQAVDYENFSCWSPGQ--VSGLPRLTYSRKKTLP							
183	QDNICEHYHNGRPSCHIRPKD-----LALFTYEIWEVETINNLGSRSDVLLD							
155	GAEGQRSPSPGFWPC--PODPLEASRCVHGAEFWSEYRLNVEYNPLG--ASTCLDVR							
232	VLDVATDPPDPAVHSRVGLLEDQLSYKVSPPALK--DFLFAKYDIRYVEDSDWK							
212	LQSLTRDPDPPGLAVESYPTGPRLLHSAWTPASWRKRPHTLL--KRLQYRPROHPAWS							
289	VDDVSNQ--TSCRLAGLKPGTYFVQVRCNPFGIYSSKKAGIWEWSHPTAATPRSER							
270	TVEIRIGLEEVITDAVAGLP-----HAVRNSANDF-----LDAGTSAWS--PEA							
347	PGGGVCCEPRGGEPSGPARRELKQFLGWLKKH							
312	-----WGTPSTGPIODEIPD--WSQGH							

Db 361 PSSGVPRELKQFLGLKRAHYCSNLSFRLYDQWRAMQKSHKTRNODGILPSGRGAA 420
 QY 421 RGPAG 425
 Db 421 RGPAG 425

RESULT 2

W59804
 ID W59804 standard; Protein; 425 AA.
 AC W59804.
 DT 26-OCT-1998 (first entry)
 DE Nucleotide sequence of the murine U4 protein.
 KW Murine; U4 protein; haematopoietin receptor superfamily;
 KW cell proliferation; immune response; antibody; cell differentiation;
 KW autoimmune disease; cancer; allergy.
 OS Mus sp.
 PN W09831811-A1.
 PD 23-JUL-1998.
 PE 15-JAN-1998; U00334.
 PR 16-JAN-1997; US-784863.
 PA (GENY) GENETICS INST INC.
 PI Collins M, Donaldson DP, Neben T, Whitters M;
 DR WPI: 98-414109/35.
 DR N-PSDB: V41688.
 PT New nucleic acid encoding U4 haematopoietin receptor superfamily
 chain - potentially useful, e.g. for modulating cell proliferation
 or immune response for treating cancer and autoimmune disease
 PS Claim 9, Pages 26-27; 38pp; English.
 CC This is the amino acid sequence of the murine U4 protein from the
 haematopoietin receptor superfamily, used in the method of the
 invention for the modulation of cell proliferation, or the immune
 response. Transformed mammalian cells are used to produce recombinant
 CC U4 protein. The U4 protein is used to screen for specific binding
 CC agents, raise antibodies. It is also used as reagents for assays and
 CC as tissue markers for isolation of cognate ligands and receptors, and
 CC in pharmaceutical compositions which may modulate cell proliferation,
 CC cell differentiation, and the immune system (e.g. for treating immune
 CC deficiency, inherited or the result of infection, autoimmune diseases,
 CC cancer, and allergy).
 SQ Sequence 425 AA;

Query Match 99.8%; Score 2313; DB 1; Length 425;
 Best Local Similarity 99.8%; Pred. No. 2, 3e-191;
 Matches 424; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAGRPVPAOSARRPRPLSLMSPLLCLVLPVGGSGAHRAVISPDPPTLLIGSSLQ 60
 Db 1 MPAGRPVPAOSARRPRPLSLMSPLLCLVLPVGGSGAHRAVISPDPPTLLIGSSLQ 60
 QY 61 ATCSHGDPGATAEGLYTLNGRRRLPSELRLNTSTLALANLNGSQSGDNLYCH 120
 Db 61 ATCSHGDPGATAEGLYTLNGRRRLPSELRLNTSTLALANLNGSQSGDNLYCH 120
 QY 121 ARDGSILAGSCLVYGLPPEKPFNISCWSRNKMDLTCRMTPGAHGEFTLHTNLSLKYKLM 180
 Db 121 ARDGSILAGSCLVYGLPPEKPFNISCWSRNKMDLTCRMTPGAHGEFTLHTNLSLKYKLM 180
 QY 181 YGQDNTECEHYHVGPHSCHIPKDLALFTPEIWEATNRLGSARSDVLTLDVLYVTTDP 240
 Db 181 YGQDNTECEHYHVGPHSCHIPKDLALFTPEIWEATNRLGSARSDVLTLDVLYVTTDP 240
 QY 241 PPDVHVSRRVGLGLEDOLSVRWSPALKDLEFOAKYQIRYVEDSVDMKYVDVSNQTSR 300
 Db 241 PPDVHVSRRVGLGLEDOLSVRWSPALKDLEFOAKYQIRYVEDSVDMKYVDVSNQTSR 300
 QY 301 LAGLKPQYVYFVQVRCNPFGIYSKAKGIMSEMSHPTAASPSEPRPGGVCGRGGE 360
 Db 301 LAGLKPQYVYFVQVRCNPFGIYSKAKGIMSEMSHPTAASPSEPRPGGVCGRGGE 360
 QY 361 PSSGVPRELKQFLGLKRAHYCSNLSFRLYDQWRAMQKSHKTRNODGILPSGRGAA 420

Db 361 PSSGVPRELKQFLGLKRAHYCSNLSFRLYDQWRAMQKSHKTRNODGILPSGRGAA 420
 QY 421 RGPAG 425
 Db 421 RGPAG 425

RESULT 3

W70862
 ID W70862 standard; Protein; 425 AA.
 AC W70862;
 DT 17-MAR-1999 (first entry)
 DE Rat zcyto5 protein.
 KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
 KW cardiac pathology; heart enlargement; zcyto5 ligand.
 OS Rattus sp.
 PN W09849307-A1.
 PD 05-NOV-1998.
 PE 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 DR N-PSDB: V70896.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiotoxin-1
 PT in blood.
 PS Claim 1; Page 75-76; 55pp; English.
 CC The present sequence represents a protein designated zcyto5, which is
 CC a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcyto5 could be used to detect cardiotoxin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SQ Sequence 425 AA;

Query Match 98.7%; Score 2288; DB 1; Length 425;
 Best Local Similarity 98.8%; Pred. No. 3, 3e-189;
 Matches 420; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPAGRPVPAOSARRPRPLSLMSPLLCLVLPVGGSGAHRAVISPDPPTLLIGSSLQ 60
 Db 1 MPAGRPVPAOSARRPRPLSLMSPLLCLVLPVGGSGAHRAVISPDPPTLLIGSSLQ 60
 QY 61 ATCSHGDPGATAEGLYTLNGRRRLPSELRLNTSTLALANLNGSQSGDNLYCH 120
 Db 61 ATCSHGDPGATAEGLYTLNGRRRLPSELRLNTSTLALANLNGSQSGDNLYCH 120
 QY 121 ARDGSILAGSCLVYGLPPEKPFNISCWSRNKMDLTCRMTPGAHGEFTLHTNLSLKYKLM 180
 Db 121 ARDGSILAGSCLVYGLPPEKPFNISCWSRNKMDLTCRMTPGAHGEFTLHTNLSLKYKLM 180
 QY 181 YGQDNTECEHYHVGPHSCHIPKDLALFTPEIWEATNRLGSARSDVLTLDVLYVTTDP 240
 Db 181 YGQDNTECEHYHVGPHSCHIPKDLALFTPEIWEATNRLGSARSDVLTLDVLYVTTDP 240
 QY 241 PPDVHVSRRVGLGLEDOLSVRWSPALKDLEFOAKYQIRYVEDSVDMKYVDVSNQTSR 300
 Db 241 PPDVHVSRRVGLGLEDOLSVRWSPALKDLEFOAKYQIRYVEDSVDMKYVDVSNQTSR 300
 QY 301 LAGLKPQYVYFVQVRCNPFGIYSKAKGIMSEMSHPTAASPSEPRPGGVCGRGGE 360

|||||
Db 301 LAGKPGTVFVQVRCNPFGLYSGSKKAGINSEMSHPTAASPSESRPGGVCPEPRGGE 360
OY 361 PSSGPVARELKQFGLKTKHAYCSNLSFRLYDQWRAMOKSHKTRNDEGILPGRGAA 420
Db 361 PSSGPVARELKQFGLKTKHAYCSNLSFRLYDQWRAMOKSHKTRNDEGILPGRGAA 420
OY 421 RGPAG 425
Db 421 RGPAG 425
RESULT 4
ID W55011 standard; Protein; 413 AA.
AC W55011;
DE 29-SEP-1998 (first entry)
KW Novel haemopoietin receptor NR6.1 protein.
KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
KW cell survival; therapeutic; neuronal proliferation; drug screening;
KW Mouse.
OS Mus sp.
PN M09811225-A2.
PR 19-MAR-1998.
PR 11-SEP-1997; G02479.
PR 11-SEP-1996; AU-002246.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PA (DZIF/) DZIGLEMSKA H E.
PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
PI Kojima T, Maeda M, Nash A, Nicolia NA, Rakar S, Willison T,
PI Zhang J;
DR MPI: 98-260970/23.
DR N-PSDB: V27140.
PT New isolated haemopoietin receptor - used for developing products
PT for modulating proliferation, differentiation and survival of cells,
PT e.g. neuronal cells
PS Claim 14; Page 77-81; 182pp; English.
CC The haemopoietin receptor (HR) NR6.1 is a form of the novel HR NR6.
CC Interaction between the novel HR and a ligand facilitates proliferation,
CC differentiation and survival of a wide variety of cells. The HR and its
CC derivatives can be used for modulating the activity of the receptors e.g.
CC to regulate development, maintenance or regeneration in an array of
CC different cells and tissues in vitro and in vivo. They can be present in
CC therapeutic used for modulating neuronal proliferation, differentiation,
CC and survival. The products can also be used for detection and diagnosis,
CC e.g. for cancers or predisposition to cancers, or for drug screening.
SQ Sequence 413 AA;

Query Match 96.1%; Score 2226.5; DB 1; Length 413;
Best Local Similarity 98.8%; Pred. No. 6.3e-184;
Matches 409; Conservative 2; Mismatches 0; Indels 3; Gaps 1;
OY 1 MPAGRPVAVASARRPRPLSLMSPLLCVLAGVPRGSGAHTAVISPODPTLLIGSSIQ 60
Db 1 MPAGRPVAVASARRPRPLSLMSPLLCVLAGVPRGSGAHTAVISPODPTLLIGSSIQ 60
OY 61 ATGSHDDTGGATGEGLYTLNGRRLPSELRLNTSTLALALANLNGSRQSGDNLYCH 120
Db 61 ATGSHDDTGGATGEGLYTLNGRRLPSELRLNTSTLALALANLNGSRQSGDNLYCH 120
OY 121 ARODSILAGSCLIVGLPPEKPFNISCWSRNKDLTCRWTGAGHETFLHTNYSKYLRLW 180
Db 121 ARODSILAGSCLIVGLPPEKPFNISCWSRNKDLTCRWTGAGHETFLHTNYSKYLRLW 180
OY 181 YGQDNTECEHTVGPSPHCHLPKDLALFTPEIWEATNRLGSARSADVLTLDVYVTTDP 240
Db 181 YGQDNTECEHTVGPSPHCHLPKDLALFTPEIWEATNRLGSARSADVLTLDVYVTTDP 240
OY 241 PPDVHVRVGGLEDQSLSVKRWSPPALKDFLFOAKYQIRYVEDSVDMKVVDDVSNQTSR 300
Db 241 PPDVHVRVGGLEDQSLSVKRWSPPALKDFLFOAKYQIRYVEDSVDMKVVDDVSNQTSR 300

|||||
OY 301 LAGKPGTVFVQVRCNPFGLYSGSKKAGINSEMSHPTAASPSESRPGGVCPEPRGGE 360
Db 301 LAGKPGTVFVQVRCNPFGLYSGSKKAGINSEMSHPTAASPSESRPGGVCPEPRGGE 360
OY 361 PSSGPVARELKQFGLKTKHAYCSNLSFRLYDQWRAMOKSHKTRNDEGILPGRGAA 420
Db 361 PSSGPVARELKQFGLKTKHAYCSNLSFRLYDQWRAMOKSHKTRNDEGILPGRGAA 420
OY 421 RGPAG 425
Db 421 RGPAG 425
RESULT 5
ID W70860 standard; Protein; 422 AA.
AC W70860;
DE 17-MAR-1999 (first entry)
KW Human zcyto5 protein sequence.
KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
KW cardiac pathology; heart enlargement; zcyto5 ligand.
OS Homo sapiens.
PN M09849307-A1.
PD 05-NOV-1998.
PR 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
DR MPI: 99-034662/03.
DR N-PSDB: V70894.
PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
PT down-regulating zcyto5 natural ligands or detecting cardiotrophin-1
PT in blood
PS Claim 1; Page 66-67; 55pp; English.
CC The present sequence represents a protein designated zcyto5, which is
CC a cytokinin-like receptor. Soluble zcyto5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC thyroid, heart, and skeletal muscle for example to lessen the effect
CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
CC enlargement. Zcyto5 could be used to detect cardiotrophin-1 in the
CC blood, and to discover other possible zcyto5 ligands. A probe
CC comprising zcyto5 DNA or RNA can be used to determine the presence
CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify zcyto5 and
CC therapeutically to modify zcyto5 ligand effects.
SQ Sequence 422 AA;

Query Match 93.8%; Score 2172.5; DB 1; Length 422;
Best Local Similarity 94.6%; Pred. No. 2.9e-179;
Matches 401; Conservative 6; Mismatches 14; Indels 3; Gaps 2;
OY 1 MPAGRPVAVASARRPRPLSLMSPLLCVLAGVPRGSGAHTAVISPODPTLLIGSSIQ 60
Db 1 MPAGRPVAVASARRPRPLSLMSPLLCVLAGVPRGSGAHTAVISPODPTLLIGSSIL 57
OY 61 ATGSHDDTGGATGEGLYTLNGRRLPSELRLNTSTLALALANLNGSRQSGDNLYCH 120
Db 61 ATGSHDDTGGATGEGLYTLNGRRLPSELRLNTSTLALALANLNGSRQSGDNLYCH 117
OY 121 ARODSILAGSCLIVGLPPEKPFNISCWSRNKDLTCRWTGAGHETFLHTNYSKYLRLW 180
Db 121 ARODSILAGSCLIVGLPPEKPFNISCWSRNKDLTCRWTGAGHETFLHTNYSKYLRLW 177
OY 181 YGQDNTECEHTVGPSPHCHLPKDLALFTPEIWEATNRLGSARSADVLTLDVYVTTDP 240
Db 181 YGQDNTECEHTVGPSPHCHLPKDLALFTPEIWEATNRLGSARSADVLTLDVYVTTDP 237
OY 241 PPDVHVRVGGLEDQSLSVKRWSPPALKDFLFOAKYQIRYVEDSVDMKVVDDVSNQTSR 300
Db 241 PPDVHVRVGGLEDQSLSVKRWSPPALKDFLFOAKYQIRYVEDSVDMKVVDDVSNQTSR 297

QY 301 LAGLPGTYEVQVRCNPFGLYSGKAGIMSESHPTASTPSEKPGGVCCEPRGGE 360
 DB 298 LAGLPGTYEVQVRCNPFGLYSGKAGIMSESHPTASTPSEKPGGVCCEPRGGE 357
 QY 361 PSSGPVRELKQFLGWLKRAKAYCSNLSFRLYDQWRAMQKSHKRNDEGILSGRGAA 420
 DB 358 PSSGPVRELKQFLGWLKRAKAYCSNLSFRLYDQWRAMQKSHKRNDEGILSGRGAA 417
 QY 421 RGRA 424
 DB 418 RGRA 421
 RESULT 6
 W59805
 ID W59805 standard; Protein; 408 AA.
 AC W59805;
 DT 26-OCT-1998 (first entry)
 DE Amino acid sequence of the human U4 protein.
 KW Human: U4 protein; haematopoietin receptor superfamily;
 KW cell proliferation; immune response; antibody; cell differentiation;
 KW auto-immune disease; cancer; allergy.
 OS Homo sapiens.
 PN W09831811-A1.
 PD 23-JUL-1998.
 PF 15-JAN-1998; US-784863.
 PR 16-JAN-1997; US-784863.
 PA (GEMT) GENETICS INST INC.
 PI Collins M, Donaldson DD, Neben T, Whitters M;
 DR WPI: 98-414109/35.
 DR N-PSDB: V41689.
 PT New nucleic acid encoding U4 haematopoietin receptor superfamily
 PT chain - potentially useful, e.g. for modulating cell proliferation
 PT or immune response, for treating cancer and auto-immune disease
 PS Claim 9; Pages 29-30; 38pp; English.
 CC This is the amino acid sequence of the human U4 protein from the
 CC haematopoietin receptor superfamily, used in the method of the
 CC invention for the modulation of cell proliferation, or the immune
 CC response. Transformed mammalian cells are used to produce recombinant
 CC U4 protein. The U4 protein is used to screen for specific binding
 CC agents, raise antibodies. It is also used as reagents for assays and
 CC as tissue markers for isolation of cognate ligands and receptors, and
 CC in pharmaceutical compositions which may modulate cell proliferation,
 CC cell differentiation, and the immune system (e.g. for treating immune
 CC deficiency, inherited or the result of infection, autoimmune diseases,
 CC cancer, and allergy).
 SQ Sequence 408 AA;

Query Match 91.3%; Score 2116.5; DB 1; Length 408;
 Best Local Similarity 95.1%; Pred. No. 1.8e-174;
 Matches 330; Conservative 5; Mismatches 12; Indels 3; Gaps 2;
 QY 15 RPRPLSLMSPLLCVLGVRGSGAHTAVISPODPTLLIGSSLOATCSIHGDRGATA 74
 DB 1 RPR-PLPL-LLLCVLGVRGSGAHTAVISPODPTLLIGSSLOATCSVHGDRGATA 57
 QY 75 EGIYTLNGRRRLPSELRLNTSTLALANLNGSRQSGDNLYCHARDGILLAGSCLVY 134
 DB 58 EGIYTLNGRRRLPSELRLNTSTLALANLNGSRQSGDNLYCHARDGILLAGSCLVY 117
 QY 135 GLPPEKPNISCSRMKMDLTCRTGAGETFLHTNYSLKTKRLMYGQDNCEEHYV 194
 DB 118 GLPPEKPNISCSRMKMDLTCRTGAGETFLHTNYSLKTKRLMYGQDNCEEHYV 177
 QY 195 PHSCHIPKDLALFTPEIWEATNRLGSASDYLTLVDVYTTDPDPVHSRKGLED 254
 DB 178 PHSCHIPKDLALFTPEIWEATNRLGSASDYLTLVDVYTTDPDPVHSRKGLED 237
 QY 255 QLSVKNVSPALKDFLFOAKYQIRIVEDSVMKVVDVSNQTSCLAGLKGTYFYV 314
 DB 238 QLSVKNVSPALKDFLFOAKYQIRIVEDSVMKVVDVSNQTSCLAGLKGTYFYV 297

QY 315 KCNPFGLYSGKAGIMSESHPTASTPSEKPGGVCCEPRGGE 374
 DB 298 KCNPFGLYSGKAGIMSESHPTASTPSEKPGGVCCEPRGGE 357
 QY 375 GMLKRAKAYCSNLSFRLYDQWRAMQKSHKRNDEGILSGRGAA 424
 DB 358 GMLKRAKAYCSNLSFRLYDQWRAMQKSHKRNDEGILSGRGAA 407
 RESULT 7
 W70841
 ID W70841 standard; Protein; 385 AA.
 AC W70841;
 DT 17-MAR-1999 (first entry)
 DE Human zcyto5 variant.
 KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
 KW cardiac pathology; heart enlargement; zcyto5 ligand; variant.
 OS Homo sapiens.
 PN W09849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiotoxin-1
 PT in blood
 PS Claim 1; Page 83-84; 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcyto5 could be used to detect cardiotoxin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SQ Sequence 385 AA;

Query Match 90.5%; Score 2097; DB 1; Length 385;
 Best Local Similarity 99.7%; Pred. No. 8.1e-173;
 Matches 384; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 41 AATAVISPODPTLLIGSSLOATCSIHGDRGATAAGLYTLNGRRRLPSELRLNTSTLA 100
 DB 1 AATAVISPODPTLLIGSSLOATCSIHGDRGATAAGLYTLNGRRRLPSELRLNTSTLA 60
 QY 101 LALANLNGSRQSGDNLYCHARDGILLAGSCLYVGLPPEKPNISCSRMKMDLTCRTWP 160
 DB 61 LALANLNGSRQSGDNLYCHARDGILLAGSCLYVGLPPEKPNISCSRMKMDLTCRTWP 120
 QY 161 GAGGETFLHTNYSLKTKRLMYGQDNCEEHYVHGPSCHIPKDLALFTPEIWEATNRL 220
 DB 121 GAGGETFLHTNYSLKTKRLMYGQDNCEEHYVHGPSCHIPKDLALFTPEIWEATNRL 180
 QY 221 GSARSDVLTLDVYTTDPDPVHSRKGLEDLSTRVSPALKDFLFOAKYQIR 280
 DB 161 GSARSDVLTLDVYTTDPDPVHSRKGLEDLSTRVSPALKDFLFOAKYQIR 240
 QY 281 VEDSVDMKVVVDVSNQTSCLAGLKGTYFYVQVNCNFGIYSGKAGIMSESHPTAAS 340
 DB 241 VEDSVDMKVVVDVSNQTSCLAGLKGTYFYVQVNCNFGIYSGKAGIMSESHPTAAS 300
 QY 341 TPSEKPGGVCCEPRGGE 400

Db 301 TPSSRGPGGVCPEPGSSGPPVREIKOFLGWLKKNAYCSNLSFRLYDQWRAMWOK 360
QY 401 SHKTRNDEGILPSGRGARGPAG 425
Db 361 SHKTRNDEGILPSGRGARGPAG 385

RESULT 8

W70861 8
ID W70861 standard; Protein: 425 AA.
AC W70861;
DE 17-MAR-1999 (first entry)
DE Allelic variant of human zcyto5.
KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
KW cardiac pathology; heart enlargement; zcyto5 ligand; allelic variant.
OS Homo sapiens.
PN MO9849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
PI WPI: 99-034662/03.
DR N-PSDB; V70895.
PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
PT down-regulating zcyto5 natural ligands or detecting cardiotrophin-1
PT in blood
PS Claim 1: Page 71-72; 55pp; English.
CC The present sequence represents an allelic variant of protein designated
CC zcyto5, which is a cytokinin-like receptor. Soluble zcyto5 may be
CC administered to down-regulate the effects of a growth and/or maintenance
CC factor in thyroid, heart, and skeletal muscle for example to lessen the
CC effect of cardiotrophin-1 on cardiac pathologies, so preventing heart
CC enlargement. zcyto5 could be used to detect cardiotrophin-1 in the
CC blood, and to discover other possible zcyto5 ligands. A probe
CC comprising zcyto5 DNA or RNA can be used to determine the presence
CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify zcyto5 and
CC therapeutically to modify zcyto5 ligand effects.
SQ Sequence 425 AA;

Query Match 90.4%; Score 2094; DB 1; Length 425;
Best Local Similarity 94.88; Pred. No. 1.7e-172;
Matches 386; Conservative 5; Mismatches 12; Indels 4; Gaps 2;
QY 1 MPAGRPVQASARRPRLSLMSPLLCVIGYRGSGAHAVISPODPTLLIGSSIQ 60
Db 1 MPAGRRPAQASARRP-PLLP-LLLCVIGAPRAGSGAHAVISPODPTLLIGSSIL 56
QY 61 ATGCSIHCDPFGATAAGLWTLNGRRRLPSELRLNTSTLALANLNGSRQOSDNTVCH 120
Db 57 ATGCSVHDDPPGATAAGLWTLNGRRRLPSELRLNTSTLALANLNGSRQOSDNTVCH 116
QY 121 ARGSTIAGSCLVYGLPEKPEFNISCSRNKKDLTCRWTPGAHGETFLHTNYSKYLKW 180
Db 117 ARGSTIAGSCLVYGLPEKPEFNISCSRNKKDLTCRWTPGAHGETFLHTNYSKYLKW 176
QY 181 YGDNCEETHTVGPCHSCHKDALTFTPEIWEATNRLGASARSVDLTDLVDTTDP 240
Db 177 YGDNCEETHTVGPCHSCHKDALTFTPEIWEATNRLGASARSVDLTDLVDTTDP 236
QY 241 PPDVHVSRRVGGLEDQSLSVRWSPALADFLFOAKYQIRYVEDSVDMKVVDDVSNQSCR 300
Db 237 PPDVHVSRRVGGLEDQSLSVRWSPALADFLFOAKYQIRYVEDSVDMKVVDDVSNQSCR 296
QY 301 LAGLPGTIVFVQVRCNPFGLYSGKAGINSEMSHPTAASPRESRPGGVCPEPGGE 360

Db 297 LAGLPGTIVFVQVRCNPFGLYSGKAGINSEMSHPTAASPRESRPGGVCPEPGGE 356
QY 361 PSSGPVREIKOFLGWLKKNAYCSNLSFRLYDQWRAMWOKSHKTRNO 407
Db 357 PSSGPVREIKOFLGWLKKNAYCSNLSFRLYDQWRAMWOKSHKTRNO 403

RESULT 9

W70839 9
ID W70839 standard; Protein: 388 AA.
AC W70839;
DE 17-MAR-1999 (first entry)
DE Human zcyto5 variant
KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
KW cardiac pathology; heart enlargement; zcyto5 ligand; variant.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc_difference 45 /note= "not specified"
FT PN MO9849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
PI WPI: 99-034662/03.
DR N-PSDB; V70895.
PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
PT down-regulating zcyto5 natural ligands or detecting cardiotrophin-1
PT in blood
PS Claim 1: Page 80-81; 55pp; English.
CC The present sequence represents a zcyto5 variant protein. zcyto5
CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC thyroid, heart, and skeletal muscle for example to lessen the effect
CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
CC enlargement. zcyto5 could be used to detect cardiotrophin-1 in the
CC blood, and to discover other possible zcyto5 ligands. A probe
CC comprising zcyto5 DNA or RNA can be used to determine the presence
CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify zcyto5 and
CC therapeutically to modify zcyto5 ligand effects.
SQ Sequence 388 AA;

Query Match 88.5%; Score 2051; DB 1; Length 388;
Best Local Similarity 96.4%; Pred. No. 7.5e-169;
Matches 373; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 38 GSGAHAVISPODPTLLIGSSIQATCSIHGDPGATAAGLWTLNGRRRLPSELRLNTS 97
Db 1 GSGAHAVISPODPTLLIGSSILATCSVHDDPPGATAAGLWTLNGRRRLPSELRLNTS 90
QY 98 TLALANLNGSRQOSDNTVCHARGOSIAGSCLVYGLPEKPEFNISCSRNKKDLTCR 157
Db 61 TLALANLNGSRQOSDNTVCHARGOSIAGSCLVYGLPEKPEFNISCSRNKKDLTCR 120
QY 158 WTPGAHGETFLHTNYSKYLKWYGDNCEETHTVGPCHSCHKDALTFTPEIWEAT 217
Db 121 WTPGAHGETFLHTNYSKYLKWYGDNCEETHTVGPCHSCHKDALTFTPEIWEAT 180
QY 218 NRLGASARSVDLTDLVDTTDPDPPVHVSRRVGGLEDQSLSVRWSPALADFLFOAKYQI 277
Db 181 NRLGASARSVDLTDLVDTTDPDPPVHVSRRVGGLEDQSLSVRWSPALADFLFOAKYQI 240
QY 278 RYVEDSVDMKVVDDVSNQSCRAGLPGTIVFVQVRCNPFGLYSGKAGINSEMSHPT 337
Db 241 RYVEDSVDMKVVDDVSNQSCRAGLPGTIVFVQVRCNPFGLYSGKAGINSEMSHPT 300

OY 338 AASTPSEBPGGGVCEPBGEPSSGVPARELKOFLGMLKKHAYCSNLSFRLYDQWRAN 397
 DB 301 AASTPSEBPGGGVCEPBGEPSSGVPARELKOFLGMLKKHAYCSNLSFRLYDQWRAN 360
 OY 398 MOKSHKTRNDEGILPSSGRGAARCPA 424
 DB 361 MOKSHKTRNDEGILPSSGRGAARCPA 387

RESULT 10

ID W70842 standard; Protein: 385 AA.
 AC W70842;
 DT 17-MAR-1999 (first entry)
 DE Human zcytoz variant.
 KW zcytoz; cytokinin-like receptor; down-regulation; growth factor;
 KM maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc. difference 42 /note="not specified"
 FT WO9849307-A1.
 PN 05-NOV-1998.
 PF 01-MAY-1998; US-074721.
 PR 13-FEB-1998; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcytoz - useful for, e.g.
 PT down-regulating zcytoz natural ligands or detecting cardiotoxin-1
 PT in blood
 PS Claim 1: Page 84-85; 55pp; English.
 CC The present sequence represents a zcytoz variant protein. zcytoz
 CC is a cytokinin-like receptor. Soluble zcytoz may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcytoz could be used to detect cardiotoxin-1 in the
 CC blood, and to discover other possible zcytoz ligands. A probe
 CC comprising zcytoz DNA or RNA can be used to determine the presence
 CC and integrity of the zcytoz gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcytoz and
 CC therapeutically to modify zcytoz ligand effects.
 SO Sequence 385 AA.

Query Match 87.8%; Score 2035; DB 1; Length 385;
 Best Local Similarity 96.4%; Pred. No. 1.8e-167;
 Matches 370; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 41 AHAHVAISPODPTLLIGSSSLAATCSIHGDPGATAEGLYWTLNRRRLPSELRLNTSTA 100
 DB 1 AHAHVAISPODPTLLIGSSSLAATCSIHGDPGATAEGLYWTLNRRRLPSELRLNTSTA 60
 OY 101 LALANLNGSRGSGDNVCHARDGSLIAGSCLVYGLPPEKPFNISCSRMKMLTORMP 160
 DB 61 LALANLNGSRGSGDNVCHARDGSLIAGSCLVYGLPPEKPFNISCSRMKMLTORMP 120
 OY 161 GAHGEFTLNTNLSLTKKLMYGGDNCEEHYVGPSPCHIPKDLAFTPEIWEATNTL 220
 DB 121 GAHGEFTLNTNLSLTKKLMYGGDNCEEHYVGPSPCHIPKDLAFTPEIWEATNTL 180
 OY 221 GSARSVDLTLDVLDVYTTDPPDVHVSRRVGLLEDQLSVRVSPALKDFLQAKYQIR 280
 DB 181 GSARSVDLTLDVLDVYTTDPPDVHVSRRVGLLEDQLSVRVSPALKDFLQAKYQIR 240
 OY 281 VEDSVDMKVYDVVSNQTSCLAGLKRGTTFVYVRCNPNPFIYSKAGIWMSESHPTAAS 340

DB 241 VEDSVDMKVYDVVSNQTSCLAGLKRGTTFVYVRCNPNPFIYSKAGIWMSESHPTAAS 300
 OY 341 TPSEBPGGGVCEPBGEPSSGVPARELKOFLGMLKKHAYCSNLSFRLYDQWRAN 400
 DB 301 TPSEBPGGGVCEPBGEPSSGVPARELKOFLGMLKKHAYCSNLSFRLYDQWRAN 360
 OY 401 SHKTRNDEGILPSSGRGAARCPA 424
 DB 361 SHKTRNDEGILPSSGRGAARCPA 384

RESULT 11

ID W70840 standard; Protein: 392 AA.
 AC W70840;
 DT 17-MAR-1999 (first entry)
 DE Human zcytoz variant.
 KW zcytoz; cytokinin-like receptor; down-regulation; growth factor;
 KM maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc. difference 42 /note="not specified"
 FT WO9849307-A1.
 PN 05-NOV-1998.
 PF 01-MAY-1998; US-074721.
 PR 13-FEB-1998; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcytoz - useful for, e.g.
 PT down-regulating zcytoz natural ligands or detecting cardiotoxin-1
 PT in blood
 PS Claim 1: Page 81-82; 55pp; English.
 CC The present sequence represents a zcytoz variant protein. zcytoz
 CC is a cytokinin-like receptor. Soluble zcytoz may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcytoz could be used to detect cardiotoxin-1 in the
 CC blood, and to discover other possible zcytoz ligands. A probe
 CC comprising zcytoz DNA or RNA can be used to determine the presence
 CC and integrity of the zcytoz gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcytoz and
 CC therapeutically to modify zcytoz ligand effects.
 SO Sequence 392 AA.

Query Match 85.4%; Score 1978; DB 1; Length 392;
 Best Local Similarity 97.0%; Pred. No. 1.5e-162;
 Matches 359; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 38 GGAHVAISPODPTLLIGSSSLAATCSIHGDPGATAEGLYWTLNRRRLPSELRLNTS 97
 DB 1 GGAHVAISPODPTLLIGSSSLAATCSIHGDPGATAEGLYWTLNRRRLPSELRLNTS 60
 OY 98 LALANLNGSRGSGDNVCHARDGSLIAGSCLVYGLPPEKPFNISCSRMKMLTORMP 157
 DB 61 LALANLNGSRGSGDNVCHARDGSLIAGSCLVYGLPPEKPFNISCSRMKMLTORMP 120
 OY 158 GAHGEFTLNTNLSLTKKLMYGGDNCEEHYVGPSPCHIPKDLAFTPEIWEATNTL 217
 DB 121 GAHGEFTLNTNLSLTKKLMYGGDNCEEHYVGPSPCHIPKDLAFTPEIWEATNTL 180
 OY 218 GSARSVDLTLDVLDVYTTDPPDVHVSRRVGLLEDQLSVRVSPALKDFLQAKYQIR 277
 DB 181 GSARSVDLTLDVLDVYTTDPPDVHVSRRVGLLEDQLSVRVSPALKDFLQAKYQIR 240
 OY 278 RRVEDSVDMKVYDVVSNQTSCLAGLKRGTTFVYVRCNPNPFIYSKAGIWMSESHPT 337

Db 241 RYRVEDSVDMKVVDDVSNQTSCLAGLKPCTVYFVQVRCPNPGIYSGSKKAGIMSEMSHPT 300
 QY 338 AASTPSEPPGCGVCEPRGEGSSGPVRRLEKQFLGWLKKHAYCSNLSFRLYDQWRAHOK 397
 Db 301 AASTPSEPPGCGVCEPRGEGSSGPVRRLEKQFLGWLKKHAYCSNLSFRLYDQWRAHOK 360
 QY 398 MOKSHKTRNQ 407
 Db 361 MOKSHKTRNQ 370

RESULT 12

W70850 standard; Protein: 389 AA.
 ID W70850.
 AC W70850: 17-MAR-1999 (first entry)
 DE Human Zcyto5 variant.
 KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1; cardiac pathology; heart enlargement; Zcyto5 ligand; variant.
 OS Homo sapiens.
 PN WO9849307-A1.
 PD 05-NOV-1998.
 PE 01-MAY-1998: US-074721.
 PR 13-FEB-1998: US-045287.
 PR 01-MAY-1997: US-850030.
 PR 13-FEB-1998: US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams R, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM, Lok S, Presnell SR, Whitmore TE.
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g. down-regulating Zcyto5 natural ligands or detecting cardiotoxin-1 in blood.
 PS Claim 1: Page 95-96; 55pp; English.
 CC The present sequence represents a Zcyto5 variant protein. Zcyto5 is a cytokinin-like receptor. Soluble Zcyto5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotoxin-1 on cardiac pathologies, so preventing heart enlargement. Zcyto5 could be used to detect cardiotoxin-1 in the blood, and to discover other possible Zcyto5 ligands. A probe comprising Zcyto5 DNA or RNA can be used to determine the presence and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcyto5 and therapeutically to modify Zcyto5 ligand effects.
 SQ Sequence 389 AA:

Query Match 84.7%; Score 1963; DB 1; Length 389;
 Best Local Similarity 97.3%; Pred. No. 2,9e-161;
 Matches 357; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 41 AHTAVISPOPTLLIGSSLATGCSIHGDTGATAGLWTLNGRRLPSELRLNTSTLA 100
 Db 1 AHTAVISPOPTLLIGSSLATGCSIHGDTGATAGLWTLNGRRLPSELRLNTSTLA 60
 QY 101 LALANLNGSRQSDNLYCHARDGSIILAGSLYGLPPEKPNISCSKNNKDLTCRMT 160
 Db 61 LALANLNGSRQSDNLYCHARDGSIILAGSLYGLPPEKPNISCSKNNKDLTCRMT 120
 QY 161 GAGETFLHTNYSILKYLKRWGQDNTCEHYTVGPHSCHIPKDLALFTPEIWEATNRL 220
 Db 121 GAGETFLHTNYSILKYLKRWGQDNTCEHYTVGPHSCHIPKDLALFTPEIWEATNRL 180
 QY 221 GSARSVLTLDVLTDPDPDVHVRVSGLEDOLSVRWVSPALDOLFQAKYQIRYR 280
 Db 181 GSARSVLTLDVLTDPDPDVHVRVSGLEDOLSVRWVSPALDOLFQAKYQIRYR 240
 QY 281 VEDSVDMKVVDDVSNQTSCLAGLKPCTVYFVQVRCPNPGIYSGSKKAGIMSEMSHPT 340
 Db 241 VEDSVDMKVVDDVSNQTSCLAGLKPCTVYFVQVRCPNPGIYSGSKKAGIMSEMSHPT 300

QY 341 TPSEPPGCGVCEPRGEGSSGPVRRLEKQFLGWLKKHAYCSNLSFRLYDQWRAHOK 400
 Db 301 TPSEPPGCGVCEPRGEGSSGPVRRLEKQFLGWLKKHAYCSNLSFRLYDQWRAHOK 360
 QY 401 SHKTRNQ 407
 Db 361 SHKTRNQ 367

RESULT 13

W70844 standard; Protein: 389 AA.
 ID W70844.
 AC W70844: 17-MAR-1999 (first entry)
 DE Human Zcyto5 variant.
 KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1; cardiac pathology; heart enlargement; Zcyto5 ligand; variant.
 OS Homo sapiens.
 PN WO9849307-A1.
 PD 05-NOV-1998.
 PE 01-MAY-1998: US-074721.
 PR 13-FEB-1998: US-045287.
 PR 01-MAY-1997: US-850030.
 PR 13-FEB-1998: US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams R, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM, Lok S, Presnell SR, Whitmore TE.
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g. down-regulating Zcyto5 natural ligands or detecting cardiotoxin-1 in blood.
 PS Claim 1: Page 87-88; 55pp; English.
 CC The present sequence represents a Zcyto5 variant protein. Zcyto5 is a cytokinin-like receptor. Soluble Zcyto5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotoxin-1 on cardiac pathologies, so preventing heart enlargement. Zcyto5 could be used to detect cardiotoxin-1 in the blood, and to discover other possible Zcyto5 ligands. A probe comprising Zcyto5 DNA or RNA can be used to determine the presence and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcyto5 and therapeutically to modify Zcyto5 ligand effects.
 SQ Sequence 389 AA:

Query Match 84.7%; Score 1962; DB 1; Length 389;
 Best Local Similarity 97.0%; Pred. No. 3.5e-161;
 Matches 356; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 41 AHTAVISPOPTLLIGSSLATGCSIHGDTGATAGLWTLNGRRLPSELRLNTSTLA 100
 Db 1 AHTAVISPOPTLLIGSSLATGCSIHGDTGATAGLWTLNGRRLPSELRLNTSTLA 60
 QY 101 LALANLNGSRQSDNLYCHARDGSIILAGSLYGLPPEKPNISCSKNNKDLTCRMT 160
 Db 61 LALANLNGSRQSDNLYCHARDGSIILAGSLYGLPPEKPNISCSKNNKDLTCRMT 120
 QY 161 GAGETFLHTNYSILKYLKRWGQDNTCEHYTVGPHSCHIPKDLALFTPEIWEATNRL 220
 Db 121 GAGETFLHTNYSILKYLKRWGQDNTCEHYTVGPHSCHIPKDLALFTPEIWEATNRL 180
 QY 221 GSARSVLTLDVLTDPDPDVHVRVSGLEDOLSVRWVSPALDOLFQAKYQIRYR 280
 Db 181 GSARSVLTLDVLTDPDPDVHVRVSGLEDOLSVRWVSPALDOLFQAKYQIRYR 240
 QY 281 VEDSVDMKVVDDVSNQTSCLAGLKPCTVYFVQVRCPNPGIYSGSKKAGIMSEMSHPT 340
 Db 241 VEDSVDMKVVDDVSNQTSCLAGLKPCTVYFVQVRCPNPGIYSGSKKAGIMSEMSHPT 300

QY 341 TPSEBPGGVCCEPBGSSGVPVRELKQFLGMLKKHAYCSNLSFRLYDQWAMOK 400
 DB 301 TPSEBPGGVCCEPBGSSGVPVRELKQFLGMLKKHAYCSNLSFRLYDQWAMOK 360
 QY 401 SHKTRNO 407
 DB 361 SHKTRNO 367

RESULT 14

ID W70851 standard; Protein: 389 AA.
 AC W70851;
 DT 17-MAR-1999 (first entry)
 DE Human zcyto5 variant.
 KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
 cardiac pathology; heart enlargement; zcyto5 ligand; variant.
 OS Homo sapiens.
 PN W09849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998: 008865.
 PR 13-FEB-1998: US-074721.
 PR 01-MAY-1997: US-045287.
 PR 01-MAY-1997: US-850030.
 PR 13-FEB-1998: US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams Rl, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
 PI Lok S, Pressnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiotoxin-1
 PT in blood
 PS Claim 1: Page 96-97; 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcyto5 could be used to detect cardiotoxin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SO Sequence 389 AA.

Query Match 84.6%; Score 1961; DB 1; Length 389;
 Best Local Similarity 96.7%; Pred. No. 4,3e-161;
 Matches 355; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 41 AHTAVISPODPTLLIGSSLOATCSIHGDPGATAGLYWTNGRLPSELRLNTSTLA 100
 DB 1 AHTAVISPODPTLLIGSSLOATCSIHGDPGATAGLYWTNGRLPSELRLNTSTLA 60
 QY 101 LALANLNGSRGSGDNLYCHARDGSIILAGSLYGLPEKPNISCSRNKMDLTCRTP 160
 DB 61 LALANLNGSRGSGDNLYCHARDGSIILAGSLYGLPEKPNISCSRNKMDLTCRTP 120
 QY 161 GAHGETFLHTNYSKLYKLRYGODNTCEHYTVGPHSCHIRKDALFTPEIWEATNRL 220
 DB 121 GAHGETFLHTNYSKLYKLRYGODNTCEHYTVGPHSCHIRKDALFTPEIWEATNRL 180
 QY 221 GSARSDVLTLDLVYTTDPPDVHVSRYGLEDQLSVRWSPALADFLFOAKYQIRYR 280
 DB 181 GSARSDVLTLDLVYTTDPPDVHVSRYGLEDQLSVRWSPALADFLFOAKYQIRYR 240
 QY 281 VEDSVDMKVVDDVSNQTSCLAGLPGTYVTVQRCNPFGLYSGKKGAGINSEMSHPPTAAS 340
 DB 241 VEDSVDMKVVDDVSNQTSCLAGLPGTYVTVQRCNPFGLYSGKKGAGINSEMSHPPTAAS 300
 QY 341 TPSEBPGGVCCEPBGSSGVPVRELKQFLGMLKKHAYCSNLSFRLYDQWAMOK 400

DB 301 TPSEBPGGVCCEPBGSSGVPVRELKQFLGMLKKHAYCSNLSFRLYDQWAMOK 360
 QY 401 SHKTRNO 407
 DB 361 SHKTRNO 367

RESULT 15

ID W70852 standard; Protein: 389 AA.
 AC W70852;
 DT 17-MAR-1999 (first entry)
 DE Human zcyto5 variant.
 KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
 cardiac pathology; heart enlargement; zcyto5 ligand; variant.
 OS Homo sapiens.
 PN W09849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998: 008865.
 PR 13-FEB-1998: US-074721.
 PR 01-MAY-1997: US-045287.
 PR 01-MAY-1997: US-850030.
 PR 13-FEB-1998: US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams Rl, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
 PI Lok S, Pressnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiotoxin-1
 PT in blood
 PS Claim 1: Page 98-99; 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcyto5 could be used to detect cardiotoxin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SO Sequence 389 AA.

Query Match 84.6%; Score 1960; DB 1; Length 389;
 Best Local Similarity 96.7%; Pred. No. 5,2e-161;
 Matches 355; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 41 AHTAVISPODPTLLIGSSLOATCSIHGDPGATAGLYWTNGRLPSELRLNTSTLA 100
 DB 1 AHTAVISPODPTLLIGSSLOATCSIHGDPGATAGLYWTNGRLPSELRLNTSTLA 60
 QY 101 LALANLNGSRGSGDNLYCHARDGSIILAGSLYGLPEKPNISCSRNKMDLTCRTP 160
 DB 61 LALANLNGSRGSGDNLYCHARDGSIILAGSLYGLPEKPNISCSRNKMDLTCRTP 120
 QY 161 GAHGETFLHTNYSKLYKLRYGODNTCEHYTVGPHSCHIRKDALFTPEIWEATNRL 220
 DB 121 GAHGETFLHTNYSKLYKLRYGODNTCEHYTVGPHSCHIRKDALFTPEIWEATNRL 180
 QY 221 GSARSDVLTLDLVYTTDPPDVHVSRYGLEDQLSVRWSPALADFLFOAKYQIRYR 280
 DB 181 GSARSDVLTLDLVYTTDPPDVHVSRYGLEDQLSVRWSPALADFLFOAKYQIRYR 240
 QY 281 VEDSVDMKVVDDVSNQTSCLAGLPGTYVTVQRCNPFGLYSGKKGAGINSEMSHPPTAAS 340
 DB 241 VEDSVDMKVVDDVSNQTSCLAGLPGTYVTVQRCNPFGLYSGKKGAGINSEMSHPPTAAS 300
 QY 341 TPSEBPGGVCCEPBGSSGVPVRELKQFLGMLKKHAYCSNLSFRLYDQWAMOK 400

Db 301 TPRESPPGGGACEPRGCEPSSGPPVRELNQFLGWLKHAACSNLSFRLYDOWRAMOK 360
OY 401 SHKTRNQ 407
Db 361 SHKTRNQ 367

Search completed: September 17, 1999, 03:08:13
Job time: 304 sec

OM protein - protein search, using sw model

Run on: September 16, 1999, 20:41:06 ; Search time 53.94 Seconds

(without alignments)
77.754 Million cell updates/sec

Title: US-09-037-657-15

Sequence: 1 MPAGRPVQASARRPRPL.....NODEGILPSGRGAARPGAG 425

Scoring table: BLOSUM62

Searched: 106577 seqs, 9868381 residues

Database :

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- 2: /cgn2-6/ptodata/2/1aa/5B.COMB.pep.*
- 3: /cgn2-6/ptodata/2/1aa/PCUS9.COMB.pep.*
- 4: /cgn2-6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	329	14.2	708	1 US-07-797-556-2	Sequence 2, Appl1
2	329	14.2	708	2 US-08-308-881-2	Sequence 2, Appl1
3	329	14.2	708	3 PCT-US95-06530-2	Sequence 2, Appl1
4	254.5	11.0	836	1 US-07-923-976-4	Sequence 4, Appl1
5	254.5	11.0	863	1 US-07-923-976-6	Sequence 4, Appl1
6	254.5	11.0	863	1 US-07-923-976-8	Sequence 4, Appl1
7	252.5	10.9	837	1 US-07-923-976-2	Sequence 2, Appl1
8	230.5	9.5	372	1 US-07-865-878A-4	Sequence 2, Appl1
9	230.5	9.5	372	1 US-07-676-647-2	Sequence 2, Appl1
10	230.5	9.5	372	1 US-08-449-329-2	Sequence 2, Appl1
11	220.5	9.5	372	1 US-08-445-073-2	Sequence 2, Appl1
12	220.5	9.5	372	3 PCT-US91-03896-2	Sequence 2, Appl1
13	217.5	9.4	862	2 US-08-685-118-2	Sequence 2, Appl1
14	217.5	9.4	862	2 US-08-915-495-2	Sequence 2, Appl1
15	216.5	9.3	602	2 US-08-419-632-6	Sequence 2, Appl1
16	206	8.9	572	2 US-08-419-652-5	Sequence 5, Appl1
17	192.5	8.3	635	1 US-08-184-327A-4	Sequence 4, Appl1
18	192.5	8.3	635	3 PCT-US95-00670-4	Sequence 4, Appl1
19	192	8.3	633	1 US-08-250-859-17	Sequence 17, Appl1
20	192	8.3	633	1 US-08-490-883-17	Sequence 17, Appl1
21	192	8.3	633	3 PCT-US94-08806-17	Sequence 17, Appl1
22	192	8.3	633	3 PCT-US95-01775-17	Sequence 17, Appl1
23	192	8.3	633	3 PCT-US95-16626-7	Sequence 7, Appl1
24	190	8.2	1001	1 US-07-797-556-6	Sequence 6, Appl1
25	190	8.2	1001	1 US-07-943-843-2	Sequence 2, Appl1
26	190	8.2	1097	1 US-07-943-843-6	Sequence 2, Appl1
27	190	8.2	1001	2 US-08-347-003-2	Sequence 2, Appl1
28	190	8.2	1097	2 US-08-347-003-6	Sequence 6, Appl1
29	186	8.0	626	1 US-08-184-327A-2	Sequence 2, Appl1
30	186	8.0	482	1 US-08-184-327A-8	Sequence 8, Appl1
31	186	8.0	626	3 PCT-US95-00670-2	Sequence 2, Appl1
32	186	8.0	482	3 PCT-US95-00670-8	Sequence 8, Appl1
33	185	8.0	719	1 US-07-943-843-4	Sequence 4, Appl1
34	185	8.0	719	1 US-08-347-003-4	Sequence 4, Appl1
35	174.5	7.5	569	2 US-08-306-231-3	Sequence 3, Appl1
36	174.5	7.5	960	2 US-08-355-888A-8	Sequence 8, Appl1
37	174.5	7.5	960	2 US-08-693-697-3	Sequence 3, Appl1
38	174.5	7.5	908	2 US-08-693-697-33	Sequence 33, Appl1
39	174.5	7.5	898	2 US-08-693-697-36	Sequence 36, Appl1

40	173.5	7.5	908	2 US-08-588-526-3	Sequence 3, Appl1
41	170	7.3	888	1 US-08-445-640-35	Sequence 35, Appl1
42	169.5	7.3	960	2 US-08-588-190-3	Sequence 3, Appl1
43	159.5	6.9	383	1 US-08-609-572-2	Sequence 2, Appl1
44	151.5	6.5	508	2 US-08-850-293-5	Sequence 5, Appl1
45	149.5	6.5	897	1 US-07-960-389-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-07-797-556-2
Sequence 2, Application US/07797556

Patent No. 5262522

GENERAL INFORMATION:
APPLICANT: Gearing, David P.
TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
TITLE OF INVENTION: Inhibitory Factor
NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle

STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/797,556
FILING DATE: 19911122

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 37,172
REFERENCE/DOCKET NUMBER: 2607

TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
TELEFAX: 206-587-0606

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear

MOLECULE TYPE: protein
US-07-797-556-2

Query Match 14.28; Score 329; DB 1; Length 708;
Best Local Similarity 28.6%; Pred. No. 1.3e-22;

Matches 88; Conservative 51; Mismatches 151; Indels 18; Gaps 8;

QY	46	ISPDPTLLIGSSIQACSIHG---DTPGATFAGELTYLTLGRRLPSLSLTLTSTALA	102
DB	31	ISPSPVQVLSHNSNTACVAKCKMDYFHVANAYIVKRTNHTFTPKQYTIINRTASVT	90
QY	103	LANNRGROSGDVLVCHARDGSLASCLYGLPPEKPNISCSHNMMDLCRTMGA	162
DB	91	FTDIASLNIOLTCILIFGQLEQVNVYGIITISGLPPEKPNISCLIVEGKMKCEMDGR	150
QY	163	HGETFTNTSLKTKLKMVQDNTCEYATVGPSPHCHIPDLALFTYEIWEATNRLGS	222
DB	151	--EHLLENFLIKSEMAHFKFADCKARDT--PTSCVDYSTVYFVNIETVEENALGR	206
QY	223	ARQVLLDLVLTVPPTPPDVHRSKRGGLDQLSVAVSWSPPALKDLFPKQIQRVE	282
DB	207	VTSIHNFDPYTKRPPPHNLSTINSELSILKLTWN-PSIKSVYI-LKYNIDYRRT	264
QY	283	DSVDMKVY---DVSNOTSCLAGLKPQTYFYQVRCNPGIIGSKKAGIWSMSHTPA	339

REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 6526-048
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 8698864/9741
 TELETYPE: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 372 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-676-647-2

Query Match 9.5%; Score 220.5; DB 1; Length 372;
 Best Local Similarity 26.2%; Pred. No. 7.3e-13;
 Matches 96; Conservative 42; Mismatches 149; Indels 79; Gaps 19;

41 AHTAVI-----SPDPTLL-----IGSSLOATCSIHGDTFGATAGLYWTNGRRRLPSLS 91
 15 AAAAAYVYQHRSPQAPHYOYERLGSVDYTLPCGTANMDAAVT-----WRVGTDLAPD-- 68
 92 RLINTSTLALANLNGSRQSGDNLVCHARGSLIAGS-CLYVGLPPEKPNISCSNRN 150
 68 -LNGSQLV-----LHGELGHSGLYACFHRQSWHLRHQVLLHVGLPPEPEV-LSCRSMT 120
 151 M-KDLTCRW-----TPGAHGETFLHTNYSKYLKRWYGODNTCEHYTVGPHSGHIK 202
 121 YPRGFCYSWMLPTPTIIPNTFNTVHLSKIM-----VCEKDPAL-KNRCHT-R 167
 203 DLALFT--PYEIVWEATNRLGSARSDVLTLDVLYTTDPPPPVHVSRRVGGLEDOLSVR 260
 168 YMHFSTIKKVSISVSNALGH-NATAITDEFITVPDPPENVAAPVSNRRLEVTW 226
 261 VSPPALKD-FLFOAKIQIRVEDSVWKYVDVSNQTSCLAGLKPGTYFYVQVRCPNF 319
 227 QTPSTWDPDESFLKFLRYRPLILDQOHV-ELSDGTAHTITDAVAKETIIIOVAAK-- 284
 320 GIYSKKAGTSEMS-----HPTASTPSEPPGCGVCEPERG 358
 284 ----DNEIGTWSWVAHAATPTWTEPRHLLTEAQAETTTSTSLAPPTTKICDP-- 338
 359 GEPSSG 364
 338 GELGSG 343

RESULT 10
 US-08-449-329-2
 Sequence 2, Application US/08449329
 Patent No. 5648334
 GENERAL INFORMATION:
 APPLICANT: Davis, Samuel
 APPLICANT: Squinto, Stephen P.
 APPLICANT: Furth, Mark E.
 APPLICANT: Yancopoulos, George D.
 TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/449,329

FILING DATE: 530
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/700,677
 FILING DATE: 15-MAY-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: MISTOCK, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 6526-065
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 8698864/9741
 TELETYPE: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 372 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-449-329-2

Query Match 9.5%; Score 220.5; DB 1; Length 372;
 Best Local Similarity 26.2%; Pred. No. 7.3e-13;
 Matches 96; Conservative 42; Mismatches 149; Indels 79; Gaps 19;

41 AHTAVI-----SPDPTLL-----IGSSLOATCSIHGDTFGATAGLYWTNGRRRLPSLS 91
 15 AAAAAYVYQHRSPQAPHYOYERLGSVDYTLPCGTANMDAAVT-----WRVGTDLAPD-- 68
 92 RLINTSTLALANLNGSRQSGDNLVCHARGSLIAGS-CLYVGLPPEKPNISCSNRN 150
 68 -LNGSQLV-----LHGELGHSGLYACFHRQSWHLRHQVLLHVGLPPEPEV-LSCRSMT 120
 151 M-KDLTCRW-----TPGAHGETFLHTNYSKYLKRWYGODNTCEHYTVGPHSGHIK 202
 121 YPRGFCYSWMLPTPTIIPNTFNTVHLSKIM-----VCEKDPAL-KNRCHT-R 167
 203 DLALFT--PYEIVWEATNRLGSARSDVLTLDVLYTTDPPPPVHVSRRVGGLEDOLSVR 260
 168 YMHFSTIKKVSISVSNALGH-NATAITDEFITVPDPPENVAAPVSNRRLEVTW 226
 261 VSPPALKD-FLFOAKIQIRVEDSVWKYVDVSNQTSCLAGLKPGTYFYVQVRCPNF 319
 227 QTPSTWDPDESFLKFLRYRPLILDQOHV-ELSDGTAHTITDAVAKETIIIOVAAK-- 284
 320 GIYSKKAGTSEMS-----HPTASTPSEPPGCGVCEPERG 358
 284 ----DNEIGTWSWVAHAATPTWTEPRHLLTEAQAETTTSTSLAPPTTKICDP-- 338
 359 GEPSSG 364
 338 GELGSG 343

RESULT 11
 US-08-445-073-2
 Sequence 2, Application US/08445073
 Patent No. 5849857
 GENERAL INFORMATION:
 APPLICANT: Davis, Samuel
 APPLICANT: Squinto, Stephen P.
 APPLICANT: Furth, Mark E.
 APPLICANT: Yancopoulos, George D.
 TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036


```

ADDRESSSEE: Pennine & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/03896
FILING DATE: 19910603
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-065-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US91-03896-2

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Query Match          9.5%; Score 220.5; DB 3; Length 372;
Best Local Similarity 26.28; Pred. No. 7.3e-13;
Matches 96; Conservative 42; Mismatches 149; Indels 79; Gaps 19;

QY      41 AHAVI-----SPDDTLL-----IGSSLAQCSIHGDPGATAGELGYTLNGRRLPSELS 91
DB      15 AAAAVVYAQRHSPQEAHPHYQYERLGSVDTLPGGTANMAAT-----WRVNGTDLAPD-- 68
QY      92 RLNTSTLALNALNNGSRQSGDNLVCHARDGSTLAGS-CLVGLPEPKPENNISCSARN 150
DB      68 -LLNGSOLV-----LHGELGSHSGLYACFHNDSWHLRHQVLLVHGLPREPY-LSRSWT 120
QY      151 M-KDLTCRW-----RPGAGETGELHNYSLAKYKLRVGGDNQCEEHYTGPHSCHLPK 202
DB      121 YPKFYFCSWHLPTPTPTPTPTPTNTVTLHSSKTM-----VCEKDPAL-KNNCHT-R 167
QY      203 DLAFET--PREIWEATNRGLSARSADVLLDLDVYTTDPPDYHVSRYVGGLEDLSRW 260
DB      168 YMHLEFSLIKYKVISISVSNALGH-NATAITPEFLTIYKDPDENVYARVPSNPRLEVTW 226
QY      261 VSPPALND-FLFAKQIQIRKRVEDSDMKYVDVDSNOTCSLAGLKPTGYVYVQRCNPF 319
DB      227 QTPTWDPDPSEFPLKFLRYRPLTLDIMOHV-ELSDGTAHITDAVAGKEYIIVAAK-- 284
QY      320 GIYSKRKAGLWSEMS-----HPTASTPREEPFGGCGGVCGERG 358
DB      284 -----DNIGTGWSDMSVAAHNPTPEERPHLTTEAOAAETTTSTTSSLAPPTTRICDP-- 338
QY      359 GEPSSG 364
DB      338 GELGSG 343

RESULT 13
US-08-683-118-2
; Sequence 2, Application US/08685118
; Patent No. 5840530
; GENERAL INFORMATION:
; APPLICANT: Gubler, Ulrich A
; APPLICANT: Presky, David H
; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12

```

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,118
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Robert A.
REGISTRATION NUMBER: 35,682
REFERENCE/DOCKET NUMBER: CD 9195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-2863
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 862 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-685-118-2

Query Match 9.4%; Score 217.5; DB 2; Length 862;
Best Local Similarity 25.6%; Pred. No. 4,8e-12;
Matches 84; Conservative 46; Mismatches 121; Indels 77; Gaps 14;

QY 53 LIGSSLAQTCIHGDTPGATNGLYWTL-----NGRRLPSELRL-L 94
DB 41 ILIGSTVNTCSL-----KPRGCFHYSRRNKLILYKFDRIINFHGHSLNSQVTLPL 94
QY 95 NSTLALANLNGSRQSGDNLVCHARDGSLIAGSCLYVGLPPEKPFNISCWSNMK-D 153
DB 95 GTTLFVCKLACINSDEIQ-----ICGAEIFVGVAPEQPONLSIQGEGGT 140
QY 154 LFCRMTPGAHGEPFLHTNYSLK-----KLRWYGO--DNCEEHYTVG-----PHSCH 200
DB 141 VACTWGRG--DTHLYTETTLQSGPKNLTWQKCKDIYC-DYLDGFINLTPESPESNFT 197
QY 201 PKDLALFTPEIWEATNRLGARSADVLTLVDVYTTDPPDVHVSRYGLEDQLSVRM 260
DB 198 AK-----VTAVNSLGSSSLPSTFTFLDIYRPLPMDIRIKFKQKASVRSCTLW 246
QY 261 VSPPALKDFLQAKQIQRIVVEDSVDMKYVDVSNQTSRLAGLKGTYFYVOVRCNPFG 320
DB 247 -----RDGGLVLLNRLRIRPSNRLMNNVNTKAKGRHDLDLKPFTEYEFQI-SSKLH 299
QY 321 IYGSKKAGIMSEWSHPTASTPSESRPG 348
DB 300 LY-----KGSWSDMSSESLRAQTPEEPTG 323

RESULT 14
US-08-915-495-2
Sequence 2, Application US/08915495
Patent No. 5832176
GENERAL INFORMATION:
APPLICANT: Gubliet, Ulrich A
APPLICANT: Presky, David H
TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.

STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,495
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,118
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Robert A.
REGISTRATION NUMBER: 35,682
REFERENCE/DOCKET NUMBER: CD 9195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-2863
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 862 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-915-495-2

Query Match 9.4%; Score 217.5; DB 2; Length 862;
Best Local Similarity 25.6%; Pred. No. 4,8e-12;
Matches 84; Conservative 46; Mismatches 121; Indels 77; Gaps 14;

QY 53 LIGSSLAQTCIHGDTPGATNGLYWTL-----NGRRLPSELRL-L 94
DB 41 ILIGSTVNTCSL-----KPRGCFHYSRRNKLILYKFDRIINFHGHSLNSQVTLPL 94
QY 95 NSTLALANLNGSRQSGDNLVCHARDGSLIAGSCLYVGLPPEKPFNISCWSNMK-D 153
DB 95 GTTLFVCKLACINSDEIQ-----ICGAEIFVGVAPEQPONLSIQGEGGT 140
QY 154 LFCRMTPGAHGEPFLHTNYSLK-----KLRWYGO--DNCEEHYTVG-----PHSCH 200
DB 141 VACTWGRG--DTHLYTETTLQSGPKNLTWQKCKDIYC-DYLDGFINLTPESPESNFT 197
QY 201 PKDLALFTPEIWEATNRLGARSADVLTLVDVYTTDPPDVHVSRYGLEDQLSVRM 260
DB 198 AK-----VTAVNSLGSSSLPSTFTFLDIYRPLPMDIRIKFKQKASVRSCTLW 246
QY 261 VSPPALKDFLQAKQIQRIVVEDSVDMKYVDVSNQTSRLAGLKGTYFYVOVRCNPFG 320
DB 247 -----RDGGLVLLNRLRIRPSNRLMNNVNTKAKGRHDLDLKPFTEYEFQI-SSKLH 299
QY 321 IYGSKKAGIMSEWSHPTASTPSESRPG 348
DB 300 LY-----KGSWSDMSSESLRAQTPEEPTG 323

RESULT 15
US-08-419-652-6
Sequence 6, Application US/08419652
Patent No. 5831007
GENERAL INFORMATION:
APPLICANT: Chua, Anne O
APPLICANT: Gubliet, Ulrich A
TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.

```

: STREET: 340 Kingsland Street
: CITY: Nutley
: STATE: New Jersey
: COUNTRY: United States of America
: ZIP: 07110-1199
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: PC compatible
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/419,652
: FILING DATE: 11-APR-1995
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/248,532
: FILING DATE: 31-MAY-1994
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/094,713
: FILING DATE: 19-JUL-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Kass, Alan P
: REGISTRATION NUMBER: 32142
: REFERENCE/DOCKET NUMBER: CD 9174
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (201) 235-4205
: TELEFAX: (201) 235-3500
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 602 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FEATURE:
: NAME/KEY: Region
: LOCATION: 1..602
: OTHER INFORMATION: /note="Represents residues 98 to
: OTHER INFORMATION: 731 of human granulocyte colony-stimulating
: OTHER INFORMATION: factor-receptor."
:
: US-08-419-652-6
    
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Query Match          9.3%; Score 216.5; DB 2; Length 602;
Best Local Similarity 31.8%; Pred. No. 3.5e-12;
Matches 68; Conservative 31; Mismatches 86; Indels 29; Gaps 11;

QY 137 PPEKPPNISC-WSRNNKIDTCRMTPGAHGETFLHTNYSIK-YKLRYGO--DNTCEHY 191
      ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3 PPAIPHNLSCMLNLTSSILICQMEPP--ETHLPFTSLKFSRSGNCQTGDSILDVCP 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 192 TVGPRSCHIP-KDLALFTFYEIWEVETNRLGSARSDVFLDVLDDV-----TTDPPP 242
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 KDGOHCCIPRHHLLLYONMGIWQAEALGTSMSPOLCLDPDYYKLEPPMLRTDPPSP 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 243 DVHVSRYVGLIEDQLSVRWSPALKDQLFOATYQIRYVE-DSVDMKYVDVDSNQT-SCR 300
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 EAAPQACIQ---LCW--EPWQGLHINQKCELRHKPQRGESALVGPFLPEALQYE 174
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 301 LAGLKPSTVYEVQVRCNPFGIYSKRKAGIWSMS 334
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 175 LCGILPATATYTLQIRCIHWPL-----PGHMSDWS 203
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    
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Search completed: September 16, 1999, 20:41:07
 Job time: 5436 sec

GenCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 16, 1999, 20:42:06 / Search time 49.27 seconds

(Without alignments)
345.602 Million cell updates/sec

Title: US-09-037-657-15

Perfect score: 2317

Sequence: 1 MPAGRPGPYAQSARPPRL.....NODEGLPSGRGAPAG 425

Scoring table: BLOSUM62

Searched: 122810 seqs, 40065486 residues

Database: PIR_60:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	331	14.3	622	2	prolactin receptor
2	329	14.2	918	2	membrane glycoprot
3	324.5	14.0	206	2	prolactin receptor
4	319.5	13.8	917	2	glycoprotein 130
5	317.5	13.7	918	2	interleukin-6 sign
6	314	13.6	830	2	prolactin receptor
7	312	13.5	610	2	prolactin receptor
8	312	13.5	610	2	prolactin receptor
9	312	13.5	412	2	prolactin receptor
10	312	13.5	310	2	prolactin receptor
11	307.5	13.3	616	2	prolactin receptor
12	307.5	13.3	303	2	prolactin receptor
13	307.5	13.3	292	2	prolactin receptor
14	307.5	13.3	608	2	prolactin receptor
15	306	13.2	831	2	prolactin receptor
16	302.5	13.1	581	2	prolactin receptor
17	261.5	11.3	630	2	prolactin receptor
18	254.5	11.0	783	2	prolactin receptor
19	254.5	11.0	771	2	prolactin receptor
20	254.5	11.0	863	2	prolactin receptor
21	252.5	10.9	837	2	prolactin receptor
22	234	10.1	372	2	prolactin receptor
23	220.5	9.5	372	1	prolactin receptor
24	209.5	9.0	422	2	prolactin receptor
25	208.5	9.0	432	2	prolactin receptor
26	208	9.0	362	2	prolactin receptor
27	202.5	8.7	460	1	prolactin receptor
28	200.5	8.7	468	1	prolactin receptor
29	199	8.6	156	2	prolactin receptor
30	194.5	8.4	440	2	prolactin receptor
31	192.5	8.3	579	2	prolactin receptor
32	192.5	8.3	635	2	prolactin receptor
33	191.5	8.3	894	2	prolactin receptor
34	191.5	8.3	900	2	prolactin receptor
35	191.5	8.3	805	2	prolactin receptor
36	190	8.2	1097	2	prolactin receptor
37	190	8.2	625	2	prolactin receptor
38	190	8.2	150	2	prolactin receptor
39	188.5	8.1	894	2	prolactin receptor

40	188.5	8.1	1162	2	PC4184
41	188.5	8.1	805	3	JC4897
42	186	8.0	626	2	S37622
43	185	8.0	1092	2	JX0312
44	185	8.0	719	2	JC2181
45	182	7.9	895	2	S74225

ALIGNMENTS

RESULT 1

A40144

prolactin receptor long form precursor, hepatoma and breast cancer cells - human

C/Species: Homo sapiens (man)

C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Sep-1998

C/Accession: A40144

R/Boutin, J.M.; Edey, M.; Shirota, M.; Jolicoeur, C.; Lesueur, L.; All, S.; Gould, D

Mol. Endocrinol 3, 1455-1461, 1989

A/Title: Identification of a cDNA encoding a long form of prolactin receptor in human

A/Reference number: A40144; MID:90114212

A/Accession: A40144

A/Residues: 1-622 <RCD>

A/Cross-references: GB:M31661; NID:q190361; PID:q190362

C/Genetics:

A/Map position: 5p13.3-5p13.1

C/Keywords: glycoprotein, transmembrane protein

F/1-24/Domain: signal sequence #status predicted <SIG>

F/25-622/Product: prolactin receptor, long form #status predicted <MAT>

F/59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.3%; Score 331; DB 2; Length 622;

Best Local Similarity 37.5%; Pred. No. 3e-19; Matches 84; Conservative 27; Mismatches 95; Indels 18; Gaps 8;

QY 126 ILASGCLYVG-LPPEKPFNISCWSRNKDLTCMTGPGAGETPLHTNYSIKYLRMYGDD 184

DB 15 LFLNTCLINQLPGRPEIFKCSPKKEFTTCWRBGTGG--LPNYSILTYHREGETLM 72

QY 185 NICEETHVWPHSCHIPKD-LALFPEIWEATNRLGASRSDVLTLVDVYTTDPPD 243

DB 73 HECPPDITGGPNSCHGKQYTSWRTYIMVYVNTNMGSSFSDELVDVYTYVQPPPLE 132

QY 244 VHSRVRGLEDQSVWV--SPALDF---LFQAKYQIRYVEDSVDRKVVDDVSNQTS 298

DB 133 LAV-EVKQPEDRKPRYIMKWSPTLLIDLTGWFTLLYEIRLKRKAWE-IHFAQQTTE 190

QY 299 CRLAGLKPGTVFYVQRCNPFGLYGSKKAGINSESHPTAASP 342

DB 191 FKLSLHPGOKYIVQRCR-----DHGYSAMSAPATFIQIP 227

RESULT 2

A36337

Membrane glycoprotein gp130 precursor - human

C/Species: Homo sapiens (man)

C/Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-Sep-1998

C/Accession: A36337

R/Hibi, M.; Murekami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.

Cell 63, 1149-1157, 1990

A/Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.

A/Reference number: A36337; MID:91084644

A/Accession: A36337

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-918 <HIB>

A/Cross-references: GB:M57230; NID:q186353; PID:q186354

A/Genes: GDB:IL6ST; GP130

A:Cross-references: GDB:126725; OMIM:600694
 A:Map position: 5q11-5q11
 C:Keywords: glycoprotein; membrane protein

Query Match 14.2%; Score 329; DB 2; Length 918;
 Best Local Similarity 28.6%; Pred. No. 7.4e-19;
 Matches 88; Conservative 51; Mismatches 151; Indels 18; Gaps 8;

QY 46 ISPODPTLLIGSSIQATCSHG--DTPGATAGLVTNLGRLLPSELSTLNTSTLALA 102
 DB 31 ISPEPVVQLHSNFTACVLCVKEKCMDFHVNANVYWKTHFTPEQYTIINRTASSVT 90
 QY 103 LANLNGSRQOSDNLVCHARDGSIILAGSCLYGLPPEKPNISCSMRNKKDLTCRTPGA 162
 DB 91 FTDIASINQLTCLNLLFQLEQNYGITIISLPPKPNLCIYNEGKMKCEMDGGR 150
 QY 163 HGETFLHTNYSKYKLRWYGQDNTCEBYHTVGHSHIPKDLAFTPEIWEATNRLGS 222
 DB 151 --ETHLETNETLKSEWATHRFADCKAKROT--FTSCVDISTYFVNIWEVAENALGR 206
 QY 223 ARSDVLTLDVLTDPDPDVVSRVSGLEDLSVRWVSPALNDFLOAKQIIRYR 282
 DB 207 VTSDFHINFDVYKRPKPPNLSVINSEELSLIKLTWN-PSIKSVTI-LKYNIQYRK 264
 QY 283 DSYDMKVY--DDVSNQTSCLAGLKPQYFVQVRCNPGIYSGSKKAGIMSEMSHPTA 339
 DB 265 DASTWQIIPEDTASTRSSTVODLKPFTVEYFRIC-----KKEGQKWSMSSEAS 319
 QY 340 STPRSERP 347
 DB 320 IT-YEDRP 326

RESULT 3
 A57018
 prolactin receptor - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-Jul-1996
 C:Accession: A57018
 R:Fun, G.; Wells, J.A.
 J. Biol. Chem. 270, 13133-13137, 1995
 A:Title: prolactin receptor antisense constructs that inhibit the growth of breast cancer cell lines
 A:Reference number: A57018; MUID:95286597
 A:Accession: A57018
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-206 <RES>
 A:Cross-references: GB:S78505; NID:999114; PID:999115

Query Match 14.0%; Score 324.5; DB 2; Length 206;
 Best Local Similarity 38.0%; Pred. No. 2.4e-19;
 Matches 81; Conservative 25; Mismatches 90; Indels 17; Gaps 7;

QY 136 LPPEKPNISCSMRNKKDLTCRTPGAHGETFLHTNYSKYKLRWYGQDNTCEYTVGP 195
 DB 2 LPPEKPNISCSMRNKKDLTCRTPGAHGETFLHTNYSKYKLRWYGQDNTCEYTVGP 195
 QY 196 HSCHIPED-LALFTPEIWEATNRLGSARSDVLTLDVLTDPDPDVVSRVSGLED 254
 DB 60 NSCHFQKQYTSMTWTYIMVYINATNGSSSEDELYDVTVQDPDPLELA-ETVQPD 118
 QY 255 QLSVRYV--SPALKDF--LEQAKQIIRKVEDSDVMKYVVDVSNQTSCLAGLKPQY 309
 DB 119 RKPLWKMSPPPLIDLTGTFELKLEIRLKPKEAWE-IRFAGQOTEFKIISLPGRK 177
 QY 310 YFVQVRCNPGIYSGSKKAGIMSEMSHPTASTP 342
 DB 178 YLVQVRCKP-----DHGYSMSKSPATFIQIP 203

RESULT 4

149699
 glycoprotein 130 - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 07-Feb-1997
 C:Accession: 149699; 148370
 R:Saito, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.
 J. Immunol. 148, 4066-4071, 1992
 A:Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer,
 A:Reference number: 148370; MUID:92291532

QY 46 ISPODPTLLIGSSIQATCSHG--DTPGATAGLVTNLGRLLPSELSTLNTSTLALA 102
 DB 31 IYPEFPVQRGSNFTACVLCVKEACLOHYVYNASYIWKNNHAAVREQYTVINRTSSVT 90
 QY 103 LANLNGSRQOSDNLVCHARDGSIILAGSCLYGLPPEKPNISCSMRNKKDLTCRTPGA 162
 DB 91 FTDVVLPVQLCNILSFQIQDQNTYGYTMSLGFPPDKPTNLTICVNECKNMLCOMDPCR 150
 QY 163 HGETFLHTNYSKYKLRWYGQD--NICEEYHTVGHSHIPKDLAFTPEIWEATNRLG 221
 DB 151 --ETILENTYITLAKS--WATEKFPQCQSHGT---SCWYSIPTTYVNIWEVAENALG 203
 QY 222 SARSDVLTLDVLTDPDPDVVSRVSGLEDLSVRWVSPALNDFLOAKQIIRYR 281
 DB 204 KYSSSINDDPDYKRPKPPNLSVINSEELSLIKLSWVSSGL--GGLDLKSIDQYRT 261
 QY 282 EDSVDMKVY--DDVSNQTSCLAGLKPQYFVQVRCNPGIYSGSKKAGIMSEMSHPTA 338
 DB 262 KDASTWQIIPEDTASTRSSTVODLKPFTVEYFRIR----SIKDSGK-GYWSMSSEAS 316
 QY 339 AST--PRSERP 347
 DB 317 GTTYEDRPSRP 327

Query Match 13.8%; Score 319.5; DB 2; Length 917;
 Best Local Similarity 29.6%; Pred. No. 4.4e-18;
 Matches 92; Conservative 50; Mismatches 146; Indels 23; Gaps 10;

QY 46 ISPODPTLLIGSSIQATCSHG--DTPGATAGLVTNLGRLLPSELSTLNTSTLALA 102
 DB 31 IYPEFPVQRGSNFTACVLCVKEACLOHYVYNASYIWKNNHAAVREQYTVINRTSSVT 90
 QY 103 LANLNGSRQOSDNLVCHARDGSIILAGSCLYGLPPEKPNISCSMRNKKDLTCRTPGA 162
 DB 91 FTDVVLPVQLCNILSFQIQDQNTYGYTMSLGFPPDKPTNLTICVNECKNMLCOMDPCR 150
 QY 163 HGETFLHTNYSKYKLRWYGQD--NICEEYHTVGHSHIPKDLAFTPEIWEATNRLG 221
 DB 151 --ETILENTYITLAKS--WATEKFPQCQSHGT---SCWYSIPTTYVNIWEVAENALG 203
 QY 222 SARSDVLTLDVLTDPDPDVVSRVSGLEDLSVRWVSPALNDFLOAKQIIRYR 281
 DB 204 KYSSSINDDPDYKRPKPPNLSVINSEELSLIKLSWVSSGL--GGLDLKSIDQYRT 261
 QY 282 EDSVDMKVY--DDVSNQTSCLAGLKPQYFVQVRCNPGIYSGSKKAGIMSEMSHPTA 338
 DB 262 KDASTWQIIPEDTASTRSSTVODLKPFTVEYFRIR----SIKDSGK-GYWSMSSEAS 316
 QY 339 AST--PRSERP 347
 DB 317 GTTYEDRPSRP 327

RESULT 5
 A44257
 interleukin-6 signal transducing molecule gp130 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
 C:Accession: A44257
 R:Wang, Y.; Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M.
 Genomics 14, 666-672, 1992
 A:Title: Molecular cloning and characterization of the rat liver IL-6 signal transducing molecule
 A:Reference number: A44257; MUID:93052397
 A:Accession: A44257
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-918 <MAN>
 A:Experimental source: liver
 A>Note: sequence extracted from NCBI backbone (NCBIP:118488)
 C:Keywords: transmembrane protein

Query Match 13.7%; Score 317.5; DB 2; Length 918;

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RESULT      6
150455
P:prolactin receptor - pigeon
C:Species: Columba livia (domestic pigeon)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Sep-1996
C:Accession: I50455
R:Chen, X.; Horseman, N.D.
Endocrinology 135, 269-276, 1994
A:Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor
A:Reference number: I50455; MUID:94283267
A:Accession: I50455
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-830 <CHE>
A:Cross-references: EMBL:U07694; NID:g466381; PID:g466382

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Biochem. Biophys. Res. Commun. 168, 415-422, 1990
 A: Title: Isolation and characterization of two novel rat ovarian lactogen receptor cDNAs
 A: Reference number: A34631; MUID:90241201
 A: Accession: A34631
 A: Status: Preliminary
 A: Molecule type: mRNA
 A: Residues: 1-610 <ZHA>
 A: Cross-references: GB:M34083; NID:9205122; PID:9205123
 A: Note: The authors translated the codon GAG for residue 533 as Gly

RESULT 8
 A36116
 prolactin receptor 2 precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 28-Mar-1991 #sequence -revision 28-Mar-1991 #text_change 10-Sep-1997
 C:Accession: A36116
 R:Shiota, M.; Banville, D.; Alt, S.; Jolicoeur, C.; Boutin, J.M.; Ederly, M.; Djiane, M.; Endocrinol. 4, 1156-1143, 1990
 A:Title: Expression of two forms of prolactin receptor in rat ovary and liver.
 A:Reference number: A36116; PMID:91155946
 A:Accession: A36116
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-610 <SH>
 A:Cross-references: GB:M57668; NID:q206366; PID:q206367; GB:M60728

Query Match	13.5%	Score 312:	DB 2:	Length 610:
Best Local Similarity	35.4%	Pred. No. 1e-17:		
Matches	80:	Conservative	35:	Mismatches 85: Indels 26: Gaps 10:
QY	125	SIAGSCLYGLPEKPEPNISCSWRNNKDLTCRWTPGAHGTEFLHTNSIKYLRMGOD	184	
DB	15	SILKQSG-----PGKPEIHKCRSPDKETTCWNPBTDGG--LPINYSILYTSKE--	65	
QY	165	NT--CEEHWYGFPSCHAPKD-LALTPPYEITWEATNRGLSASDVLLTDVYVTTDPP	241	
DB	66	TYECPDKITSGPNSCFEFSKQYTSIMWYIYITYNATQWOMSSSDPLVDVYVYVEPEPP	125	
QY	242	PDVHVSIRGGLEDLSTRWV--SPPALKDF--LDAQYQIRRVSDSDMKYDVDSNQ	296	
DB	126	RNLL-ETKQAKDKKJILWYKMSPTITTDYKGTGFTWNEIRIKPEAEWE-INTGHQ	183	
QY	297	TSCRLAGIKPGTYIVFVQVRCNPFGLYGSKAGIWMSESHPTAASP	342	
DB	184	TQKVFDFLYPGQKLYVTRCKP-----DHGYSMASQSSSESVEMP	222	
RESULT	9			
AA1070				
Prolactin receptor Nb2 precursor - rat				

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 10-Sep-1997
 C:Accession: A41070; 153417
 R:Ali, S.; Pellegrini, I.; Kelly, P.A.
 J. Biol. Chem. 266, 20110-20117, 1991
 A:Title: A prolactin-dependent immune cell line (Nb2) expresses a mutant form of prolactin
 A:Reference number: A41070; MUID:92041834
 A:Accession: A41070
 A:Molecule type: mRNA
 A:Residues: 1-412 <ALI>
 A:Cross-references: GB:M74152; NID:g206389; PID:g206390
 R:O'Neal, K.D.; Yu-Lee, L.Y.
 J. Biol. Chem. 269, 26076-26082, 1994
 A:Title: Differential signal transduction of the short, Nb2, and long prolactin receptor
 A:Reference number: 153417; MUID:95014432
 A:Accession: 153417
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-412 <RES>
 A:Cross-references: EMBL:U07567; NID:g641963; PID:g641964
 A:Experimental source: Nb2-11C cell line
 C:Keywords: transmembrane protein

Query Match 13.5%; Score 312; DB 2; Length 412;
 Best Local Similarity 35.4%; Pred. No. 6.2e-18;
 Matches 80; Conservative 35; Mismatches 85; Indels 26; Gaps 10;

QY 125 SLLAGSCLYVGLPEKPFNISCWNRMDLTCRWTPGANGFELHNTSLKRLMYGOD 184
 15 SLLKGS-----PPGKPELHKCRSPKKEFTCWANFGDGG--LPTNLSLTSKE--GEK 65
 DB 185 NR--CEEYHTVGPBHSCHIRKDLAETPEYIWEATNRLGSARSDLTLDVDTTDP 241
 66 TYEECPDYKTSQPNSCFEFSKOYTSIKWYIITVYATNNGSSSDPLYDVDTYIYEPEP 125
 QY 242 PNVHVSRYVGLDGLDQSVKRV--SPPLAKDF--LEQAKQIYRVEDSVDMKRVDDVSNQ 296
 126 RMLTL-EVAKQLDKTKTYLWVKMSPPTITDVKGTGWTMEYELKKEEAEME-IHFTGHQ 183
 QY 297 TSCRLAGLPGTYVYFVQVRCNPFGIYGSKKAGIWMSEMSHPTAASP 342
 184 TQFKVFDLYPGQKYLVTQRCR-----DHGYMSRMSSESSVEMP 222
 DB

RESULT 10

prolactin receptor precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 20-Mar-1998
 C:Accession: A29884
 R:Boutin, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Edery, M.; Shiotto, M.; Bannyille
 Cell 53, 69-77, 1988
 A:Title: Cloning and expression of the rat prolactin receptor, a member of the growth ho
 A:Reference number: A29884; MUID:86165059
 A:Accession: A29884
 A:Molecule type: mRNA
 A:Residues: 1-310 <BOU>
 A:Cross-references: GB:M19304; NID:g206364; PID:g206365
 C:Keywords: transmembrane protein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-310/Product: prolactin receptor #status predicted <MAT>

Query Match 13.5%; Score 312; DB 2; Length 310;
 Best Local Similarity 35.4%; Pred. No. 4.3e-18;
 Matches 80; Conservative 35; Mismatches 85; Indels 26; Gaps 10;

QY 125 SLLAGSCLYVGLPEKPFNISCWNRMDLTCRWTPGANGFELHNTSLKRLMYGOD 184
 15 SLLKGS-----PPGKPELHKCRSPKKEFTCWANFGDGG--LPTNLSLTSKE--GEK 65
 DB 185 NR--CEEYHTVGPBHSCHIRKDLAETPEYIWEATNRLGSARSDLTLDVDTTDP 241

DB 66 TYEECPDYKTSQPNSCFEFSKOYTSIKWYIITVYATNNGSSSDPLYDVDTYIYEPEP 125
 QY 242 PNVHVSRYVGLDGLDQSVKRV--SPPLAKDF--LEQAKQIYRVEDSVDMKRVDDVSNQ 296
 126 RMLTL-EVAKQLDKTKTYLWVKMSPPTITDVKGTGWTMEYELKKEEAEME-IHFTGHQ 183
 QY 297 TSCRLAGLPGTYVYFVQVRCNPFGIYGSKKAGIWMSEMSHPTAASP 342
 184 TQFKVFDLYPGQKYLVTQRCR-----DHGYMSRMSSESSVEMP 222
 DB

RESULT 11

prolactin receptor 2 precursor - rabbit
 A:Accession: A30304
 A:Residues: 1-616 <EDB>
 A:Cross-references: GB:J04510; NID:g165669; PID:g165670
 R:Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I.
 Int. J. Biochem. 22, 1089-1095, 1990
 A:Title: Purification and partial sequence of the rabbit mammary gland prolactin rec
 A:Reference number: A60380; MUID:91146782
 A:Accession: A60380
 A:Molecule type: protein
 A:Residues: 41-58, 'X', 60-66, 90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108, 150-164, 'XX'
 A:Note: the amino end of the mature protein was blocked
 C:Keywords: blocked amino end; glycoprotein; transmembrane protein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-616/Product: prolactin receptor 2 #status predicted <MAT>
 F:235-258/Domain: transmembrane #status predicted <TM>
 F:59,104,132,347,389,411/Binding site: carbohydrate (asn) (covalent) #status predict

Query Match 13.3%; Score 307.5; DB 2; Length 616;
 Best Local Similarity 36.3%; Pred. No. 2.4e-17;
 Matches 77; Conservative 26; Mismatches 90; Indels 17; Gaps 7;

QY 137 PPKPFNISCWNRMDLTCRWTPGANGFELHNTSLKRLMYGODNCEHYHTVGP 196
 DB 27 PPKPFNISCWNRMDLTCRWTPGANGFELHNTSLKRLMYGODNCEHYHTVGP 196
 QY 197 SCHI-PRDLAETPEYIWEATNRLGSARSDLTLDVDTTDPDPVHVSRYVGLDQ 255
 85 SCYRSKHTSTWYIITVYATNNGSSSDPLYDVDTYIYEPEPVLTL-EVAKHEDR 143
 DB 256 LSVHVS--SPPLAKDF--LEQAKQIYRVEDSVDMKRVDDVSNQSCRLAGLPGTYV 310
 144 KPYLWVKMSPPTITDVKGTGWTMEYELKKEEAEME-IHFAQOQTFKLSLTPQOKY 202
 QY 311 FVQVRCNPFGIYGSKKAGIWMSEMSHPTAASP 342
 DB 203 LVQVRCR-----DHGYMSRMSSESSVEMP 222

RESULT 12

prolactin receptor precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 02-Aug-1996
 C:Accession: I77524
 R:Davis, J.A.; Linzer, D.I.H.
 Mol. Endocrinol. 3, 674-680, 1989
 A:Title: Expression of multiple forms of the prolactin receptor in mouse liver.
 A:Reference number: 157699; MUID:89261834

A:Accession: J01655
A:Molecule type: mRNA
A:Residues: 1-831 <TAN>
A:CROSS-references: DDBJ:D13154; NITD:G222848; PTD:d1002939; PTD:G222849
A:Experimental source: Kidney
C:Keywords: glycoprotein; transmembrane protein
F:1-33/Domains: signal sequence [status predicted <SIG>
F:24-83/Product: prolactin receptor [status predicted <MAT>
F:439-642/Domains: transmembrane [status predicted <MEM>
F:59, 91, 100, 112, 132, 262, 303, 315, 335, 647, 701, 800/Binding site: carbohydrate (Asn) (coval)

Query Match	13.2%;	Score 306;	DB 2;	length 831;
Best Local Similarity	35.0%;	Pred. NO. 4.8e-17;		
Matches	76;	Conservative	27;	Mismatches 96;
			Indels	18;
			Gaps	8;

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QY 137 PPEPENTSCSRNNKDLTCWTEGAGETFLH-TNYSLAYKULRWGQDNCEHNYGP 155
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 230 PPEKPTIKCSPEKEFTTCMKWGLDGG---HPTNTILKSGEGEQVTECPDYFTAG 286
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 196 HSCHI-PRDALLFTPEYIWEATNRLKSARSVDYLLTDVLTDDVTTPPEPDY--HVSRYGGL 252
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 287 NSCFDKKHITSFTIYNTIVATNEMGSSNDPHYVDYTIYQDPYVNTLEKPKINR 346
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 253 EDOLSVKRVSPALKDF---LFQAKYIIRKRVEDSDVMKVVDDVSNQTSCLAGLRPGTV 309
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 347 KPYLYLTW-SPPPLADVRSGWLTLEYELRLRKPPEGEGEMETI-FVGQOTQYKMFSLNPGKK 404
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 310 YFVQVRCPFGITGSKNAGISESHPTLASTPESER 346
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 405 YTIQHKCP-----DHGGSNWSSESNYIQIPDPR 435
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

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Search completed: September 16, 1999, 20:42:07
Job time: 5400 sec

1	333	14.3	622	1	PRLR_HUMAN
2	329	14.2	918	1	IL6B_HUMAN
3	319.5	13.8	917	1	IL6B_MOUSE
4	317.5	13.7	918	1	IL6B_RAT
5	314	13.6	830	1	PRLR_COLTI
6	312	13.5	610	1	PRLR_RAT
7	307.5	13.3	608	1	PRLR_MOUSE
8	307.5	13.3	831	1	PRLR_RABIT
9	306	13.2	831	1	PRLR_CHICK
10	305	13.2	831	1	PRLR_CHELSEA
11	303	13.1	581	1	PRLR_BOVINE
12	302.5	13.1	581	1	PRLR_ORENI
13	261.5	11.3	630	1	GCSR_HUMAN
14	254.5	11.0	836	1	GCSR_MOUSE
15	252.5	10.9	837	1	CNTR_RAT
16	234	10.1	372	1	CNTR_HUMAN
17	222.5	9.6	372	1	CNTR_CHICK
18	208	9.0	362	1	IL6A_HUMAN
19	202.5	8.7	460	1	IL6A_RAT
20	200.5	8.7	468	1	LIFR_HUMAN
21	196.5	8.5	462	1	LIFR_MOUSE
22	192.5	8.3	635	1	LIFR_HUMAN
23	191.5	8.3	1162	1	LIFR_MOUSE
24	190	8.2	1097	1	LIFR_HUMAN
25	190	8.2	625	1	LIFR_MOUSE
26	185	8.0	1092	1	LIFR_HUMAN
27	175	7.6	427	1	LIFR_MOUSE
28	174.5	7.5	1165	1	LIFR_HUMAN
29	170	7.3	888	1	UPO_MOUSE
30	164.5	7.1	638	1	GHR_RABBIT
31	158.5	6.8	508	1	EPOR_HUMAN
32	157	6.8	507	1	EPOR_RAT
33	156.5	6.8	638	1	EPOR_PIG
34	155	6.7	507	1	EPOR_MOUSE
35	151	6.5	638	1	GHR_HUMAN
36	148.5	6.4	897	1	AXOL_RAT
37	147	6.3	1040	1	AXOL_MOUSE
38	146.5	6.3	424	1	IL3_MOUSE
39	145	6.3	634	1	GHR_SHEEP
40	143.5	6.2	380	1	IL32_HUMAN
41	143	6.2	638	1	GHR_RAT
42	140.5	6.1	650	1	GHR_MOUSE
43	140.5	6.1	297	1	GHR_MOUSE
					P16471 homo sapien
					P40188 homo sapien
					O00560 mus musculu
					P40190 rattus norv
					O00374 columba liv
					P05710 rattus norv
					O08501 mus musculu
					P14787 cryotolagus
					O04394 gallus gall
					O28325 meleagris g
					O28325 cervus elap
					O28172 bos taurus
					O91513 oreochromis
					O090652 homo sapien
					P40223 mus musculu
					O08406 rattus norv
					P26992 homo sapien
					P51641 gallus gall
					P22272 mus musculu
					P08887 homo sapien
					P22273 rattus norv
					P40238 homo sapien
					P48356 mus musculu
					P42702 homo sapien
					O08351 mus musculu
					P42703 mus musculu
					P78552 homo sapien
					P48357 homo sapien
					O00993 mus musculu
					P19941 cryotolagus
					P19235 homo sapien
					O07303 rattus norv
					P19756 sus scrofa
					P14753 mus musculu
					P10912 homo sapien
					P32527 homo sapien
					P22063 rattus norv
					O09030 mus musculu
					O28575 ovls aries
					O41657 homo sapien
					P16130 rattus norv
					P16882 mus musculu
					P16590 mus musculu

Best Local Similarity 37.5%; Pred. No. 1.8e-19;
Matches 84; Conservative 37; Mismatches 46

Query	Match	Best Local Similarity	Score	DB 1:	Length
Matches	88	Conservative	51	Mismatches	151
				Indels	18
				Gaps	
QY	46	ISPDPTLLIGSSLSQATCSING--DTPGATAEGLYTLNLRRLPSELSRLNSTLALA	107		
Db	31	ISPESPVQLHSNFTLAVCLNEKCMDFHVNANIVKTNFTLPRQYTIINNTASSVT	90		
QY	103	LANLNGSQSGDNILVCHARGSLIAGSCLYGLPPEKPERNISCSWRNMKDLTCRWTPGA	165		
Db	91	FTDIASLNIQTLNCILFFGLEQHWYGIITISGLPPEKPKNLSCIVNEGKMKRCMEWGR	156		
QY	163	HGETFLATNTYSLAKTKLRWYGDNCEEHWTGSPHSCHIKDLAFTPEIWEATNRLGS	222		
Db	151	--EHLLENFLKEMATHKRADKARDT--PISCTVDISTYFVNIENWAEENLKG	206		
QY	223	ARSDVLIDVLVDVTTTPPDVHVSRYGLEDQLSVKWSVPALKDELFOAKYIRRYVE	283		
Db	207	VTSIDHNEPDYKPKPNPHLSYINSEELSSILKLTMTN-PSIKSVYII-LKYNIOYRTK	265		
QY	283	DSYVMKVY---DVSNQTSCLAGLKGTYFYVQRCNPNPGIYSSKNAQINSESHPTAA	333		
Db	265	DASTWSQIPEPDITASTRSSFTVDLKEPTEYFIRIC---MKEDGKGYMSDWEASG	319		
QY	340	STPSRSP 347			
Db	320	IT-YEDR 326			
RESULT	3				
IL6B_MOUSE	STANDARD;	PRT;	917 AA.		
AC	000560;				
DT	01-FEB-1995 (REL. 31, CREATED)				
DT	01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)				
DT	15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)				
DE	INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKININ-6 SIGNAL TRANSUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).				
GN	IL6ST.				
OS	MUS MUSCULUS (MOUSE).				

CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC RODENTIA; SCURIONATHI; MORIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ICR; TISSUE-MACROPHAGE;
 RX MEDLINE; 92291532.
 RA SAITO M., YOSHIDA K., HIRI M., TAGA T., KISHIMOTO T.;
 RT "Molecular cloning of a murine IL-6 receptor-associated signal
 transducer, gp130, and its regulated expression in vivo."
 J. IMMUNOL. 148:4066-4071(1992).
 CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
 IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
 SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
 RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
 AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
 EMBRYONIC DEVELOPMENT.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: FOUND IN TISSUES SUCH AS BRAIN, HEART, THYMUS,
 SPLEEN, KIDNEY, LUNG AND LIVER. FOUND IN ALL THE CELL LINES TESTED
 EXCEPT BAF-B03. EXPRESSION NOT RESTRICTED TO IL-6-RESPONSIVE
 CELLS.
 CC -1- DEVELOPMENTAL STAGE: IN EMBRYONIC STEM CELLS IT IS FOUND FROM DAY
 6 OF GESTATION. IT REACHES A PEAK ON DAY 8 AND GRADUALLY DECLINES
 DURING THE REST OF EMBRYOGENESIS.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -----
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 CC -----
 CC EMBL; X62646; G840817;
 CC EMBL; M83336; G193592;
 CC MGD; MGI:96560; IL6ST.
 CC PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
 CC PFM; PF00041; fn3; 3.
 CC HSSP; P40189; IL6U.
 CC RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
 CC REPEAT.
 CC SIGNAL.
 CC CHAIN 1 22
 CC DOMAIN 23 917 POTENTIAL.
 CC TRANSMEM 618 617 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
 CC DOMAIN 640 917 EXTRACELLULAR (POTENTIAL).
 CC DOMAIN 26 120 POTENTIAL.
 CC DOMAIN 221 322 CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 323 420 IG-LIKE C2-TYPE DOMAIN.
 CC DOMAIN 516 611 FIBRONECTIN TYPE-III.
 CC DOMAIN 723 741 FIBRONECTIN TYPE-III.
 CC DISULFID 134 144 SER-RICH.
 CC DISULFID 172 180 BY SIMILARITY.
 CC CARBOHYD 43 43 POTENTIAL.
 CC CARBOHYD 61 61 POTENTIAL.
 CC CARBOHYD 83 83 POTENTIAL.
 CC CARBOHYD 131 131 POTENTIAL.
 CC CARBOHYD 157 157 POTENTIAL.
 CC CARBOHYD 225 225 POTENTIAL.
 CC CARBOHYD 388 388 POTENTIAL.
 CC CARBOHYD 476 476 POTENTIAL.
 CC CARBOHYD 551 551 POTENTIAL.
 CC SEQUENCE 917 AA; 102452 MW; A5DCD259 CRC32;
 CC Query Match 13.8%; Score 319.5; DB 1; Length 917;

Best Local Similarity 29.6%; Pred. No. 2,5e-18;
 Matches 92; Conservative 50; Mismatches 146; Indels 23; Gaps 10;
 QY 46 ISPDPTLLISSSLQACNSHG---DTPGATAEGLWTLNCRRLPSLSRLNTSTALA 102
 DB 31 IYPEPVPVQRSNFTALCVLKEACLOHYVNAVSYIWKNTNAAPRQVYINNTTSVT 90
 QY 103 LANNGSMQSGDULVCHARDGSLIAGSLYGPPEKPFISCSWNRMDLCRTWPGA 162
 DB 91 FTDVVLSVQLTCLISLFGQEQONVAVTMLSGPPKPNLTICIVEGNMLCQMPGR 150
 QY 163 HGEFLTNLSLKLKRWYGD-NTCEHYHVGPHSCHIRDLALFPEYELWATNRGL 221
 DB 151 -EYLENTLTKAE-WAKRFPDCKSKGT---SCWSTMPYTYNIEVWEAENALG 203
 QY 222 SARSDVLTLDVLTTPDPDVHVSNGVGLDLSYRWSPALKDFLQAKYQIRRV 281
 DB 204 KVSSESIINFPDVKRPTLPYKNTSVTSESLSLKSWSSG--GGLLDKSDIORYT 261
 QY 282 EDSVDKTV---DVSNOTGCRAGLAPGVYVQVQCNPFGLYSGKKAGIWEWSHPTA 338
 DB 262 KDASTWQVLEDTMSRTSTFYQDLKPFTEYFRIR---SIRDSGK-GYMSDWSSEAS 316
 QY 339 ASR--PSESRP 347
 DB 317 GTTYEDRPSRP 327
 RESULT 4
 ID IL6B_RAT STANDARD; PRT; 918 AA.
 AC P40130;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
 DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN I30) (GP130).
 GN IL6ST.
 OS RATUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC RODENTIA; SCURIONATHI; MORIDAE; MURINAE; RATIUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER;
 RX MEDLINE; 93052397.
 RA WANG Y., NESBITT J.E., FUENTES N.L., FULLER G.M.;
 RT "Molecular cloning and characterization of the rat liver IL-6 signal
 transducing molecule, gp130."
 RL GENOMICS 14:666-672(1992).
 CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
 IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
 SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
 RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
 AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
 EMBRYONIC DEVELOPMENT (BY SIMILARITY).
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS
 AND ENDOTHELIAL CELLS.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M92340; --; NOT_ANNOTATED_CDS.

DR PIR: A44257: A44257.
 DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR PFAM: PF00041; fn3; 3.
 DR HSSP: P40189; 1BOU.
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
 REPEAT
 FT SIGNAL 1 22
 FT CHAIN 23 918
 FT DOMAIN 23 618
 FT TRANSMEM 619 640
 FT DOMAIN 641 918
 FT DOMAIN 26 120
 FT DOMAIN 124 221
 FT DOMAIN 222 323
 FT DOMAIN 324 422
 FT DOMAIN 423 516
 FT DOMAIN 517 612
 FT DOMAIN 724 754
 FT DISULFID 134 144
 FT DISULFID 172 181
 FT CARBOHYD 43 43
 FT CARBOHYD 61 61
 FT CARBOHYD 83 83
 FT CARBOHYD 131 131
 FT CARBOHYD 157 157
 FT CARBOHYD 205 205
 FT CARBOHYD 226 226
 FT CARBOHYD 382 382
 FT CARBOHYD 389 389
 FT CARBOHYD 477 477
 FT CARBOHYD 552 552
 SQ SEQUENCE 918 AA; 102450 MW; E6EDFCD0 CRC32;

Query Match 13.7%; Score 317.5; DB 1; Length 918;
 Best Local Similarity 29.8%; Pred. No. 3.7e-18;
 Matches 92; Conservative 51; Mismatches 145; Indels 21; Gaps 10;

QY 46 ISQODFTLIGSLQATCSHG--DTPGATAGLYWTNGRLPSELRLNTSTLATA 102
 DB 31 IYEFYVVOGSGNFTATVLEKELQVSYNATYIWKTHNVAPEQVTVINRTASSVT 90
 QY 103 LANLNGSROOSGNLYCHARDGSIILAGSCLYVGLPREKPNISGSRNKKDLTCRTPCA 162
 DB 91 FTVVVEQVQVQVLCNLTISFGQIEQVNYGITILSGYPPDIPNLNLSINEKMKLCQDPPR 150
 QY 163 HGEFTLHTNSLKYKLRMTGOD-NTCEHYTVGPHSCHIPKDLALTPYEIWEATNRUG 221
 DB 151 --ETIETINTLKSE--WATEKPPDRTKH--GTSSCMAGYPIIYVNIWEAENALG 204
 QY 222 SARSDVLTLDVLDVTTDPDPVHVSRYVGLLEDOLSVRWVSPALNDLFOAYQIRYEV 281
 DB 205 NYSSEPIINFDVQKVPSPHNLSTNSELISILKIAVNSGL--DSILRLKSDIQYRT 262
 QY 282 EDSVDKVV--DDVSNQISCRAGLAKPGIVYVQVRCNPFGLYSGKAKGINSNSHPA 338
 DB 263 KASTAIQVPLEDTVSPRSTFVQDKPTEYVFRIR---SIKENGK-GYSDWSE-RA 316
 QY 339 ASTPSEPR 347
 DB 317 SGTTYEDRP 325

RESULT 5
 PRIR COLLI STANDARD; PRT: 830 AA.
 ID 090374:
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
 GN PRLR.
 OS COLUMBA LIVIA (DOMESTIC PIGEON).

CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
 CC NEOGNATHAE; COLUMBIFORMES; COLUMBIDAE; COLUMBA.
 RN [1]
 RC SEQUENCE FROM N.A.
 RX TISSUE-CROPSAC.
 RA MEDLINE: 94283267.
 RA CHEN X., HORSEMAN N.D.;
 FT "Cloning, expression, and mutational analysis of the pigeon prolactin
 RT receptor".
 RL ENDOCRINOLOGY 135:269-276(1994).
 CC - FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC - SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC - SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC
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DR EMBL: U07694; G466382;
 DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 2.
 DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 2.
 DR PFAM: PF00041; fn3; 4.
 DR HSSP: P16471; 1BP3.

KM RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
 FT SIGNAL 1 23
 FT CHAIN 24 830
 FT DOMAIN 24 439
 FT TRANSMEM 440 460
 FT DOMAIN 461 830
 FT DOMAIN 23 122
 FT DOMAIN 123 226
 FT DOMAIN 229 326
 FT DOMAIN 327 429
 FT DISULFID 36 46
 FT DISULFID 75 86
 FT CARBOHYD 59 59
 FT CARBOHYD 91 91
 FT CARBOHYD 100 100
 FT CARBOHYD 112 112
 FT CARBOHYD 132 132
 FT CARBOHYD 263 263
 FT CARBOHYD 304 304
 FT CARBOHYD 316 316
 FT CARBOHYD 336 336
 SQ SEQUENCE 830 AA; 94507 MW; 5EPAD051 CRC32;

Query Match 13.6%; Score 314; DB 1; Length 830;
 Best Local Similarity 37.1%; Pred. No. 6.2e-18;
 Matches 76; Conservative 29; Mismatches 82; Indels 18; Gaps 8;

QY 137 PREKPNISGSRNKKDLTCRTPCAAGETPIH-INYSLKYLAHNYGDNTEEHYVGP 195
 DB 231 PEKPTIILKCRSPKEETFCWKRPGSDG--HPNITLLYSKEEERYECPPDYKTGP 287
 QY 196 HSCHT-PRDLAFTPEYIWEATNRLGSARSDVLTLDVYVTTDPDPV--HYSRVGL 252
 DB 288 NSCFYDKHTSWITINITYKATINIGSVSDPLVYDTYIYOTDPPVAVTILEKKTYYNR 347
 QY 253 EDQLSVRWVSPALDGF--LEQAYQIRYEVSDVKRVVDVSNQTSCLAGLPGTV 309
 DB 348 KRYLVLTW-SPPLADVSGMLTLDYELRLKPEEALEMETI-FVGOQTHYKAFSLNPGKK 405
 QY 310 FVVOVRCNPFGLYSGKAKGINSNS 334
 DB 406 IYVQIHCKP-----DHGGSWSEWS 424

RESULT 6
PRLR_RAT 6
STANDARD: PRT: 610 AA.
ID PRLR_RAT 063451: 063723: 062832: 064274: 063479;
AC 05710: 063451: 063723: 062832: 064274: 063479;
DT 01-NOV-1988 (REL. 09, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (LACTOGEN RECEPTOR).
PR: PRL.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCURIONATHI; MORIDA; MORINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91155946.
RA SHIROTA M., BANVILLE D., ALI S., JOLICOEUR C., BOUTIN J.M.,
EDERY M., DJIANE J., KELLY P.A.;
RT "Expression of two forms of prolactin receptor in rat ovary and
liver."
RL MOL. ENDOCRINOL. 4:1136-1143(1990).
[2]
RP SEQUENCE FROM N.A. (LONG FORM AND SHORT FORM).
RX STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY;
MEDLINE: 90241201.
RA ZHANG R., BUCCIO E., TSAI-MORRIS C.H., HU Z.Z., DUFAY M.L.;
RT "Isolation and characterization of two novel rat ovarian lactogen
receptor cDNA species."
RL BIOCHEM. BIOPHYS. RES. COMMUN. 168:415-422(1990).
[3]
RP SEQUENCE OF 281-610 FROM N.A.
RX BANVILLE D., STOCO R., MURTHY K.K., BOIE Y., KELLY P.A.;
SUBMITTED (MAR-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
[4]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (MEDIUM FORM).
RX TISSUE-LIVER;
MEDLINE: 88165059.
RA BOUTIN J.M., JOLICOEUR C., OKAMURA H., GAGNON J., EDERY M.,
SHIROTA M., BANVILLE D., DUSANTER-FOUR I., DJIANE J., KELLY P.A.;
RT "Cloning and expression of the rat prolactin receptor, a member of
the growth hormone/prolactin receptor gene family."
RL CELL 53:69-77(1988).
[5]
RP SEQUENCE FROM N.A. (FORM NB2).
RX TISSUE-LYMPHOMA;
MEDLINE: 92041834.
RA ALI S., PELLIGRINI I., KELLY P.A.;
RT "A prolactin-dependent immune cell line (NB2) expresses a mutant form
of prolactin receptor."
RL J. BIOL. CHEM. 266:20110-20117(1991).
[6]
RP SEQUENCE FROM N.A. (FORM NB2).
RX MEDLINE: 95014432.
RA O'NEAL K.D., YU-LEE L.Y.;
RT "Differential signal transduction of the short, NB2, and long
prolactin receptors. Activation of interferon regulatory factor-1 and
cell proliferation."
RL J. BIOL. CHEM. 269:26076-26082(1994).
[7]
RP FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
PROLACTIN.
[8]
RP SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
[9]
RP ALTERNATIVE PRODUCTS: DIFFERENT FORMS ARE PRODUCED BY ALTERNATIVE
SPLICING OF THE PRLR GENE.
[10]
RP SIMILARITY: BELONGS TO THE CYTOKINE FAMILY III-LIKE DOMAINS.
[11]
RP SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
[12]
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CC EMBL: M57668; G206367; -
DR EMBL: M34083; G205123; -
DR EMBL: L48060; G1019651; -
DR EMBL: U34730; G1223859; -
DR EMBL: M19304; G206365; -
DR EMBL: M74152; G206380; -
DR EMBL: U07567; G641964; -
DR PIR: A29884; A29884.
DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
DR PFAM: PF00041; fn3; 2.
DR HSSP: P16471; 1B3.
KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT;
RV ALTERNATIVE SPLICING.
FT SIGNAL 1 19
FT CHAIN 20 610
FT DOMAIN 20 229
FT TRANSMEM 230 253
FT DOMAIN 254 610
FT DOMAIN 20 117
FT DOMAIN 119 222
FT DISULFID 31 41
FT DISULFID 70 81
FT CARBOHYD 34 54
FT CARBOHYD 99 99
FT CARBOHYD 127 127
FT CARBOHYD 131 150
FT VARSPPLIC 151 610
FT VARSPPLIC 281 310
FT VARSPPLIC 311 610
FT VARSPPLIC 342 539
FT CONFLICT 236 236
FT CONFLICT 345 345
FT CONFLICT 465 465
FT CONFLICT 466 466
FT CONFLICT 469 469
FT CONFLICT 541 541
FT CONFLICT 555 555
SQ SEQUENCE 610 AA; 68599 MW; C579BC43 CRC32;

Query Match 13.5%; Score 312; DB 1; Length 610;
Best Local Similarity 35.4%; Pred. No. 6e-18;
Matches 80; Conservative 35; Mismatches 85; Indels 26; Gaps 10;

QY 125 SIAGSCLYVGLPEKPFNISCMSRMKDLGKTPGANGETFLHNTSLKTKLRMYGOD 184
DB 15 SILKGS-----PQKPELHCKRSPDKETFTWMNGDGG--LPTNLSLYSKE--GEK 65
QY 185 NT--CEEYTVGPHSCHIPKD-LAFTPEIWEATNRLGARSVDLVTDVDTTPDP 241
DB 66 TYECPDYKTSGPSNCFKSYSTIMKIIITVNAITNMGSSSPLVYDVYIYEPSP 125
QY 242 PNYHNRVGGLEDQSLVKNV--SPALRDE--LEQARYQIYRVEDSDVMDVVDVSNQ 296
DB 126 RNLTL-ERKQLDKKTYLWVKWSPPTIDVKTGFTMEYELRLKEALEME--HFTGHQ 183
QY 297 TSCRLAGLKGIVYVVOYRQCNPFYIGSKKAGIWEHSPRAASP 342
DB 184 TQFKFDLYPGQKLYVQTRCKP-----DHGYSRWQSSSEVEMP 222

RESULT 7
PRLR_MOUSE
ID PRLR_MOUSE STANDARD: PRT: 608 AA.
AC 008501: 062099: P15213: P15212;
DT 01-APR-1990 (REL. 14, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
 GN PRLR.
 OS MUS MUSCULUS (MOUSE).
 OC EUDARTOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC ROENTIA; SCIROGNATHI; MORIDA; MORINAE; MOS.
 RN [1]
 RP SEQUENCE FROM N.A. (FORM PRL-R3).
 RC STRAIN-C3H; TISSUE-MAMMARY GLAND;
 RX MEDLINE: 94085788.
 RA MOORE R.C., OKA T.;
 RT "Cloning and sequencing of the cDNA encoding the murine mammary gland
 RT long-form prolactin receptor.";
 RL GENE 134:263-265(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (FORM PRL-R3).
 RC STRAIN-SWISS WEBSTER; TISSUE-LIVER;
 RX MEDLINE: 93307149.
 RA CLARKE D.L., LINZER D.I.H.;
 RT "Changes in prolactin receptor expression during pregnancy in the
 RT mouse ovary.";
 RL ENDOCRINOLOGY 133:224-232(1993).
 RN [3]
 RP SEQUENCE FROM N.A. (FORM PRL-R3).
 RA SASAKI M.;
 RL SUBMITTED (JUL-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [4]
 RP SEQUENCE FROM N.A. (FORM PRL-R3).
 RC STRAIN-BALB/C; TISSUE-MAMMARY GLAND;
 RA EDERY M., PEZET A., NANDI S., KELLY P.A.;
 RL SUBMITTED (JUN-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [5]
 RP SEQUENCE FROM N.A. (FORMS PRL-R2 AND PRL-R1).
 RC STRAIN-SWISS WEBSTER; TISSUE-LIVER;
 RX MEDLINE: 89261824.
 RA DAVIS J.A., LINZER D.I.H.;
 RT "Expression of multiple forms of the prolactin receptor in mouse
 RT liver.";
 RL MOL. ENDOCRINOL. 3:674-680(1989).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN, AS WELL AS PLACENTAL LACTOGEN I AND II.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: THREE FORMS, PRL-R1, PRL-R2 AND PRL-R3
 CC (SHOWN HERE) ARE PRODUCED BY ALTERNATIVE SPLICING OF THE PRLR
 CC GENE.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: L13593; G347842; -
 DR EMBL: L14811; G283770; -
 DR EMBL: D10214; G220576; -
 DR EMBL: X73372; G312697; -
 DR EMBL: M22959; G200482; -
 DR EMBL: M22958; G200480; -
 DR PIR: J06711; J06711.
 DR MGD: MGI:9763; PRLR.
 DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
 DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; FALSE-NEG.
 DR HSSP: P16471; IBS3; 2.
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT;
 KM ALTERNATIVE SPLICING.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 608 PROLACTIN RECEPTOR.
 FT DOMAIN 20 229 EXTRACELLULAR (BY SIMILARITY).
 FT TRANSMEM 230 253 BY SIMILARITY.

FT DOMAIN 254 608 CYTOPLASMIC (BY SIMILARITY).
 FT CHAIN 20 117 FIBRONECTIN TYPE-III.
 FT DOMAIN 119 222 FIBRONECTIN TYPE-III.
 FT DISULFID 31 41 BY SIMILARITY.
 FT DISULFID 70 81 BY SIMILARITY.
 FT CARBOHYD 54 54 POTENTIAL.
 FT CARBOHYD 99 99 POTENTIAL.
 FT CARBOHYD 127 127 POTENTIAL.
 FT VARSPLIC 281 292 MISSING (IN PRL-R1).
 FT VARSPLIC 293 608 MISSING (IN PRL-R2).
 FT VARSPLIC 281 303 MISSING (IN PRL-R2).
 FT VARSPLIC 304 608 MISSING (IN PRL-R1).
 FT CONFLICT 558 558 MISSING (IN REF. 2).
 SO SEQUENCE 608 AA; 68240 MR; AA01E67 CAC32.
 Query Match 13.3%; Score 307.5; DB 1; Length 608;
 Best Local Similarity 32.6%; Pred. No. 1,4e-17;
 Matches 85; Conservative 37; Mismatches 92; Indels 47; Gaps 11;
 QY 90 LSRLLNTSTALALANNGSRHSGDNLVCHARDGSLAGSCLVGLPEKPEFNSICMR 149
 Db 1 MSSALAYMLLYLSISLNG--OS-----PPGKPEIHKCRSP 34
 QY 150 NMKDLTCRWTPGAHGETFLHTNYSLKXKLRWYGODNT--CEHYTVGPHSCHIRPD-LAL 206
 Db 35 DKETFTWMPNPGSDG--LPTNLSITSKE--GKNYECEDYITSGPNSCFEKOITSI 90
 QY 207 FTPEYIWEATNRLGSASDVLTLVDVYTTDPDPVHSRVGLEDOLSVRWVS--PP 264
 Db 91 WKIIIVNATNENGSSDPLVDYVYIYEPEPRNLTLEVKQLDKTKYLVWKMPLP 149
 QY 265 ALKDF--LFOAKQIQRVEDSDVKVVDVSNQTSCLAGLKPQYVYPOVACNPGCI 321
 Db 150 TITVTKGWFLMEYELIKSEADEWE-IHTGQIOFKYFDLPQGYLVOTRCKP--- 206
 QY 322 YGSKKAGIWSHPTASTP 342
 Db 206 ----DRGYWNRGQKSEIEP 222
 RESULT 8
 PRLR_RABIT STANDARD; PRT; 616 AA.
 AC P14787;
 DT 01-APR-1990 (REL. 14, CREATED)
 DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
 GN PRLR.
 OS ORCTOLAGUS CUNICULUS (RABBIT).
 OC EUDARTOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC EUDARTOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC LAGOMORPHA; LEPORIDAE; ORCTOLAGUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-MAMMARY GLAND;
 RX MEDLINE: 89184578.
 RA EDERY M., JOLICOEUR C., LEVI-MEYRUEIS C., DUSANTER-FOURT I.,
 RA PETERIDOU B., BOUFIN J.M., LESUEUR L., KELLY P.A., DIANE J.;
 RT "Identification and sequence analysis of a second form of prolactin
 RT receptor by molecular cloning of complementary DNA from rabbit
 RT mammary gland.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 86:2112-2116(1989).
 RN [2]
 RP 3D-STRUCTURE MODELING OF 30-228.
 RX MEDLINE: 97248733.
 RA HALASY D., THORAU E., DIANE J., MORON J.P.;
 RT "homology modeling of rabbit prolactin hormone complexed with its
 RT receptor.";
 RL PROTEINS 27:459-468(1997).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.


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RT      the cDNA sequence ".
CC      BIOCHEM. BIOPHYS. RES. COMMUN. 188:490-496(1992).
CC      -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC      PRLACTIN.
CC      -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC      -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC      -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC      This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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CC      or send an email to license@1sb-slb.ch).
CC      -----
DR      EMBL; D13154; G222849; .
DR      PIR; J01655; J01655
DR      PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 2.
DR      PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 2.
DR      PRAM; PF00041; fn3; 4.
DR      HSSP; P16471; 1BP3.
KW      RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
FT      SIGNAL 1 23
FT      CHAIN 24 831 POTENTIAL
FT      DOMAIN 24 438 EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM 439 459 POTENTIAL.
FT      DOMAIN 460 831 CYTOPLASMIC
FT      DOMAIN 25 122 FIBRONECTIN (POTENTIAL).
FT      DOMAIN 123 225 FIBRONECTIN TYPE-III.
FT      DOMAIN 228 325 FIBRONECTIN TYPE-III.
FT      DOMAIN 326 428 FIBRONECTIN TYPE-III.
FT      DOMAIN 429 528 FIBRONECTIN TYPE-III.

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[illegible]

15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (PRLR).
GN PRLR.
OS EULEYGRIS GALLOPADO (COMMON TURKEY).
OC EULEYGRIS GALLOPADO; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
OC NEOGNATHAE; GALLIFORMES; MELEAGRIDAE; MELEAGRIS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-KIDNEY;
RA ZHOU J.F., ZADWORYN D., GUENENE D., KUNHEIN U.
RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDJ DATA BANKS.
RN [2]
RP SEQUENCE OF 82-121 AND 473-522 FROM N.A.
RC TISSUE-Ovary;
RA PITS G.R., YOO S.K., FOSTER D.N., EL HALAMANI M.E.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDJ DATA BANKS.
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC EMBL: L76587; G1345365; -
DR EMBL: U22947; G973165; -
DR EMBL: U22944; G973166; -
DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 2.
DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 2.
DR PFAM: PF00041; fn3; 4.
DR HSSP: P16471; 1BP3.
KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
FT SIGNAL 1 23
FT CHAIN 24 831
FT DOMAIN 24 438
FT TRANSMEM 439 459
FT DOMAIN 460 831
FT DOMAIN 25 122
FT DOMAIN 123 225
FT DOMAIN 228 325
FT DOMAIN 326 428
FT DISULFID 36 46
FT DISULFID 75 86
FT DISULFID 59 59
FT CARBOHYD 91 91
FT CARBOHYD 100 100
FT CARBOHYD 112 112
FT CARBOHYD 132 132
FT CARBOHYD 262 262
FT CARBOHYD 303 303
FT CARBOHYD 315 315
FT CARBOHYD 335 335
SQ SEQUENCE 831 AA; 94394 MW; F8715C98 CRC32;
Query Match 13.2%; Score 305; DB 1; Length 831;
Best Local Similarity 35.5%; Pred. No. 3.3e-17;
Matches 77; Conservative 25; Mismatches 97; Indels 18; Gaps 8;

253 EDOLSVRWYSPALADFE---LFQANYQIRVYEDSVKRVVDVSNQTSCLRAGKPGTV 309
DB 347 KPYLMILTM-SPPLADVRGSGFLTLDEYELRLKREGEEMETV-FVGGQOTQKMFSLNPKK 404
QY 310 YFVQVRGNPFQYIGSKKAGINSESHPTAASPRSR 346
DB 405 YIVQIHCRP-----DHGSGWSESENIEIPNDR 435
RESULT 11
PRLR_CEREL
ID PRLR_CEREL STANDARD; PRT; 581 AA.
AC 028235;
DE 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DE 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS CERVUS ELAPHUS (RED DEER).
OC EURKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ARTIODACTYLIA; RUMINANTIA; PECORA; CERVOIDEA; CERVIDAE; CERVINAE;
OC CERVUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER;
RA MEDLINE: 96030711.
RA CLARKE L.A., EDERY M., LOUDON A.S., RANDALL V.A., POSTEL-VINAY M.C.,
RA KELLY P.A., JABBOUR H.N.;
RT "Expression of the prolactin receptor gene during the breeding and non-breeding seasons in red deer (Cervus elaphus): evidence for the expression of two forms in the testis".
RL J. ENDOCRINOL. 146:313-321(1995).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC EMBL: X94953; E218406; -
DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
DR PFAM: PF00041; fn3; 2.
DR HSSP: P14787; 1AN3.
KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
FT SIGNAL 1 24
FT CHAIN 25 581
FT DOMAIN 25 234
FT TRANSMEM 235 258
FT DOMAIN 259 581
FT DOMAIN 25 122
FT DOMAIN 123 227
FT DISULFID 36 46
FT DISULFID 75 86
FT DISULFID 59 59
FT CARBOHYD 132 132
FT CARBOHYD 233 233
SQ SEQUENCE 581 AA; 65159 MW; 721F0366 CRC32;
Query Match 13.1%; Score 303; DB 1; Length 581;
Best Local Similarity 33.6%; Pred. No. 3.1e-17;
Matches 76; Conservative 36; Mismatches 92; Indels 22; Gaps 8;

DB 18 NASLNGOS-----PPGKPKIKCSPEKETFTCWEPGSDG--LPNTYTLTYHREGT 70

QY 183 QDNTEEEHTWGPSSCHT-PKDLALFTPEIWEATNRLGSASDVLTLVDLYVTTDP 241

DB 71 LIHECPDYKTGPNCTYFSKHTSIWKIYIVTNAINQGVSSDLYVDYIYIEPEP 130

QY 242 PDVHVSFVGLDOLSVRWVS--PALADF--LFOAKQIYIRVEDSVDMKRVVDVSNQ 296

DB 131 ANLTL-ELKHPEDRPYLWIKWFPPLTLTVKSGWFMWQYERIKRPELADWE-IHFAKO 188

QY 297 TSCRLAGLPGTVYVQVRCNPFGLYSGKAGIEMSWHPTAASP 342

DB 189 TOLKFSLYPCKYLVQVRCN-----DHGIVSEWSPSSIQIP 227

RESULT 12

PRLR BOVIN STANDARD: PRT: 581 AA.

AC 028172:

DT 01-NOV-1997 (REL. 35, CREATED)

DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).

GN PRLR.

OS BOS TAURUS (BOVINE).

OC EURAKOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; ARTIODACTYLA; RUMINANTIA; PECORA; BOVIDEA; BOVINAE; BOS.

[1]

SEQUENCE FROM N.A.

RP TISSUE-ENDOMETRIUM.

RX MEDLINE: 93246019.

RA SCOTT P., KESSLER M.A., SCHULER L.A.;

RT "Molecular cloning of the bovine prolactin receptor and distribution of prolactin and growth hormone receptor transcripts in fetal and utero-placental tissues."

MO. CELL. ENDOCRINOL. 89:47-58(1992).

CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC

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CC EMBL: L02549; G163618; -

CC PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.

CC PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.

CC PFAM: PF00041; fn3; 2.

CC HSSP: P14787; IAN3.

CC RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.

CC SIGNAL 1 24 POTENTIAL.

CC CHAIN 1 24 POTENTIAL.

CC DOMAIN 25 581 PROLACTIN RECEPTOR.

CC TRANSMEM 23 234 EXTRACELLULAR (POTENTIAL).

CC DOMAIN 23 234 POTENTIAL.

CC DOMAIN 25 581 CYTOPLASMIC (POTENTIAL).

CC DOMAIN 25 122 FIBRONECTIN TYPE-III.

CC DOMAIN 123 227 FIBRONECTIN TYPE-III.

CC DISULFID 36 46 BY SIMILARITY.

CC T T 36 46 BY SIMILARITY.

CC T T 86 86 BY SIMILARITY.

CC CARBOHYD 59 59 POTENTIAL.

CC CARBOHYD 132 132 POTENTIAL.

CC SEQUENCE 581 AA; 65153 MW; COECA0A2 CRC32;

Query Match 13.1%; Score 302.5; DB 1; Length 581;

Best Local Similarity 31.9%; Pred. No. 3,4e-17;

Matches 83; Conservative 38; Mismatches 92; Indels 47; Gaps 10;

QY 91 SLTLNTSLTALANLNGSRGSDNLYCHARDGSLAGSLYGLPEKPFNISCSRN 150

DB 7 SHVFTLLFLTSVSLNG-----OS-----PEKRLVXCRSPG 40

QY 151 MEDLCRTPGARGETFTNTYSLTKRLRWGODWTCCEHTVGHSHCHT-PKDLALTP 209

DB 41 KETFTCWEPGADG--LPNTYTLTYHREGTLLHECPDYKTGPNCTYFSKHTSIWKI 98

QY 210 YEIWEATNRLGSASDVLTLVDLYVTTDPDPVHVSFVGLDOLSVRWV--SPALK 267

DB 99 YIIVTNAINQGVSSDLYVHVIYIEPEPANTL-ELKHPEDRKRYLWIKWSPPTMT 157

QY 268 D-----LFOAKQIYIRVEDSVDMKRVVDVSNQTSCLAGLKPQYVQVRCNPFGLY 322

DB 158 DVKSGWFMWQYERIKRPELADWE-THTLKQTKLFIWLYGQVLYQIRCKP----- 211

QY 323 GSKAGIEMSWHPTAASP 342

DB 211 ---DHGIVSEWSPSSIQIP 227

RESULT 13

PRLR ORENI STANDARD: PRT: 630 AA.

AC 091513:

DT 01-NOV-1997 (REL. 35, CREATED)

DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).

GN PRLR.

OS OREOCROMIS NILOTICUS (NILE TILAPIA) (TILAPIA NILOTICA).

OC EURAKOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII; OC TELEOSTEI; EUTELEOSTEI; ACANTHOPTERYGII; PERCOMORPHA; PERILOFORMES; RN LABROIDEI; CICHLIDAE; TILAPIA.

[1]

RP SEQUENCE FROM N.A.

RC TISSUE-KIDNEY;

RX MEDLINE: 95320210.

RA SANDRA O., SOHN F., DE LUZE A., PRUNET P., EDERY M., KELLY P.A.;

RT "Expression cloning of a cDNA encoding a fish prolactin receptor."

RL PROC. NATL. ACAD. SCI. U.S.A. 92:6037-6041(1995).

CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC

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CC EMBL: L34783; G903847; -

CC PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.

CC PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.

CC PFAM: PF00041; fn3; 2.

CC HSSP: P16471; IBP3.

CC RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.

CC SIGNAL 1 23 BY SIMILARITY.

CC CHAIN 1 23 BY SIMILARITY.

CC DOMAIN 24 630 PROLACTIN RECEPTOR.

CC TRANSMEM 23 234 EXTRACELLULAR (POTENTIAL).

CC DOMAIN 23 234 POTENTIAL.

CC DOMAIN 25 630 CYTOPLASMIC (POTENTIAL).

CC DOMAIN 24 123 FIBRONECTIN TYPE-III.

CC DOMAIN 124 228 FIBRONECTIN TYPE-III.

CC DISULFID 37 47 BY SIMILARITY.

CC T T 37 47 BY SIMILARITY.

CC T T 76 87 BY SIMILARITY.

CC CARBOHYD 92 92 POTENTIAL.

CC CARBOHYD 101 101 POTENTIAL.

SQ SEQUENCE 630 AA; 70810 MW; E9A4E553 CRC32;
 Query Match 11.38; Score 261.5; DB 1; Length 630;
 Best Local Similarity 33.28; Pred. No. 8.1e-14;
 Matches 71; Conservative 26; Mismatches 94; Indels 23; Gaps 9;
 QY 138 PERPNISCSRNKMDLTCMTGAGHETFLHNSKYKLYRGDNCCEHYHYGPHS 197
 DB 29 PGKPTLKRSPEKETTCMKKQSDG--LPPTLYALYKESDVAVHECPDYHTAGKNS 86
 QY 198 CHIPKDAL-FTPEYIWEATNRLGSARSDVLTLDVYTTDPPDVHSRYGGLDQ- 256
 DB 87 CFENKNTLWISYNTIVATNLGKYSDPDIDVYIYQPPPEKLEVT---YAKDQG 143
 QY 256 ---LSRWSPALKDF---LFAKQIQRVVD-SYDWKVVDDVSNGTSCRLAGLPGT 308
 DB 144 WPELRVSW-EPKPKADTSGMILTILRYKLEDESEME-NNAAGQKKFNIFSLRSG 201
 QY 309 VFEVQVRCNPFYIGSKAGIEMSHPTAATP 342
 DB 202 TYLIQVRCR-----DHGFSEMSSTIVKVP 228
 RESULT 14
 GCSR_HUMAN
 ID GCSR_HUMAN STANDARD: PRT; 836 AA.
 AC 09062;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE GRANULOCYTE COLONY STIMULATING FACTOR RECEPTOR PRECURSOR (G-CSF-R)
 DE (CD114 ANTIGEN)
 GN CSFR OR GCSR.
 OS HOMO SAPIENS (HUMAN)
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RX MEDLINE: 91011257.
 RA LARSEN A., DAVIS T., CURTIS B.M., GIMPEL S., SIMS J.E., COSMAN D.,
 RT PARK L., SORESENSEN E., MARCH C.J., SMITH C.A.;
 RT "A cDNA clone expressed in natural killer and T cells that likely
 RT encodes a secreted protein.";
 RT J. EXP. MED. 172:1559-1570(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RX MEDLINE: 91062348.
 RA FUKUNAGA R., SETO Y., MIZUSHIMA S., NAGATA S.;
 RT "Three different mRNAs encoding human granulocyte colony-stimulating
 RT factor receptor.";
 RT PROC. NATL. ACAD. SCI. U.S.A. 87:8702-8706(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92091782.
 RA SETO Y., FUKUNAGA R., NAGATA S.;
 RT "Chromosomal gene organization of the human granulocyte colony-
 RT stimulating factor receptor.";
 RT J. IMMUNOL. 148:259-266(1992).
 RN [4]
 RP DOMAINS STRUCTURE.
 RX MEDLINE: 92007729.
 RA FUKUNAGA R., ISHIZAKA-IREDA E., PAN C.-X., SETO Y., NAGATA S.;
 RT "Functional domains of the granulocyte colony-stimulating factor
 RT receptor.";
 RT EMBO J. 10:2855-2865(1991).
 RN [5]
 RP STRUCTURE BY NMR OF 227-334.
 RX MEDLINE: 97331327.
 RA YAMASAKI K., NAITO S., ANAGUCHI H., OHKUBO T., OTA Y.;
 RT "Solution structure of an extracellular domain containing the WXXWS

RT motif of the granulocyte colony-stimulating factor receptor and its
 RT interaction with ligand.";
 RT NAT. STRUCT. BIOL. 4:498-503(1997).
 RN [6]
 RP 3D-STRUCTURE MODELLING OF 125-331.
 RX MEDLINE: 98037802.
 RA LAYTON J.E., IARIA J., SMITH D.K., TREUTLEIN H.R.;
 RT "Identification of a ligand-binding site on the granulocyte colony-
 RT stimulating factor receptor by molecular modeling and mutagenesis.";
 RT J. BIOL. CHEM. 272:29735-29741(1997).
 CC -1- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR (G-
 CC CSF). IN ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION
 CC EVENTS AT THE CELL SURFACE.
 CC -1- SUBUNIT: DIMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE GCSR-2 FORM,
 CC WHICH LACKS THE TRANSMEMBRANE DOMAIN, MAY REPRESENT A SOLUBLE FORM
 CC OF THE RECEPTOR.
 CC -1- TISSUE SPECIFICITY: ONE OR SEVERAL FORMS HAVE BEEN FOUND IN
 CC MELOGENOUS LEUKEMIA CELL LINE KG-1, LEUKEMIA U937 CELL LINE, IN
 CC BONE MARROW CELLS, PLACENTA, AND PERIPHERAL BLOOD GRANULOCYTES.
 CC THE GCSR-2 FORM HAS BEEN FOUND ONLY IN LEUKEMIA U937 CELLS. THE
 CC GCSR-3 FORM IS HIGHLY EXPRESSED IN PLACENTA.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST FOUR FORMS, GCSR-1 (SHOWN UNDER),
 CC GCSR-2, GCSR-3 AND GCSR-4/D7, ARE PROBABLY PRODUCED BY
 CC ALTERNATIVE SPLICING OF THE SAME GENE. THEY DIFFER IN THEIR C-
 CC TERMINAL PORTION.
 CC -1- DISEASE: DEFECTS IN GCSR3 ARE A CAUSE OF KOSTMANN SYNDROME;
 CC ALSO KNOWN AS SEVERE CONGENITAL NEUTROPENIA (SCN).
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- DATABASE: NAME-PROV: NOTE-CD guide CD114 entry;
 CC WWW-"http://www.ncbi.nlm.nih.gov/prov/cd/cd114.htm".
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL; X55721; G31697; -
 DR EMBL; X55720; G31699; -
 DR EMBL; S71484; G240884; -
 DR EMBL; M59818; G183047; -
 DR EMBL; M59819; G485364; -
 DR EMBL; M59820; G183049; -
 DR PIR; JH0329; JH0329; -
 DR PIR; JH0330; JH0330; -
 DR PIR; A38252; A38252; -
 DR PDB; 1A271; 28-JAN-96.
 DR MIM; 138971; -
 DR MIM; 202700; -
 DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
 DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR PFAM; PF00041; fn3; 3.
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
 KW REPEAT; ALTERNATIVE SPLICING; 3D-STRUCTURE.
 FT SIGNAL 1 24
 FT CHAIN 25 836
 FT DOMAIN 25 627
 FT TRANSMEM 628 650
 FT DOMAIN 651 836
 FT DOMAIN 117 227
 FT DOMAIN 121 227
 FT DOMAIN 228 332
 FT DOMAIN 333 428
 FT DOMAIN 429 525
 FT DOMAIN 526 621
 FT DISULFID 131 142
 GRANULOCYTE COLONY STIMULATING FACTOR
 RECEPTOR.
 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.
 CYTOPLASMIC (POTENTIAL).
 IG-LIKE C2-TYPE DOMAIN.
 FIBRONECTIN TYPE-III.
 FIBRONECTIN TYPE-III.
 FIBRONECTIN TYPE-III.
 FIBRONECTIN TYPE-III.
 FIBRONECTIN TYPE-III.
 BY SIMILARITY.

Query Match	11.08;	Score 254.5;	DB 1;	Length 836;
Best Local Similarity	28.98;	Pred. No. 4,4e-13;		
Matches 97; Conservative	48;	Mismatches 148;	Indels 43;	Gaps 16

Query Match 10.9%; Score 252.5; DB 1; Length 837;
Best Local Similarity 27.8%; Pred. No. 6.3e-13;
Matches 107; Conservative 56; Mismatches 163; Indels 59; Gaps 20;

```

QY      29 LCVLGVPGGGGAMTAVISPODPFLLLGSSLAQCSIHGTPGATAG- LYWTLNGRL- 87
Db      14 LIFLLPRLPSLESCHIEISP--PVVRJGDDPLVASCTISPMCKSDQAKLMLADEP10 71
QY      87 PSELRL--NTSTLALALANGLSRROSGNLTGCHARDSILAGSCLYGLPERKFN1 144
Db      72 PGDRQHLPDGTQESLILPLANT-QAFLECLVPMWDSVQLLDQALHNGYPPASPSNL 130
QY      145 SCWR-SKKDLTCMTGAGGTFLHTNYSLK-YKLR--WYGDNTCEEYHTVGPASH 199
Db      131 SCLMLHTTNSLYCQMEGPP--ETLLPFSILKSPRSADQYGGDTIPDCVAKRQNNCS 188
QY      200 IP-NDLALFPELEYVEATNRLNGSABDVLTDLDVYTTDP-----PVRYSKRG 250
Db      189 IPRKRLILQYMALWQAEENLGSSEPKCLDPMDDVKLEPPLQALDIPVVSHP0 248
QY      251 GLEQLSVRWVS-PPALKDELFOKQYIRRYVE-DSVDMKYDDV-SNOTSCLAGLKP0 307
Db      249 CL-----WLSKPKPKPSEYMEDECLRQPOPKAGNMTLVHLBSSKQFELCLHQA 301
QY      308 TVIVVOYRCNDFGIYSSKKAGIWSWS-----HPT-AASTPSEERPGGCVCEPGRGE 361
Db      302 PVTYLOMRC-----IRSLDGFMSPMSPGQLRLRTMKAPYIRLDT-----WCQRKQDP 350
QY      362 SS-----GPVARELKGFLGWL 377
Db      351 GIVSVOLFMRKPTPLQEDSGQIQGL 375

```

Search completed: September 17, 1999, 03:10:12
Job time: 292 sec.

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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:40:05 / Search time 68.96 Seconds

(without alignments)
379.293 Million cell updates/sec

Title: US-09-037-657-15

Sequence: 1 MPAGRPGVPAQSARRPPRL.....NODEGILPSGRGAARPG 425

Scoring table: BLOSUM62

Searched: 201082 seqs, 61543640 residues

Database:

SPTREMBL_10: *
1: sp.archaea: *
2: sp.bacteria: *
3: sp.fungi: *
4: sp.human: *
5: sp.invertebrate: *
6: sp.mammal: *
7: sp.mhc: *
8: sp.organelle: *
9: sp.phage: *
10: sp.plant: *
11: sp.todent: *
12: sp.virus: *
13: sp.vertebrate: *
14: sp.unclassified: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2176.5	93.9	422	4	075462
2	355.5	15.3	881	13	057519
3	324.5	14.0	206	4	016354
4	306	13.2	581	6	046561
5	302.5	13.1	296	6	018880
6	268.5	11.6	346	13	093404
7	234.5	10.1	217	6	046386
8	230.5	9.9	198	6	018985
9	226.5	9.8	335	6	P79203
10	226	9.8	372	11	088507
11	217.5	9.4	862	4	099665
12	215.5	9.3	874	11	P97378
13	209.5	9.0	422	4	016542
14	208.5	9.0	432	11	064385
15	201	8.7	432	11	P70225
16	194.5	8.4	440	11	000343
17	193.5	8.4	710	13	057520
18	187.5	8.1	1165	6	002671
19	182	7.9	895	11	062960
20	177	7.6	316	11	035545
21	174.5	7.5	958	4	092920
22	174.5	7.5	1165	4	092921
23	174.5	7.5	958	4	013592
24	174.5	7.5	906	4	013593
25	174.5	7.5	896	4	013594
26	174.5	7.5	896	4	029219
27	163	7.0	1093	11	070535
28	162	7.0	427	4	095646
29	159.5	6.9	383	11	088786

30	156.5	6.8	971	11	070458	070458 mus musculus
31	156.5	6.8	970	11	088821	088821 mus musculus
32	153.5	6.6	229	6	027950	027950 bos indicus
33	153.5	6.6	229	6	028206	028206 bos taurus
34	153.5	6.6	228	11	035228	035228 bos taurus
35	149.5	6.5	229	4	075269	075269 homo sapien
36	149	6.4	1896	4	060468	060468 homo sapien
37	149	6.4	1571	4	060469	060469 homo sapien
38	149	6.4	890	11	092140	092140 cavia porce
39	143	6.2	279	11	064236	064236 rattus norv
40	142.5	6.2	86	6	018853	018853 mustela put
41	141.5	6.1	229	4	014213	014213 homo sapien
42	136.5	5.9	634	6	046600	046600 bos taurus
43	136.5	5.9	269	6	P79195	P79195 macaca mula
44	133	5.7	396	4	014631	014631 homo sapien
45	133	5.7	420	4	014633	014633 homo sapien

ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	422 AA.
075462	AC	075462:		
DT	01-NOV-1998	(TREMBLrel. 08, Created)		
DT	01-NOV-1998	(TREMBLrel. 08, Last sequence update)		
DT	01-MAY-1999	(TREMBLrel. 10, Last annotation update)		
DE	CYTOKINE-LIKE FACTOR-1 PRECURSOR.			
GN	CLF-1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Homidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	ELSON G.C.A., GRABER P., LOSBERGER P., HERREN S., GREUTNER D.,			
RA	MENUD L.N., WELLS T.N.C., KOSCO-VILBOIS M.H., GAUCHAT J.F.,			
RT	CLF-1, a Novel Soluble Protein Shares Homology with Members of the			
RT	Cytokine Type-I Receptor Family."			
RL	J. Immunol. 0:0-0(1998).			
DR	EMBL: AF059293; AAC28335.1;			
DR	PEAM: PF00041; fn3; 2.			
KW	Signal.			
FT	SIGNAL.			
FT	CHAIN			
SQ	SEQUENCE	422 AA; 46301 MW; 877F9BC9 CRC32;		

Query Match 93.9%; Score 2176.5; DB 4; Length 422;
Best Local Similarity 94.8%; Pred. No. 4.6e-184;
Matches 402; Conservative 5; Mismatches 14; Indels 3; Gaps 2;

QY	1	MPAGRPGVPAQSARRPPRLSLMSPILLCLVGRGSGGANTAVISQDPLLIGSSIQ	60
DB	1	MPAGRPGVPAQSARRPP-PLPL-LLLCVAGPARAGSGANTAVISQDPLLIGSSIL	57
QY	61	ATCSIHGDTPTAGTGLTYLNGRLPESELNTSTLALALANLNSROSGDNVCH	120
DB	58	ATCSVHGDPPTAGTGLTYLNGRLPESELNTSTLALALANLNSROSGDNVCH	117
QY	121	ARDGSLIAGSLYGLPEPEKPNISCSWNNKDLTCRTPGAHGTFPLHTNYSLEKYLKW	180
DB	118	ARDGSLIAGSLYGLPEPEKPNISCSWNNKDLTCRTPGAHGTFPLHTNYSLEKYLKW	177
QY	181	YGDMTCCEHYTVGPHSHIPKDLALFTPEIWEATNRLSANSADVLTLDVLYVTTDP	240
DB	178	YGDMTCCEHYTVGPHSHIPKDLALFTPEIWEATNRLSANSADVLTLDVLYVTTDP	237
QY	241	PPDVYTSVVGLEDDLSRTVSPALKDPLFOAKYQIYRVDSVDKVVVDVDSNOTSCR	300
DB	238	PPDVYTSVVGLEDDLSRTVSPALKDPLFOAKYQIYRVDSVDKVVVDVDSNOTSCR	297
QY	301	LAGLPGTVTVVQVRCNPFGLYSGKAGIMSEWSHPAASIPRSEBPGGVCPEPRGE	360

DB 298 LAGKPGTYEYVGRCPFGIYSGKAGIEMSHPTAATPSSRPGGCGCEPGE 357
 OY 361 PSSGPPARELKOFLGMLKKAAYCSNLSFRLYDQWRAMQKSHKTNODEGILPSGRGAA 420
 DB 358 PSSGPPARELKOFLGMLKKAAYCSNLSFRLYDQWRAMQKSHKTNODEGILPSGRGAA 417
 OY 421 RGA 424
 DB 418 RGA 421

RESULT 2

057519 PRELIMINARY; PRT: 881 AA.
 ID 057519;
 AC 057519; (Tremblrel. 06, Created)
 DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
 DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
 DE GP130P1.
 GN XGP130.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
 OC Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae; Xenopodinae;
 OC Xenopus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA CHEN J., GRACE A., CHEN K.R.,
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF041845; AAC03531.1;
 DR PFM; PF00041; fn3; 4.
 SQ SEQUENCE 881 AA; 99003 MW; 647E152E CRC32;

Query Match 15.3%; Score 355.5; DB 13; Length 881;
 Best Local Similarity 30.5%; Pred. No. 4.2e-23;
 Matches 100; Conservative 43; Mismatches 136; Indels 49; Gaps 11;

OY 50 DFTLLIGS-SLOATCSIHGDTGATAGLTYLNGRRRLPSELRLNTSTLALANNG 108
 DB 33 DGTGHERGERTAYCIVINOTCREDASRYLWYKGVKPEYELINOTTSVTEPNTLT 92
 OY 109 SROSGDNLVCHARDGSLAGSCLVGLPPEKFNISCSRMKMLTGTWPGANGEPFL 168
 DB 93 LNSPLTNCNMGAVANTLYGFFFLGPPDPPLTCLIVNODMLCTWPGGR--PNTL 150
 OY 169 HTNLSLKYKLR-----YGDNTCEHYHTVGPCHSHIPKDLALFPYEIWEATNRL 220
 DB 151 PNTYLSH--RWAHFGANVCRGANNSC-----TIHSP-GPGFYIDTFOVEATNEL 198
 OY 221 GSARDVLTLDVLYTTDPPPDVAVSRVGLDQLSVRWVSPPALKDLFOAKQIYR 280
 DB 199 GLOKSETLTIDPVNIVKPNPOLSELISLELPNALKIEMKNPT--NAFNKYNIXR 255
 OY 281 VEDSVDMKV--DDVNOTSCRLAGLKPQVYFVQVNCNPGIYSGKAGIEMSHPT 337
 DB 256 PKTIDWEMVPEEDASRDSFTLDDLPNTVYEVSIRC-----IHKDGHGFWSDWSLX 310
 OY 338 AASTPSEPPGPGGCVCEPGEPSGCP 365
 DB 311 KQVTP--EAP-----PGRCP 323

RESULT 3

016354 PRELIMINARY; PRT: 206 AA.
 ID 016354;
 AC 016354;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE PROLACTIN RECEPTOR (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 95286597.
 RA FUH G., WELLS J.A.,
 RT "Prolactin receptor antagonists that inhibit the growth of breast
 cancer cell lines."
 RT J. Biol. Chem. 270:13133-13137(1995).
 RL EMBL; S78505; AAB34470.1;
 DR PFM; PF00041; fn3; 2.
 FT NON-TER
 SQ SEQUENCE 206 AA; 23950 MW; D7E57266 CRC32;

Query Match 14.0%; Score 324.5; DB 4; Length 206;
 Best Local Similarity 38.0%; Pred. No. 3.4e-21;
 Matches 81; Conservative 25; Mismatches 90; Indels 17; Gaps 7;

OY 136 LPPEKFNISCSRMKDLTCRMTGANGETFLHTNLSLKYKLRWYGODNTCEHYTGP 195
 DB 2 LPPEKFNISCSRMKDLTCRMTGANGETFLHTNLSLKYKLRWYGODNTCEHYTGP 59
 OY 196 HSCHPKD-LALFTYEIWEATNRLGARSVDLTLDVLYTDDPPDVHVRVGLD 254
 DB 60 NSCHGKQYTSWMTYIMVATNMGSSFSDELVDVYIYQPPLELAV-EVKQPED 118
 OY 255 QLSVRW--SPPAKDF--LFOAKQIYRVEDSVDMKVDDVNOTSCRLAGIPEY 309
 DB 119 KPYIMINWSPPLTDLKTGWFLLYELTRPKAWE-THFAGQOTEFILSLHPGOK 177
 OY 310 YFVGRCPFGIYSGKAGIEMSHPTAATP 342
 DB 178 YLVGRCKP-----DHGYWSAMSPATFIQIP 203

RESULT 4

046561 PRELIMINARY; PRT: 581 AA.
 ID 046561;
 AC 046561;
 DT 01-JUN-1998 (Tremblrel. 06, Created)
 DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
 DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
 DE PROLACTIN RECEPTOR LONG FORM PRECURSOR.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 OC Caprinae; Ovis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 98001468.
 RA BIGON C., BINART N., ORMANDY C., SCHUIER L.A., KELLY P.A.,
 RA DIANE J.,
 RT "Long and short forms of the ovine prolactin receptor: cDNA cloning
 and genomic analysis reveal that the two forms arise by different
 alternative splicing mechanisms in ruminants and in rodents."
 RT J. Mol. Endocrinol. 19:109-120(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA BIGON C., DIANE J.,
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF041257; AAB96795.1;
 DR PFM; PF00041; fn3; 2.
 KW Signal.
 FT SIGNAL.
 FT CHAIN
 SQ SEQUENCE 581 AA; 65235 MW; 6792A7C7 CRC32;

Query Match 13.2%; Score 306; DB 6; Length 581;
 Best Local Similarity 34.8%; Pred. No. 5.6e-19;
 Matches 78; Conservative 32; Mismatches 92; Indels 22; Gaps 8;

OY 125 SIAGSLYGLPPEKFNISCSRMKDLTCRMTGANGETFLHTNLSLKYKLRWYGOD 184

```

Db 20 SLNQGS-----PPKPKLRCRSPGKETFTCMWPGADG--LPTNYTLTYRKGETLI 72
QY 185 MTCEHYHTVGHSPCHIPD-LALFTPEIWEATNRGASRSDVLTLDVYTTDPPD 243
Db 73 HECDDYKGTGNSCYFSKRYTKMYITVTSALNOMGSISSDPDLYVTYVEPEPVN 132
QY 244 VHSRVGGLDQLSVRWY--SPALKDF--LFOAKYQIRYRVEDSVDMKYVDVSNOTS 298
Db 133 LTL-ELKHPEDRKRYLTKMSPPPLTDVKSQMFSLQYIRLKPENATWME-THPAPKLTQ 190
QY 299 CRLAGLPGRYTYFQVRCNPGYIGSKAGIWSKSHPTAASP 342
Db 191 LKIFNLXPGRKYLVQIRKRP-----DHGYWSEMSPESTIQIP 227

RESULT 5
ID 018880 PRELIMINARY; PRT; 296 AA.
AC 018880;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE PROLACTIN RECEPTOR SHORT FORM.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
[1]
RP SEQUENCE FROM N.A.
RP MEDLINE: 97373450.
RA SCHULER L.A., NAGEL R.J., GAO J., HORSEMAN N.D., KESSLER M.A.;
RT "Prolactin receptor heterogeneity in bovine fetal and maternal
RT tissues.";
RT Endocrinology 138:3187-3194(1997).
DR EMBL: AF027403; AAB8399.1; -
DR PFAM: PF00041; fn3: 2.
SQ SEQUENCE 296 AA; 33854 MW; 8B40CCD8 CRC32;

Query Match 13.18; Score 302.5; DB 6; Length 296;
Best Local Similarity 31.98; Pred. No. 4.7e-19;
Matches 83; Conservative 38; Mismatches 92; Indels 47; Gaps 10;

QY 91 SRLNTSTLALANLNGSQSGDNLYCHAROSIAGCLYGLPPEKPNISCSRN 150
Db 7 SRVYFLLFLSLSLNG--QS-----PPKPKLYKCRSPG 40
QY 151 MKDLTCRWTPGAGETFLHTNYSILKRYMGODNTCEHYHTVGHSPCHI-PRDLALFTP 209
Db 41 KEFTCMWEPGADG--LPTNYTLTYRKGETLIHECPDYKGTGPNCSYFSKRYTKMY 98
QY 210 YELTVATNRGASRSDVLTLDVYTTDPPDVAHSRVGGLDQLSVRWY--SPALK 267
Db 99 YIYTVAINQMGSISSDPDLYVTYVEPEPVNLT-LKHPEDRKRYLTKMSPPPLT 157
QY 268 D-----FLFOAKYQIRYRVEDSVDMKYVDVSNOTSRLGLPGRYTYFQVRCNPGYIT 322
Db 158 DVKSGFIIO--YELTKPEKARDWE-THTLTLOTOLKIFNLXPGRKYLVQIRKRP---- 211
QY 323 GSKKAGIWSKSHPTAASP 342
Db 211 ---DHGYWSEMSPESTIQIP 227

RESULT 6
ID 093404 PRELIMINARY; PRT; 346 AA.
AC 093404;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE PROLACTIN RECEPTOR (FRAGMENT).

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OS Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica);
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Perciformes;
OC Perciformes; Labroidae; Cichlidae; Tilapia.
[1]
RP SEQUENCE FROM N.A.
RP TISSUE-GILL;
RA SHIRAIASHI K., MATSUDA M., MORI T., TENGUYA H.;
RT "Expression of prolactin and cortisol receptor gene in early-life
RT stages of tilapia (Oreochromis mossambicus).";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF080247; AAC31825.1; -
DR PFAM: PF00041; fn3: 2.
FT NON_TER 346
SQ SEQUENCE 346 AA; 39203 MW; 1E8A63B9 CRC32;

Query Match 11.64; Score 268.5; DB 13; Length 346;
Best Local Similarity 33.28; Pred. No. 5.0e-16;
Matches 71; Conservative 28; Mismatches 92; Indels 23; Gaps 9;

QY 138 PEKPNISCSNRNKKDLTCRWTPGAGETFLHTNYSILKRYMGODNTCEHYHTVGHSP 197
Db 29 PKRPTETCRSPKETEFTCMWPGSDG--LPTTYALTYRKESDVAHECPDYHTAGKNS 86
QY 198 CHIRK-DLALFTPEIWEATNRGASRSDVLTLDVYTTDPPDVAHSRVGGLDQ- 256
Db 87 CFENKNDTLTWVSYNITVAVTNALGKYSDDVIDVYIYKPHPEKLEVT--VMDQG 143
QY 256 ---LSRVNSPPALKDF--LFOAKYQIRYRVED-SVDMKYVDVSNOTSRLAGLKPRT 308
Db 144 WPLRYNSW-EPKPADRSMTITLYELRYKLEDESEWE-NHAAGQKKYNTFLSRSG 201
QY 309 VYFQVRCNPGYIGSKAGIWSKSHPTAASP 342
Db 202 TYLIQVRCRP-----DHGFWSMSTSYVXP 228

RESULT 7
ID 046386 PRELIMINARY; PRT; 217 AA.
AC 046386;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE PROLACTIN RECEPTOR (FRAGMENT).
GN PRLR.
OS Mustela vison (American mink).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.
[1]
RP SEQUENCE FROM N.A.
RP TISSUE-TESTIS;
RA DOUGLAS D.A., SONG J.-H., HOUDE A., MURPHY B.D.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF028294; AAB88899.1; -
DR PFAM: PF00041; fn3: 1.
FT NON_TER 217
SQ SEQUENCE 217 AA; 24850 MW; F77A3B9D CRC32;

Query Match 10.18; Score 234.5; DB 6; Length 217;
Best Local Similarity 32.38; Pred. No. 3.1e-13;
Matches 61; Conservative 30; Mismatches 81; Indels 17; Gaps 7;

QY 160 PCHAGETFLHTNYSILKRYMGODNTCEHYHTVGHSPCHI-PRDLALFTPEIWEATN 218
Db 2 PEGDGG--LPTTYLTYHKEGETTTHCEPDYITSGPNSCYFSKRYTKMYITVTSALN 59
QY 219 RLGSARSDVLTLDVYTTDPPDVAHSRVGGLDQLSVRWY--SPALKF---LFOA 273
Db 60 EMGSSSDPRYTVTYVEPEPVNLT-LKHPEDRKRYLTKMYPPPLTDVVRSGWTLT 118

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QY 274 KTOIRVEDSDVMKRVDDVDSNOTSCRLAGLPGVYVQVACNPFYIGSKAGIWSM 333
 DB 119 QVEIRLKPKEATEME-THRAGLOTOFKILSLYPGOKYLVQVCKP-----DHGFWSEM 170
 QY 334 SHPTAASP 342
 DB 171 SPKRSIOIP 179

RESULT 8

QY 018985 PRELIMINARY: PRT: 198 AA.
 AC 018985;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE SOLUBLE PROLACTIN RECEPTOR.
 OS Cervus elaphus nelsoni (American elk).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
 OC Cervinae; Cervus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA JABBOUR H.N.;
 RL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL: Y14753; CAA75048.1;
 DR PFAM: PF00041; fn3; 1.
 SQ SEQUENCE 198 AA; 22652 MW; COABAB0 CRC32;

Query Match 9.9%; Score 230.5; DB 6; Length 198;
 Best Local Similarity 33.7%; Pred. No. 6, 2e-13;
 Matches 62; Conservative 31; Mismatches 76; Indels 15; Gaps 7;

QY 123 DGSILAGSLYGLPPEKPFNISCNRKKDLTCRNTPEAHGETFLHNTSYKILRWY 182
 DB 18 NASLNGOS----PGKPKIKCRSPKXETFCWEPGSDG--LPTVYTLTHKEGET 70
 QY 183 QNTCEHYTVGPHSCHI-PKDLALTPYEIVWEATNRLGSARDVLTLVDVYTTDP 241
 DB 71 LHCEPDYITGPNCTYSEKHTSTIKIYIVTNALNQGVSDDLYDVYIYEPPEP 130
 QY 242 PVHVSRRVGLDQLSVRWVS--PPALKDF---LFOAKTOIRVEDSDVMKRVDDV 296
 DB 131 ANULTL-ELKHPRDKRYLTIKMFPPILTVYKSGFMIOYEIRLKPETATDWE-HDDLHP 188
 QY 297 TSCR 300
 DB 189 TSSR 192

RESULT 9

QY 018985 PRELIMINARY: PRT: 335 AA.
 AC 018985;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE PROLACTIN RECEPTOR (FRAGMENT).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae; Bovidae;
 OC Caprinae; Ovis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-422/80; TISSUE-ANTERIOR PITUITARY;
 RC TORONTO D.T.; BROOKS J.; INGLETON P.; MCNEILLY A.S.;
 RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL: Y10578; CAA71597.1;
 DR PFAM: PF00041; fn3; 1.
 FT NON_TER 1 1
 FT NON_TER 335 335

SQ SEQUENCE 335 AA; 38326 MW; 88A05AB1 CRC32;

Query Match 9.8%; Score 226.5; DB 6; Length 335;
 Best Local Similarity 31.4%; Pred. No. 2, 8e-12;
 Matches 58; Conservative 28; Mismatches 68; Indels 31; Gaps 7;

QY 164 GETFLHNTSYKILRWYGDNTCEHYTVGPHSCHI-PKDLALTPYEIVWEATNRLGS 222
 DB 8 GETLIH-----ECPDYITGPNCTYSEKHTSTIKIYIVTNALNQGVSDDLYDVYIYEPPEP 51
 QY 223 ARSDVLTLDVLYTTDPPVHVSRRVGLDQLSVRWVS--SPALKDF---LFOAKTOI 277
 DB 52 SSDDPLVDVYIYEPPEPVLTL-ELKHPRDKRYLTIKMFPPILTVYKSGFMIOYEIR 110
 QY 278 KRVVEDSDVMKRVDDVDSNOTSCRLAGLPGVYVQVACNPFYIGSKAGIWSM 337
 DB 111 RLPKPKATDWE-THRAPRLTOLKIFNLPGOKYLVQVCKP-----DHGFWSEMSPES 162
 QY 338 AASP 342
 DB 163 FIQIP 167

RESULT 10

QY 088507 PRELIMINARY: PRT: 372 AA.
 AC 088507;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE CILIARY NEUROTROPHIC FACTOR RECEPTOR ALPHA PRECURSOR.
 GN CNFR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE-BRAIN, SKELETAL MUSCLE;
 RC MAMDA M.; YACUCHI N.; HANYU C.; MAKATA Y.; ONODA N.; TULIN E.E.;
 RA KOJIMA T.; HASEGAWA M.; KIRUCHI Y.; NOMURA H.;
 RL "Mouse homolog of human ciliary neurotrophic factor receptor."
 DR EMBL: AF068615; AAC25711.1;
 DR PFAM: PF00041; fn3; 1.
 DR PFAM: PF00047; 19; 1.
 KW Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 336 CILIARY NEUROTROPHIC FACTOR RECEPTOR
 FT ALPHA.
 SQ SEQUENCE 372 AA; 40831 MW; 9A40FE12 CRC32;

Query Match 9.8%; Score 226; DB 11; Length 372;
 Best Local Similarity 26.0%; Pred. No. 3, 5e-12;
 Matches 97; Conservative 45; Mismatches 157; Indels 74; Gaps 18;

QY 30 CYLSVPRGSGAHNVISPOPTLLIGSSLOATCISHDTPGATF---GLYTLNGRRL 86
 DB 9 CCAYLAANAAYVYOKHSPQEPAPHYOYERLGDVTL----PCGTASWDAAYATWRNGTDL 64
 QY 87 PSELRLNTSTIALALANLNGSRQSGDNLYCHARDSSILAGS-CLVYGLPPEKPFN 145
 DB 65 APD---LNGSOLILRSLELGHSGIYA-----CFHRDSMHLRHQVLLHAGLPPEPVL 115
 QY 146 CWSRNM-FDLTCRW-----TPGAHGETFLHNTSYKILRWYGDNTCEHYTVGPHS 197
 DB 116 CSNSTYPRGFCYSHLPPTIYPTNFNTVYLVHSGRIM-----VCEKDPAL-KNR 163
 QY 198 CHIPDLALFT--PYEIVWEATNRLGSARDVLTLDVYTTDPPVHVSRRVGLDQ 255
 DB 164 CHI-RYMLFSTIKIKVSIYSVNLGH-NTAIFTDEFITVKKDPPENVAVRAPPSNDR 221

256 LSVRWSPALAKD-FLFOAKYQIRYVEDSDVKNVVDVSNQTSCLAGLPGTVYFVQV 314
222 LEVYMQTPSTWPDSEFPLKFLRYRPLIIDQONV-ELSDGAHTITDVAKEVITIQV 280
315 RCPNPFYISKRGKIGSSENS-----HPTAATSPSEPPGPGGV 353
281 AAK-----DNEIGTWSVSAHAATPTEPRHLTTEAQAPEITTTSTSLAPPTKI 334
354 CEP-----RGCEPS 362
335 CDPGLSGSGGPRS 347
ESULT 11
199665
D 099665 PRELIMINARY: PRT: 862 AA.
C 099665:
01-MAY-1997 (TREMBLrel. 03, Created)
01-MAY-1997 (TREMBLrel. 03, Last sequence update)
01-NOV-1998 (TREMBLrel. 08, Last annotation update)
IL-12 RECEPTOR BETA2.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
[1]
SEQUENCE FROM N.A.
PRESKY D.H., YANG H., MINETTI L.J., CHUA A.O., NABAVI N., WOU C.Y.,
GATELY M.K., GUBLER U.,
Submitted (Jul-1996) to the EMBL/GenBank/DBJ databases.
EMBL: U64198; AAB36675.1; -
PFAM: PF00041; fn3; 3.
RPFAM: PF00041; fn3; 3.
O SEQUENCE 862 AA; 97134 MW; 5FE4FBD5 CRC32;
Query Match 9.4%; Score 217.5; DB 4; Length 862;
Best Local Similarity 25.6%; Pred. No. 6e-11;
Matches 84; Conservative 46; Mismatches 121; Indels 77; Gaps 14;
Y 53 LLIGSLQNTCSIHDDTGATAGLYWTL-----NGRRLSELRL-L 94
41 ILIGSTVITSL-----KPRQGFHYSRRNKLILYKFRDRINFHHGSLNSOVYGLPL 94
95 NTSTLALALANLNGSRQSGDNLVCHARDGSIAGSLYGLPPEKPFNISQSRNKK-D 153
95 GTTFVCKLACINSEIQ-----ICGAEIVGVAPEQPONLSCTIQKEQGT 140
154 LTCRTPGASGETFLHNYSLKY-----KLRYGQ--DMTCEYHYVG-----PHSCHI 200
141 VACTWENGR--DTHLYETYLQLSGPKMLTQKCKDIYC-DYLDGILMLTPESPESNFT 197
201 PKDLALTFPEYEWATNRGLSARSDVLTLDVLYTTDPPPDVHVSRYGLEDQLSVRW 260
198 AK-----VTAVNSLGSSSLPSTFTFLDIYRPLPPMDIRIKFOKASVSCTIYW 246
261 VSPALAKDFOAKYQIRYVEDSDVKNVVDVSNQTSCLAGLPGTVYFVQVGNPFG 320
247 -----RDEGLVLNRLKRYRPSNSRLKNNVNTAKGRHDLDLPLTEYEFQI--SKLH 299
321 IYSGKKGAGIWEWSHPTAATSPRSEPG 348
300 LY-----KGSWSDWSESLRAQTPREEPTG 323
ESULT 12
97378
D 97378 PRELIMINARY: PRT: 874 AA.
C 97378:
01-MAY-1997 (TREMBLrel. 03, Created)
01-MAY-1997 (TREMBLrel. 03, Last sequence update)
01-NOV-1998 (TREMBLrel. 08, Last annotation update)
INTERLEUKIN 12 RECEPTOR, BETA 2 (IL-12 RECEPTOR BETA2).
Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
SEQUENCE FROM N.A.
PRESKY D.H., YANG H., MINETTI L.J., CHUA A.O., NABAVI N., WOU C.Y.,
GATELY M.K., GUBLER U.,
Submitted (Jul-1996) to the EMBL/GenBank/DBJ databases.
EMBL: U64199; AAB36676.1; -
DR MGI:1270861; IL12RB2.
DR PFAM: PF00041; fn3; 4.
DR PFAM: PF00041; fn3; 4.
O SEQUENCE 874 AA; 98196 MW; 9890EB47 CRC32;
Query Match 9.3%; Score 215.5; DB 11; Length 874;
Best Local Similarity 25.3%; Pred. No. 9.1e-11;
Matches 96; Conservative 59; Mismatches 145; Indels 79; Gaps 19;
OY 9 VASARPPRPLISLMSPLL-----CYLGPFGSGAHNAVISPDPPTLLIGSLQAT 62
DB 1 MOTVRECSLALLFLFMWLLIRANIDVCKLG-----TVYQPA-PVPIPGSAANIS 50
OY 63 CSIH-----GDPFGATA-----EGLYWTLNGRRL-----PSELRLNST-LATAL 103
DB 51 CSUNPQSGSHYPSSEWELLILAFVNDVLYENHAGKRVHDHGHSTFOYTNLSLQTLFV 110
OY 104 AALNGSRQSGDNL-VCHARDGSIAGSLYGLPPEKPFNISQSRNKK-DLTCRWTPG 161
DB 111 CKLNGSNQSKRPYPVC-----GVEISGVAPEPPQNSICQGEENGVAASWMSG 161
OY 162 ANGTEFLHNTYSLAKYKRLRYGQDN-TCE-EHTTVPHSC-----HFKDLALTPPEI 212
DB 162 K--VYLLKNTVYIQLS-----GPNLTCQKQCFSDNRONCRDLGINSPLDA-ESRFIV 214
OY 213 WYEATNRLGSASADVLTLDVLYTTDPPPDVHVSRYGLEDQLSVRWSPALAKDFLQ 272
DB 215 RYTAINDLNGSSSLHHTFTFLDIYRPLPPMDIRINFHAGSGRGLQW-----EDSGV 268
OY 273 AKYQIRYVEDSDVKNVVDVSNQTSCLAGLPGTVYFVQVRCNPFYISK--KAGI 329
DB 269 VLNQRLYQPLNSTSWNNVNAVAKGKYDLRLRPTREYEFQI-----SKKLHSGGS 320
OY 330 WSEWSHPTAATSPRSEPG 348
DB 321 WSNWSESLRTRTPEEPVG 339
RESULT 13
016542
ID 016542 PRELIMINARY: PRT: 422 AA.
AC 016542: 014626;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE INTERLEUKIN-11 RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
[1]
SEQUENCE FROM N.A.
RC TISSUE-MUSCLE;
RX MEDLINE: 95399754.
RA CHEREL M., SOREL M., LEBEAU B., DOBOIS S., MOREAU J.F., BATAILLE R.,
MINVIELLE S., JACQUES Y.,
RT "Molecular cloning of two isoforms of a receptor for the human
hematopoietic cytokine Interleukin-11."
RL Blood 86:2534-2540(1995).
[2]
SEQUENCE FROM N.A.
RP VAN LIEUVEN F., STAS L., HILLIKER C., MIYAKE Y., GOSSLER A.,
RU Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 3-390 FROM N.A.
RC TISSUE-PLACENTA;

RA CHEREL M., SOREL M., DUBOIS S., LEBEAU B., MOREAU J., JACQUES Y.,
 RA MINVILLE S.,
 RA Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U32324; AAB36492.1; -
 DR EMBL: Z38102; CAAB6224.1; -
 DR EMBL: U32323; AAB36491.1; -
 DR EMBL: Z46595; CAAB6570.1; -
 DR PFM: PF00041; fn3: 2.
 DR PFM: PF00047; fn3: 1.
 SO SEQUENCE 422 AA; 45222 MW; 29011292 CRC32;

Query Match 9.0%; Score 209.5; DB 4; Length 422;
 Best Local Similarity 23.9%; Pred. No. 1.2e-10;
 Matches 89; Conservative 53; Mismatches 136; Indels 93; Gaps 18;

QY 43 TAVISPODPTLLI-----GSSLOATCSINGDPGATA-EGLYWTNG--RLPS 88
 DB 17 TALVASASPCQAMGPPEVQKGPGRSVKLC-----PGYAGDPVWFMEDGPKLLQG 70
 QY 89 ELRLNLTSTLALANLNGSGDNLVCHARDGSLAAGCLVGLPPKPNISGWS 148
 DB 71 PDGSGHGLVLAQADSTDEGR-----YICQTLGALGCTVTLQIGPPAPV-VSCQA 122
 QY 149 RNMDLTCRTPGAGETFLHTNTSLKYLWYGODNTCEYHTWGPSCHIPRO----- 204
 DB 123 ADYENFSCSTWSPSQ--ISGLPTRYLTSYRKRTYGLADGQRSPSTGPPC--PDDPLGA 178
 QY 204 -----LALFTPEIWEATNRLSARSVDLTLLVDVTTDPDPVHVSRYGLEQDLS 257
 DB 179 RCYVGAFFWQYRINTVEVNPGL-ASTRLDVSLSQSLRDPDGLVESEVPGPRRLR 237
 QY 258 VRWVSP---PALKDELFOAKQIYRYVEDSDWKVYVDVSNQTSCLAGL-----PG 307
 DB 238 ASWTPYASWPCQPHLL--KRLDYRPAQHPAMSTVEP-----AGLEEVTTDAVAG 286
 QY 308 TVYFQVACNPFYIGSKAGIMSEMSHPTASTPRSPRPGGVCEPRGSESSGPVR 367
 DB 287 LPHAVRVSARDF-----LDAGTWSWS-PEA-----WGTSTGTITP 321
 QY 368 RELKQFLGWLKX 380
 DB 322 KEIP---AMGOLH 331

RESULT 14
 ID 064385 PRELIMINARY; PTR; 432 AA.
 AC 064385;
 DT 01-JAN-1998 (Tremblrel. 05, Created)
 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 1 PRECURSOR (NRL) (ETL2)
 DE (IL-11ALPHA) (IL11RA1).
 GN IL11RA1 OR IL11RA OR ETL2 OR ETL2/IL11 REC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6 X CBA; TISSUE-LIVER;
 RX MEDLINE: 95045367.
 RA HILTON D.J., HILTON A.A., RAICEVIC A., RAKAR S., HARRISON-SMITH M.,
 RA GONGE N.M., BEGLEY C.G., METCALF D., NICOLA N.A., WILLSON T.A.;
 RA "Cloning of a murine IL-11 receptor alpha-chain; requirement for
 RA gp130 for high affinity binding and signal transduction.";
 RL EMBO J. 13:4765-4775(1994).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN-BALB/C, AND C57BL/6; TISSUE-EMBRYO;
 RA NEUBAUS H., BETENHAUSEN B., BILINSKI P., SIMON-CHAOTTES D.,
 RA GUBERT J.L., GOSSLER A.;
 RL Dev. Biol. 166:521-542(1994).

RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C, AND C57BL/6;
 RA GOSSLER A.;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97129000.
 RA BILINSKI P., HALL M.A., NEUBAUS H., GISEL C., HEATH J.K.,
 RA GOSSLER A.;
 RT "Two differentially expressed Interleukin-11 receptor genes in the
 RT mouse genome.";
 RL Biochem. J. 320:359-363(1996).
 CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11.
 CC -1- BINDS TO IL-11 WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A
 CC SIGNAL.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- CONTRAINS ONE IG-LIKE DOMAIN.
 DR EMBL: X74953; CAAS2908.1; -
 DR EMBL: U14412; AAAS3248.1; -
 DR EMBL: X94163; CAAG3873.1; -
 DR EMBL: X94163; CAAG3873.1; JOINED.
 DR MCD; MG1:107426; IL11RA1.
 DR PFM: PF00041; fn3: 2.
 DR PFM: PF00047; fn3: 1.
 KM Receptor; Transmembrane; Glycoprotein; Immunoglobulin fold; Signal.
 FT SIGNLF 1 23
 FT CHAIN 24 432
 FT DOMAIN 24 367
 FT TRANSMEM 368 393
 FT DOMAIN 394 432
 FT DOMAIN 41 102
 FT CARBOHYD 127 127
 FT CARBOHYD 194 194
 FT POTENTIAL.
 SO SEQUENCE 432 AA; 46655 MW; F65B3060 CRC32;

Query Match 9.0%; Score 208.5; DB 11; Length 432;
 Best Local Similarity 23.9%; Pred. No. 1.5e-10;
 Matches 94; Conservative 51; Mismatches 136; Indels 113; Gaps 20;

QY 7 GPVAGSARRPRPLSLMSPLLCVGLVPRGSGAHTAVISPODPTLLIGSSLOATCSIH 66
 DB 31 GPVQVQGGGR-----PYMLCCPEVSAG----- 55
 QY 67 GDIPGATAEGLYWTNGRLRLPSELRLN--TSTLA--LALANLNGSGDNLVCHAR 122
 DB 55 --TP-----VSWFRDSD-----SRLLQGPDSGLGRLVLAQVSDPE---GTYVQTL 97
 QY 123 DGSILAGSCLVGLPPKPNISGWSNMMDLTCRTPGAGETFLHTNTSLKYLWYG 182
 DB 98 DGVSGGVNTLKLGPAPRP--EVSCQAVDYENFCTWSPGQ--VSGLPTRLTSYRKRTLP 154
 QY 183 QDWTCEHYHVGPHSCHIPRO-----LALFTPEIWEATNRLSARSADVTLTD 231
 DB 155 GASQSRSPSTGPPC--PDDPLASRCVHGAFMEYRINTVEVNPGL-ASCLLDVR 211
 QY 232 VLDVTTDPDPVHVSRYGLEQDLSRYVSPALK---DFLFOAKQIYRYVEDSDWK 288
 DB 212 LOSLRDDPDQGRVSEVSPYPRLLASWTYPAWRRQPHLL--KRLDYRPAQHPAWS 269
 QY 289 VVDVSNQ--TSRLAGLKGCTYFQVQVNRNPGIYSGKAGIMSEMSHPTASTPRSER 346
 DB 270 TVEIGLEEVTTDAVAGLP---HAYVVSARDP-----LDAGTWSAWS-PEA----- 312
 QY 347 PGRGGVCEPRGSESSGPVRELKQFLGWLKX 380
 DB 312 -----WGTSTGTITPDEIIPD---WSQGH 331

RESULT 15
 ID P70225 PRELIMINARY; PRT; 432 AA.
 AC P70225: 009074:
 DT 01-FEB-1997 (TREMBLERel. 02, Created)
 DT 01-FEB-1997 (TREMBLERel. 02, Last sequence update)
 DT 01-NOV-1998 (TREMBLERel. 08, Last annotation update)
 DE INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 2 PRECURSOR (IL11RA2)
 DE (IL-11RETA) (INTERLEUKIN-11 RECEPTOR BETA CHAIN)
 GN IL11RA2 OR IL-11RETA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 (1)
 SEQUENCE FROM N.A.
 RC STRAIN-CD1: TISSUE-TESTIS;
 MEDLINE: 97129000.
 RA BILINSKI P., HALL M.A., NEUHAUS H., GISSEL C., HEATH J.K.,
 RA GOSSLER A.;
 RA "Two differentially expressed Interleukin-11 receptor genes in the
 RA mouse genome.";
 RA Biochem. J. 320:359-363(1996).
 (2)
 SEQUENCE FROM N.A.
 RC STRAIN-CD-1: TISSUE-TESTIS;
 MEDLINE: 96278810.
 RA ROBB L., HILTON D.J., WILLSON T.A., BEGLEY C.G.;
 RA "Structural analysis of the gene encoding the murine Interleukin-11
 RA receptor alpha-chain and a related locus.";
 RA J. Biol. Chem. 271:13754-13761(1996).
 (3)
 SEQUENCE FROM N.A.
 RC STRAIN-CD-1: TISSUE-TESTIS;
 MEDLINE: 97230451.
 RA ROBB L., HILTON D.J., BROOK-CARTER P.T., BEGLEY C.G.;
 RA "Identification of a second murine interleukin-11 receptor
 RA alpha-chain gene (IL11RA2) with a restricted pattern of expression.";
 RA Genomics 40:387-394(1997).
 C -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN-11.
 C -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 C -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 C -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 C -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 C -1- CONTAINS ONE IG-LIKE DOMAIN.
 C -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 C EMBL: X94157; CAA63872.1; -
 C EMBL: X94158; CAA63872.1; JOINED.
 C EMBL: X94159; CAA63872.1; JOINED.
 C EMBL: X94160; CAA63872.1; JOINED.
 C EMBL: X94161; CAA63872.1; JOINED.
 C EMBL: X98519; CAA67144.1; -
 C EMBL: 069491; AAC53114.1; -
 C MGD: MGI:109123; IL11RA2.
 C PFM: PFM0041; fn3; 2.
 C PFM: PFM0047; lg; 1.
 C Receptor; Transmembrane; Glycoprotein; Immunoglobulin fold; Signal.
 C SIGNAL 1 23
 C CHAIN 1 24 432
 C DOMAIN 24 367 INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 2.
 C TRANSMEM 368 393 EXTRACELLULAR (POTENTIAL).
 C DOMAIN 394 432 CYTOPLASMIC (POTENTIAL).
 C DOMAIN 41 102 IG-LIKE C2-TYPE DOMAIN.
 C CARBOHYD 127 127 POTENTIAL.
 C CARBOHYD 194 194 POTENTIAL.
 C CONFLICT 200 200 S -> P (IN CAA63872).
 C CONFLICT 384 384 V -> L (IN CAA63872).
 C SEQUENCE 432 AA: 46721 MW: C4FD7DEC CRC32;

QY 7 GPVQASARRPRPLSSLSKSPILLCLVLPVPGSGAHTAVISPODPTILLIGSSLOATCSIH 66
 Db 31 GPPEVOYQOPGR-----PYMLCCPGVSAG----- 55
 QY 67 GDTFGATAEGLYWTNLNRRRLPSELRLN--TSTLA--LALANLNGSRQSGDNLVCHAR 122
 Db 55 --TV-----VSRPDD-----SRLLQPPDSGLGRVLAQVDSDE--GRYVQTL 97
 QY 123 DGSILAGSCLYVGLPPEKPNISCSMRMDLCRTWPGAHGETFLHTNLSLKYLHWY 182
 Db 98 DGVSQGWTLKLGPPARP--EVSCQAVDYENFSGTWSPG--VSGLTRILTSYRKTLP 154
 QY 183 QDNTCEETHVGPESHCHPND-----LALTPYEIWEATNRLGARSADVLTLD 231
 Db 155 GAEQRESPESTGPPFC--PODPLEASRCVHGAEFMEYENINVTENVSLG--ASTCLLDVR 211
 QY 232 VLDVYTDPPPDVHVSNGVLEQOLSVRWSPFALK--DFLQAKYQIYRVEDSVDK 288
 Db 212 LQSLRPDPPOGLVESVPEYPRRLHNSWTYPASWRQPHLL--KRLQYRPAQHPAWS 269
 QY 289 VVDVSNQ--TSCRLAGLKPGTYFYVQRCNPFGIYSKKAQIINSESHPTASTP--- 343
 Db 270 TVEPIGLEEYITDTVAGLP---HAYVSAEDF-----LDAGTWSAMS--PEAWGTPTSTGL 319
 QY 343 -RSERP---GPGGVCCEPRGSGPSSGPPVRELEK 371
 Db 320 LQDEIPWMSGHGCQLEAVVAQEDSLAPAPPSIQ 353

Search completed: September 16, 1999, 20:40:05
 Job time: 5556 sec

Query Match 8.7%; Score 201; DB 11; Length 432;
 Best Local Similarity 24.6%; Pred. No. 6,9e-10;
 Matches 97; Conservative 49; Mismatches 148; Indels 100; Gaps 20;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 17, 1999, 03:08:13; Search time 64.1 Seconds

(without alignments)
57.275 Million cell updates/sec

ALIGNMENTS

44 72 8.3 525 1 W36846
45 72 8.3 304 1 W23155

Human fusion polyp
Human endonuclease

Title: US-09-037-657-17

Perfect score: 864

Sequence: 1 GTYVFWQVNCNPFQIGYSKK.....RTSGCPADGVREYVSG 155

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database: A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	864	100.0	155	1 W55013	Novel haemopoietin
2	631.5	73.1	350	1 W55015	Amino acid sequenc
3	631.5	73.1	389	1 W70846	Human zcyto5 vari
4	631.5	73.1	389	1 W70847	Human zcyto5 vari
5	631.5	73.1	389	1 W70848	Human zcyto5 vari
6	631.5	73.1	389	1 W70849	Human zcyto5 vari
7	631.5	73.1	389	1 W70850	Human zcyto5 vari
8	631.5	73.1	389	1 W70851	Human zcyto5 vari
9	631.5	73.1	389	1 W70852	Human zcyto5 vari
10	631.5	73.1	392	1 W70853	Human zcyto5 vari
11	631.5	73.1	392	1 W70854	Human zcyto5 vari
12	631.5	73.1	389	1 W70844	Human zcyto5 vari
13	631.5	73.1	425	1 W55011	Novel haemopoietin
14	577	66.8	413	1 W55012	Novel haemopoietin
15	573	66.3	425	1 W55012	Novel haemopoietin
16	573	66.3	425	1 W55012	Novel haemopoietin
17	573	66.3	385	1 W55804	Nucleotide sequenc
18	573	66.3	425	1 W70862	Human zcyto5 vari
19	569	65.9	408	1 W59805	Rat zcyto5 protei
20	569	65.9	388	1 W70839	Amino acid sequenc
21	569	65.9	385	1 W70842	Human zcyto5 vari
22	569	65.9	422	1 W70860	Human zcyto5 vari
23	209	24.2	303	1 W70843	Human zcyto5 vari
24	209	24.2	303	1 W70843	Human zcyto5 vari
25	166	19.2	31	1 W70845	Human zcyto5 vari
26	121	14.0	278	1 W70858	Human zcyto5 vari
27	84	9.7	2237	1 W55014	Human zcyto5 vari
28	78.5	9.1	500	1 R33550	Sequence of the al
29	78	9.0	1931	1 W36847	Sequence of the al
30	78	9.0	2339	1 R27649	Human fusion polyp
31	78	9.0	2339	1 R33549	Human calcium chan
32	78	9.0	2337	1 R71005	Sequence of the al
33	78	9.0	2337	1 R71006	Human neuronal cal
34	78	9.0	434	1 R66420	Peptide fragment o
35	78	9.0	2337	1 W37878	Human calcium chan
36	78	9.0	2339	1 W63141	Human calcium chan
37	75	8.7	2237	1 P93284	Sequence of clone
38	74	8.6	3025	1 W56293	Babesia microti BM
39	73.5	8.5	712	1 R07094	Protein having imm
40	73.5	8.5	240	1 R22597	Foetal oncogene pe
41	72.5	8.4	211	1 R24273	Truncated human pr
42	72.5	8.4	630	1 R93120	Tilapia prolactin
43	72.5	8.4	606	1 R93121	Tilapia prolactin

RESULT 1

W55013
ID W55013 standard; Protein; 155 AA.

AC W55013; 29-SEP-1998 (first entry)

DE Novel haemopoietin receptor NR6.3 protein.

KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer; cell survival; therapeutic; neuronal proliferation; drug screening;

KW Mouse.

OS Mus sp.

PN W09811225-A2.

PD 19-MAR-1998.

PE 11-SEP-1997; G02479.

PR 11-SEP-1996; AU-002246.

PA (AMRA-) AMRAD OPERATIONS PTY LTD.

PI (DIE/) DIELEWISKA H B.

PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,

PI Kojima T, Maeda M, Nash A, Nicola NA, Nakar S, Willison T,

PI Zhang J;

PI WPI; 98-260970/23.

DR N-PSDE; V27142.

PT New isolated haemopoietin receptor - used for developing products

PT for modulating proliferation, differentiation and survival of cells,

PT e.g. neuronal cells

PS Claim 16; Page 90-92; 182pp; English.

CC The haemopoietin receptor (HR) NR6.3 is a form of the novel HR NR6.

CC Interaction between the novel HR and a ligand facilitates proliferation,

CC differentiation and survival of a wide variety of cells. The HR and its

CC derivatives can be used for modulating the activity of the receptors e.g.

CC to regulate development, maintenance or regeneration in an array of

CC different cells and tissues in vitro and in vivo. They can be present in

CC therapeutics used for modulating neuronal proliferation, differentiation

CC and survival. The products can also be used for detection and diagnosis,

CC e.g. for cancers or predisposition to cancers, or for drug screening.

CC Sequence 155 AA.

SQ

Query Match

Best Local Similarity 100.0%; Score 864; DB 1; Length 155;

Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GTYYFWQVNCNPFQIGYSKKAGIWSMSHPTAASPPRSPGPGGVCPEPRGESSGPV	60
DB	1	GTYYFWQVNCNPFQIGYSKKAGIWSMSHPTAASPPRSPGPGGVCPEPRGESSGPV	60
QY	61	RELKQFLGMLKKHAYCSLFRLDQWPAAMQSKHTRNOYKLGACVGGAGEERD	120
DB	61	RELKQFLGMLKKHAYCSLFRLDQWPAAMQSKHTRNOYKLGACVGGAGEERD	120
QY	121	PEQPPQHTLLSKHRTGSCPRADGVREYVSG	155
DB	121	PEQPPQHTLLSKHRTGSCPRADGVREYVSG	155

RESULT 2

W55015
ID W55015 standard; Protein; 350 AA.

AC W55015; 29-SEP-1998 (first entry)

DE Amino acid sequence of clone HFR-66 encoding human NR6.

KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer; cell survival; therapeutic; neuronal proliferation; drug screening;

KW Human.

OS Homo sapiens.

PN W09811225-A2.

PD 19-MAR-1998.

PF 11-SEP-1997: G02479.
 PR (AMRA-) AMRAD OPERATIONS PVT LTD.
 PA (DZIE/) DZIEGLEWSKA H E.
 PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
 PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
 PI Zhang J;
 DR WPI: 98-260970/23.
 DR N-PSDB: V27144.
 PI New isolated haemopoietin receptor - used for developing products
 PI for modulating proliferation, differentiation and survival of cells,
 PT e.g. neuronal cells
 PS Claim 18: Page 102-104: 182pp; English.
 CC The NR6 protein is a novel haemopoietin receptor (HR). Interaction
 CC between the novel HR and a ligand facilitates proliferation.
 CC differentiation and survival of a wide variety of cells. The HR and its
 CC derivatives can be used for modulating the activity of the receptors e.g.
 CC to regulate development, maintenance or regeneration in an array of
 CC different cells and tissues in vitro and in vivo. They can be present in
 CC therapeutics used for modulating neuronal proliferation, differentiation
 CC and survival. The products can also be used for detection and diagnosis,
 CC e.g. for cancers or predisposition to cancers, or for drug screening.
 SQ Sequence 350 AA;

Query Match 73.1%; Score 631.5; DB 1; Length 350;
 Best Local Similarity 76.8%; Pred. No. 1.3e-58;
 Matches 116; Conservative 0; Mismatches 2; Indels 33; Gaps 1;

QY 1 GTVYFVQVRCNPFYIGSKKAGIWSHPTASTPRSERPGGVCPEPGGESSGPV 60
 DB 228 GTVYFVQVRCNPFYIGSKKAGIWSHPTASTPRSERPGGVCPEPGGESSGPV 287
 QY 61 RRELKQFLGWLKKAHAYCSNLSFRLYDQWRAMQSKHTRNOVGKLGACVGGKAEERD 120
 DB 288 RRELKQFLGWLKKAHAYCSNLSFRLYDQWRAMQSKHTRNOVGKLGACVGGKAEERD 329
 QY 121 PGEOPQHRITLSKHTRGSCPRADGVREV 151
 DB 329 -----HTRGSCPRADGVREV 345

RESULT 3
 W70846
 ID W70846 standard; Protein: 389 AA.
 AC W70846;
 DT 17-MAR-1999 (first entry)
 DE Human zcyto5 variant.
 KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KW cardiac pathology; heart enlargement; zcyto5 ligand; variant.
 OS Homo sapiens.
 PN WO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998: U08865.
 PR 13-FEB-1998: US-074721.
 PR 01-MAY-1997: US-045287.
 PR 01-MAY-1997: US-850030.
 PR 13-FEB-1998: US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.,
 PT down-regulating zcyto5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1: Page 89-90: 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcyto5 could be used to detect cardiotrophin-1 in the

CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SQ Sequence 389 AA;

Query Match 73.1%; Score 631.5; DB 1; Length 389;
 Best Local Similarity 76.8%; Pred. No. 1.5e-58;
 Matches 116; Conservative 0; Mismatches 2; Indels 33; Gaps 1;

QY 1 GTVYFVQVRCNPFYIGSKKAGIWSHPTASTPRSERPGGVCPEPGGESSGPV 60
 DB 267 GTVYFVQVRCNPFYIGSKKAGIWSHPTASTPRSERPGGVCPEPGGESSGPV 326
 QY 61 RRELKQFLGWLKKAHAYCSNLSFRLYDQWRAMQSKHTRNOVGKLGACVGGKAEERD 120
 DB 327 RRELKQFLGWLKKAHAYCSNLSFRLYDQWRAMQSKHTRNOVGKLGACVGGKAEERD 368
 QY 121 PGEOPQHRITLSKHTRGSCPRADGVREV 151
 DB 368 -----HTRGSCPRADGVREV 384

RESULT 4
 W70847
 ID W70847 standard; Protein: 389 AA.
 AC W70847;
 DT 17-MAR-1999 (first entry)
 DE Human zcyto5 variant.
 KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KW cardiac pathology; heart enlargement; zcyto5 ligand; variant.
 OS Homo sapiens.
 PN WO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998: U08865.
 PR 13-FEB-1998: US-074721.
 PR 01-MAY-1997: US-045287.
 PR 01-MAY-1997: US-850030.
 PR 13-FEB-1998: US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.,
 PT down-regulating zcyto5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1: Page 91-92: 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcyto5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SQ Sequence 389 AA;

Query Match 73.1%; Score 631.5; DB 1; Length 389;
 Best Local Similarity 76.8%; Pred. No. 1.5e-58;
 Matches 116; Conservative 0; Mismatches 2; Indels 33; Gaps 1;

QY 1 GTVYFVQVRCNPFYIGSKKAGIWSHPTASTPRSERPGGVCPEPGGESSGPV 60
 DB 267 GTVYFVQVRCNPFYIGSKKAGIWSHPTASTPRSERPGGVCPEPGGESSGPV 326
 QY 61 RRELKQFLGWLKKAHAYCSNLSFRLYDQWRAMQSKHTRNOVGKLGACVGGKAEERD 120

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Db 327 RRELKQFLGMLKKHAYCNSLSPRLTDQRAWAKSHKTRNQ----- 368
OY 121 PGEOPPOHRTLLSKHRTGSCPRADGVRREV 151
Db 368 -----HRTGSCPRADGARREV 384

RESULT 5
W70848 standard; Protein; 389 AA.
ID W70848;
AC W70848;
DT 17-MAR-1999 (first entry)
DE Human Zcyto5 variant.
KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
KW cardiac pathology; heart enlargement; Zcyto5 ligand; variant.
OS Homo sapiens.
MO9849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO ) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
PI WPI: 99-034662/03.
PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.
PT down-regulating Zcyto5 natural ligands or detecting cardiotrophin-1
PT in blood
PT Claim 1; Page 92-93; 55pp; English.
CC The present sequence represents a Zcyto5 variant protein. Zcyto5
CC is a cytokinin-like receptor. Soluble Zcyto5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC thyroid, heart, and skeletal muscle for example to lessen the effect
CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
CC enlargement. Zcyto5 could be used to detect cardiotrophin-1 in the
CC blood, and to discover other possible Zcyto5 ligands. A probe
CC comprising Zcyto5 DNA or RNA can be used to determine the presence
CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify Zcyto5 and the
CC therapeutically to modify Zcyto5 ligand effects.
CC Sequence 389 AA.

Query Match 73.1%; Score 631.5; DB 1; Length 389;
Best Local Similarity 76.8%; Pred. No. 1.5e-58;
Matches 116; Conservative 0; Mismatches 2; Indels 33; Gaps 1;

OY 1 GVTYFVQVNCNPFGLTIGSKKAGIWSHPTAASPRSRPDPGGVCPRGEPSSGVP 60
DB 267 GTYFVQVNCNPFGLTIGSKKAGIWSHPTAASPRSRPDPGGVCPRGEPSSGVP 326
DE Human Zcyto5 variant.
KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
KW cardiac pathology; heart enlargement; Zcyto5 ligand; variant.
OS Homo sapiens.
MO9849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO ) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
PI WPI: 99-034662/03.
PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.
PT down-regulating Zcyto5 natural ligands or detecting cardiotrophin-1
PT in blood
PT Claim 1; Page 92-93; 55pp; English.
CC The present sequence represents a Zcyto5 variant protein. Zcyto5
CC is a cytokinin-like receptor. Soluble Zcyto5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC thyroid, heart, and skeletal muscle for example to lessen the effect
CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
CC enlargement. Zcyto5 could be used to detect cardiotrophin-1 in the
CC blood, and to discover other possible Zcyto5 ligands. A probe
CC comprising Zcyto5 DNA or RNA can be used to determine the presence
CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify Zcyto5 and the
CC therapeutically to modify Zcyto5 ligand effects.
CC Sequence 389 AA.

OY 61 RRELKQFLGMLKKHAYCNSLSPRLTDQRAWAKSHKTRNOVGKIGLACVGGKGAEEEND 120
DB 327 RRELKQFLGMLKKHAYCNSLSPRLTDQRAWAKSHKTRNOVGKIGLACVGGKGAEEEND 368
DE Human Zcyto5 variant.
KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
KW cardiac pathology; heart enlargement; Zcyto5 ligand; variant.
OS Homo sapiens.
MO9849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO ) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
PI WPI: 99-034662/03.
PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.
PT down-regulating Zcyto5 natural ligands or detecting cardiotrophin-1
PT in blood
PT Claim 1; Page 92-93; 55pp; English.
CC The present sequence represents a Zcyto5 variant protein. Zcyto5
CC is a cytokinin-like receptor. Soluble Zcyto5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC thyroid, heart, and skeletal muscle for example to lessen the effect
CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
CC enlargement. Zcyto5 could be used to detect cardiotrophin-1 in the
CC blood, and to discover other possible Zcyto5 ligands. A probe
CC comprising Zcyto5 DNA or RNA can be used to determine the presence
CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify Zcyto5 and the
CC therapeutically to modify Zcyto5 ligand effects.
CC Sequence 389 AA.

RESULT 6
W70849 standard; Protein; 389 AA.
ID W70849;
AC W70849;
DT 17-MAR-1999 (first entry)
DE Human Zcyto5 variant.
KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
KW cardiac pathology; heart enlargement; Zcyto5 ligand; variant.
OS Homo sapiens.
MO9849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO ) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
PI WPI: 99-034662/03.
PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.
PT down-regulating Zcyto5 natural ligands or detecting cardiotrophin-1
PT in blood
PT Claim 1; Page 92-93; 55pp; English.
CC The present sequence represents a Zcyto5 variant protein. Zcyto5
CC is a cytokinin-like receptor. Soluble Zcyto5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC thyroid, heart, and skeletal muscle for example to lessen the effect
CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
CC enlargement. Zcyto5 could be used to detect cardiotrophin-1 in the
CC blood, and to discover other possible Zcyto5 ligands. A probe
CC comprising Zcyto5 DNA or RNA can be used to determine the presence
CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify Zcyto5 and the
CC therapeutically to modify Zcyto5 ligand effects.
CC Sequence 389 AA.

```

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OS Homo sapiens.
PN MO9849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO ) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
PI WPI: 99-034662/03.
PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.
PT down-regulating Zcyto5 natural ligands or detecting cardiotrophin-1
PT in blood
PT Claim 1; Page 94-95; 55pp; English.
CC The present sequence represents a Zcyto5 variant protein. Zcyto5
CC is a cytokinin-like receptor. Soluble Zcyto5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC thyroid, heart, and skeletal muscle for example to lessen the effect
CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
CC enlargement. Zcyto5 could be used to detect cardiotrophin-1 in the
CC blood, and to discover other possible Zcyto5 ligands. A probe
CC comprising Zcyto5 DNA or RNA can be used to determine the presence
CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify Zcyto5 and the
CC therapeutically to modify Zcyto5 ligand effects.
CC Sequence 389 AA.

Query Match 73.1%; Score 631.5; DB 1; Length 389;
Best Local Similarity 76.8%; Pred. No. 1.5e-58;
Matches 116; Conservative 0; Mismatches 2; Indels 33; Gaps 1;

OY 1 GVTYFVQVNCNPFGLTIGSKKAGIWSHPTAASPRSRPDPGGVCPRGEPSSGVP 60
DB 267 GTYFVQVNCNPFGLTIGSKKAGIWSHPTAASPRSRPDPGGVCPRGEPSSGVP 326
DE Human Zcyto5 variant.
KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
KW cardiac pathology; heart enlargement; Zcyto5 ligand; variant.
OS Homo sapiens.
MO9849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO ) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
PI WPI: 99-034662/03.
PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.
PT down-regulating Zcyto5 natural ligands or detecting cardiotrophin-1
PT in blood
PT Claim 1; Page 95-96; 55pp; English.
CC The present sequence represents a Zcyto5 variant protein. Zcyto5
CC is a cytokinin-like receptor. Soluble Zcyto5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC thyroid, heart, and skeletal muscle for example to lessen the effect
CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
CC enlargement. Zcyto5 could be used to detect cardiotrophin-1 in the
CC blood, and to discover other possible Zcyto5 ligands. A probe
CC comprising Zcyto5 DNA or RNA can be used to determine the presence
CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify Zcyto5 and the
CC therapeutically to modify Zcyto5 ligand effects.
CC Sequence 389 AA.

OY 121 PGEOPPOHRTLLSKHRTGSCPRADGVRREV 151
DB 368 -----HRTGSCPRADGARREV 384

RESULT 7
W70850 standard; Protein; 389 AA.
ID W70850;
AC W70850;
DT 17-MAR-1999 (first entry)
DE Human Zcyto5 variant.
KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
KW cardiac pathology; heart enlargement; Zcyto5 ligand; variant.
OS Homo sapiens.
MO9849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO ) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
PI WPI: 99-034662/03.
PT New mammalian cytokinin-like receptor Zcyto5 - useful for, e.g.
PT down-regulating Zcyto5 natural ligands or detecting cardiotrophin-1
PT in blood
PT Claim 1; Page 95-96; 55pp; English.
CC The present sequence represents a Zcyto5 variant protein. Zcyto5
CC is a cytokinin-like receptor. Soluble Zcyto5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC thyroid, heart, and skeletal muscle for example to lessen the effect
CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
CC enlargement. Zcyto5 could be used to detect cardiotrophin-1 in the
CC blood, and to discover other possible Zcyto5 ligands. A probe
CC comprising Zcyto5 DNA or RNA can be used to determine the presence
CC and integrity of the Zcyto5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify Zcyto5 and the
CC therapeutically to modify Zcyto5 ligand effects.
CC Sequence 389 AA.

```


CC is a cytokinin-like receptor. Soluble Zcytors may be administered to down-regulate the effects of a growth and/or maintenance factor in CC thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytors could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytors ligands. A probe comprising Zcytors DNA or RNA can be used to determine the presence and integrity of the Zcytors gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytors and therapeutically to modify Zcytors ligand effects.

SO Sequence 389 AA;

Query Match 73.1%; Score 631.5; DB 1; Length 389;
Best Local Similarity 76.8%; Pred. NO. 1.5e-58;
Matches 116; Conservative 0; Mismatches 2; Indels 33; Gaps 1;

QY 1 GTTFFVQVRCNPFGIYSKKGAGIWSHPTASTPRSERPGGVCGERGESSGPV 60
DB 267 GTTFFVQVRCNPFGIYSKKGAGIWSHPTASTPRSERPGGVCGERGESSGPV 326
QY 61 RRELKQFLGWLKKAHACSNLSFRLYDQWRAMQSKHTRNQVKGLEACVGGAGEERD 120
DB 327 RRELKQFLGWLKKAHACSNLSFRLYDQWRAMQSKHTRNQVKGLEACVGGAGEERD 368
QY 121 PGEQPPQHTLSKHRTGSCPRADGVRREV 151
DB 368 -----HRTGSCPRADGVRREV 384

RESULT 8

ID W70851 standard; Protein: 389 AA.

AC W70851; 17-MAR-1999 (first entry)
DE Human Zcytors variant.
KW Zcytors; cytokinin-like receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1; cardiac pathology; heart enlargement; Zcytors ligand; variant.
OS Homo sapiens.
PN W09849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM, Lok S, Presnell SR, Whitmore TE;
PI WPI: 99-034662/03.
DR New mammalian cytokinin-like receptor Zcytors - useful for, e.g. down-regulating Zcytors natural ligands or detecting cardiotrophin-1 in blood
PT Claim 1; Page 96-97; 55pp; English.
PS The present sequence represents a Zcytors variant protein. Zcytors is a cytokinin-like receptor. Soluble Zcytors may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytors could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytors ligands. A probe comprising Zcytors DNA or RNA can be used to determine the presence and integrity of the Zcytors gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytors and therapeutically to modify Zcytors ligand effects.

SO Sequence 389 AA;

Query Match 73.1%; Score 631.5; DB 1; Length 389;
Best Local Similarity 76.8%; Pred. NO. 1.5e-58;
Matches 116; Conservative 0; Mismatches 2; Indels 33; Gaps 1;

QY 1 GTTFFVQVRCNPFGIYSKKGAGIWSHPTASTPRSERPGGVCGERGESSGPV 60
DB 267 GTTFFVQVRCNPFGIYSKKGAGIWSHPTASTPRSERPGGVCGERGESSGPV 326
QY 61 RRELKQFLGWLKKAHACSNLSFRLYDQWRAMQSKHTRNQVKGLEACVGGAGEERD 120
DB 327 RRELKQFLGWLKKAHACSNLSFRLYDQWRAMQSKHTRNQVKGLEACVGGAGEERD 368
QY 121 PGEQPPQHTLSKHRTGSCPRADGVRREV 151
DB 368 -----HRTGSCPRADGVRREV 384

RESULT 9

ID W70852 standard; Protein: 389 AA.

AC W70852; 17-MAR-1999 (first entry)
DE Human Zcytors variant.
KW Zcytors; cytokinin-like receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1; cardiac pathology; heart enlargement; Zcytors ligand; variant.
OS Homo sapiens.
PN W09849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM, Lok S, Presnell SR, Whitmore TE;
PI WPI: 99-034662/03.
DR New mammalian cytokinin-like receptor Zcytors - useful for, e.g. down-regulating Zcytors natural ligands or detecting cardiotrophin-1 in blood
PT Claim 1; Page 98-99; 55pp; English.
PS The present sequence represents a Zcytors variant protein. Zcytors is a cytokinin-like receptor. Soluble Zcytors may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytors could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytors ligands. A probe comprising Zcytors DNA or RNA can be used to determine the presence and integrity of the Zcytors gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytors and therapeutically to modify Zcytors ligand effects.

SO Sequence 389 AA;

Query Match 73.1%; Score 631.5; DB 1; Length 389;
Best Local Similarity 76.8%; Pred. NO. 1.5e-58;
Matches 116; Conservative 0; Mismatches 2; Indels 33; Gaps 1;

QY 1 GTTFFVQVRCNPFGIYSKKGAGIWSHPTASTPRSERPGGVCGERGESSGPV 60
DB 267 GTTFFVQVRCNPFGIYSKKGAGIWSHPTASTPRSERPGGVCGERGESSGPV 326
QY 61 RRELKQFLGWLKKAHACSNLSFRLYDQWRAMQSKHTRNQVKGLEACVGGAGEERD 120
DB 327 RRELKQFLGWLKKAHACSNLSFRLYDQWRAMQSKHTRNQVKGLEACVGGAGEERD 368
QY 121 PGEQPPQHTLSKHRTGSCPRADGVRREV 151
DB 368 -----HRTGSCPRADGVRREV 384

RESULT 10

ID W70853 standard; Protein: 389 AA.

Accession	Protein	Gene	Species	Source	Reference
W70840	standard; Protein; 392 AA.				
W70840.1					
W70840.2					
W70840.3					
W70840.4					
W70840.5					
W70840.6					
W70840.7					
W70840.8					
W70840.9					
W70840.10					
W70840.11					
W70840.12					
W70840.13					
W70840.14					
W70840.15					
W70840.16					
W70840.17					
W70840.18					
W70840.19					
W70840.20					
W70840.21					
W70840.22					
W70840.23					
W70840.24					
W70840.25					
W70840.26					
W70840.27					
W70840.28					
W70840.29					
W70840.30					
W70840.31					
W70840.32					
W70840.33					
W70840.34					
W70840.35					
W70840.36					
W70840.37					
W70840.38					
W70840.39					
W70840.40					
W70840.41					
W70840.42					
W70840.43					
W70840.44					
W70840.45					
W70840.46					
W70840.47					
W70840.48					
W70840.49					
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W70840.73					
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W70840.78					
W70840.79					
W70840.80					
W70840.81					
W70840.82					
W70840.83					
W70840.84					
W70840.85					

RESULT	12	
W0844		
ID	W70844	standard; Protein; 389 AA.
AC	W70844;	
DT	17-MAR-1999	(first entry)
DE	Human Zcytor5 variant.	
KW	Zcytor5; cytokinin-like receptor; down-regulation; growth factor;	
KW	maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;	
OS	cardiac pathology; heart enlargement; Zcytor5 ligand; variant.	
PN	Homio sapiens.	
PD	MO8849307-A1.	
PR	05-NOV-1998.	
PR	01-MAY-1998; U08865.	
PR	13-FEB-1998; US-074721.	
PR	01-MAY-1997; US-045287.	
PR	01-MAY-1997; US-850030.	
PR	13-FEB-1998; US-022890.	
PA	(Zymo) ZYMOGENETICS INC.	
PI	Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,	
PI	Lok S, Presnell SR, Whitmore TE;	
DR	WPI; 99-034662/03.	
PT	New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.	
PT	down-regulating Zcytor5 natural ligands or detecting cardiotoxin-1	
PT	in blood	
PS	Claim 1; Page 87-88; 55pp; English.	
PS	The present sequence represents a Zcytor5 variant protein. Zcytor5	
CC	is a cytokinin-like receptor. Soluble Zcytor5 may be administered to	
CC	down-regulate the effects of a growth and/or maintenance factor in	
CC	thyroid heart, and skeletal muscle for example to lessen the effect	
CC	of cardiotoxin-1 on cardiac pathologies, so preventing heart	
CC	enlargement. Zcytor5 could be used to detect cardiotoxin-1 in the	
CC	blood, and to discover other possible Zcytor5 ligands. A probe	
CC	comprising Zcytor5 DNA or RNA can be used to determine the presence	
CC	and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the	
CC	anti-idiotypic antibody could be used to purify Zcytor5 and	
CC	therapeutically to modify Zcytor5 ligand effects.	
CC	Sequence 389 AA;	

Query Match 73.1%; Score 631.5; DB 1; Length 389;
Best Local Similarity 76.8%; Pred. No. 1.5e-58;
Matches 116; Conservative 0; Mismatches 2; Indels 33; Gaps 1;

QY 1 GTVYFVQVNCNPGIGYSGKAGIWMSEMSHPTASTPSPRSPGGGVCCEPRGEPSSGPV 60
DB 267 GTVYFVQVNCNPGIGYSGKAGIWMSEMSHPTASTPSPRSPGGGVCCEPRGEPSSGPV 326
QY 61 RRELKQFLGMLKKHAYCSNLSFRLYDQWRAMQKSHKTRNOYKLGACVGGKGAEEEND 120
DB 327 RRELKQFLGMLKKHAYCSNLSFRLYDQWRAMQKSHKTRNOYKLGACVGGKGAEEEND 368
QY 121 PGEOPPHRTLSKHKTRGSCPRADGVREV 151
DB 368 -----HRTGSCPRADGVREV 384

RESULT 13

W70861
ID W70861 standard; Protein; 425 AA.
AC W70861;
DT 17-MAR-1999 (first entry)
DE Allelic variant of human zcytors.
KW Zcytors; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
KW cardiac pathology; heart enlargement; zcytors ligand; allelic variant.
OS Homo sapiens.
PN W09849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jernberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
DR WPI; 99-034652/03.
DR N-PSDB; V70895.
PT New mammalian cytokinin-like receptor zcytors - useful for, e.g.
PT down-regulating zcytors natural ligands or detecting cardiostrophin-1
PT in blood
PS Claim 1; Page 71-72; 55pp; English.
CC The present sequence represents an allelic variant of protein designated
CC zcytors, which is a cytokinin-like receptor. Soluble zcytors may be
CC administered to down-regulate the effects of a growth and/or maintenance
CC factor in thyroid, heart, and skeletal muscle for example to lessen the
CC effect of cardiostrophin-1 on cardiac pathologies, so preventing heart
CC enlargement. Zcytors could be used to detect cardiostrophin-1 in the
CC blood, and to discover other possible zcytors ligands. A probe
CC comprising zcytors DNA or RNA can be used to determine the presence
CC and integrity of the zcytors gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify zcytors and
CC therapeutically to modify zcytors ligand effects.
SQ Sequence 425 AA;

Query Match 73.1%; Score 631.5; DB 1; Length 425;
Best Local Similarity 76.8%; Pred. No. 1.6e-58;
Matches 116; Conservative 0; Mismatches 2; Indels 33; Gaps 1;

QY 1 GTVYFVQVNCNPGIGYSGKAGIWMSEMSHPTASTPSPRSPGGGVCCEPRGEPSSGPV 60
DB 303 GTVYFVQVNCNPGIGYSGKAGIWMSEMSHPTASTPSPRSPGGGVCCEPRGEPSSGPV 362
QY 61 RRELKQFLGMLKKHAYCSNLSFRLYDQWRAMQKSHKTRNOYKLGACVGGKGAEEEND 120
DB 363 RRELKQFLGMLKKHAYCSNLSFRLYDQWRAMQKSHKTRNOYKLGACVGGKGAEEEND 404
QY 121 PGEOPPHRTLSKHKTRGSCPRADGVREV 151
DB 404 -----HRTGSCPRADGVREV 420

RESULT 14

W55011
ID W55011 standard; Protein; 413 AA.
AC W55011;
DT 29-SEP-1998 (first entry)
DE Novel haemopoietin receptor NR6.1 protein.
KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
KW cell survival; therapeutic; neuronal proliferation; drug screening;
OS Mus sp.
PN W09811225-A2.
PD 19-MAR-1998.
PF 11-SEP-1997; G02479.
PR 11-SEP-1996; AU-002246.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PA (DZIE/) DZIEGLEWSKA H E.
PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
PI Kojima T, Maeda M, Nash A, Nicola NA, Raker S, Willson T,
PI Zhang J;
DR WPI; 98-260970/23.
DR N-PSDB; V27140.
PT New isolated haemopoietin receptor - used for developing products
PT for modulating proliferation, differentiation and survival of cells,
PS e.g. neuronal cells
PS Claim 14; Page 77-81; 182pp; English.
CC The haemopoietin receptor (HR) NR6.1 is a form of the novel HR NR6.
CC Interaction between the novel HR and a ligand facilitates proliferation,
CC differentiation and survival of a wide variety of cells. The HR and its
CC derivatives can be used for modulating the activity of the receptors e.g.
CC to regulate development, maintenance or regeneration in an array of
CC different cells and tissues in vitro and in vivo. They can be present in
CC therapeutics used for modulating neuronal proliferation, differentiation
CC and survival. The products can also be used for detection and diagnosis,
CC e.g. for cancers or predisposition to cancers, or for drug screening.
SQ Sequence 413 AA;

Query Match 66.8%; Score 577; DB 1; Length 413;
Best Local Similarity 100.0%; Pred. No. 8.2e-53;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTVYFVQVNCNPGIGYSGKAGIWMSEMSHPTASTPSPRSPGGGVCCEPRGEPSSGPV 60
DB 307 GTVYFVQVNCNPGIGYSGKAGIWMSEMSHPTASTPSPRSPGGGVCCEPRGEPSSGPV 366
QY 61 RRELKQFLGMLKKHAYCSNLSFRLYDQWRAMQKSHKTRNOY 102
DB 367 RRELKQFLGMLKKHAYCSNLSFRLYDQWRAMQKSHKTRNOY 408

RESULT 15

W55012
ID W55012 standard; Protein; 425 AA.
AC W55012;
DT 29-SEP-1998 (first entry)
DE Novel haemopoietin receptor NR6.2 protein.
KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
KW cell survival; therapeutic; neuronal proliferation; drug screening;
OS Mus sp.
PN W09811225-A2.
PD 19-MAR-1998.
PF 11-SEP-1997; G02479.
PR 11-SEP-1996; AU-002246.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PA (DZIE/) DZIEGLEWSKA H E.
PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
PI Kojima T, Maeda M, Nash A, Nicola NA, Raker S, Willson T,
PI Zhang J;
DR WPI; 98-260970/23.
DR N-PSDB; V27141.

PT New isolated haemopoietin receptor - used for developing products
 PT for modulating proliferation, differentiation and survival of cells,
 PS e.g. neuronal cells
 PS Claim 15: Page 84-87; 182pp; English.
 CC The haemopoietin receptor (HR) NR6.2 is a form of the novel HR NR6.
 CC Interaction between the novel HR and a ligand facilitates proliferation,
 CC differentiation and survival of a wide variety of cells. The HR and its
 CC derivatives can be used for modulating the activity of the receptors e.g.
 CC to regulate development, maintenance or regeneration in an array of
 CC different cells and tissues in vitro and in vivo. They can be present in
 CC therapeutics used for modulating neuronal proliferation, differentiation
 CC and survival. The products can also be used for detection and diagnosis,
 CC e.g. for cancers or predisposition to cancers, or for drug screening.
 SQ Sequence 425 AA:

Query Match 66.3%; Score 573; DB 1; Length 425;
 Best Local Similarity 100.0%; Pred. No. 2.2e-52;
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTVYFVQVRCNPFQIGSKKAGIMSEWSHPTAASPRSERPGGVCCEPRGSSGPV 60
 DB 307 GTVYFVQVRCNPFQIGSKKAGIMSEWSHPTAASPRSERPGGVCCEPRGSSGPV 60
 QY 61 RRELKQFLGWLKKAHAYCSNLSFRLYDQWRAMQKSHKTRNQ 101
 DB 367 RRELKQFLGWLKKAHAYCSNLSFRLYDQWRAMQKSHKTRNQ 407

Search completed: September 17, 1999, 03:08:14
 Job time: 305 sec

RESULT 2
US-08-337-602-3
Sequence 3, Application US/08337602
Patent No. 5623051
GENERAL INFORMATION:
APPLICANT: Catterall, William A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
NUMBER OF SEQUENCES: 4
TITLE OF INVENTION: FOR PRESYNAPTIC CALCIUM CHANNEL BLOCKERS
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98042-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,602
FILING DATE: 10-NOV-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.602
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANDBERRY
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: 1linear
US-08-337-602-3

Query Match 9.0%; Score 78; DB 1; Length 434;
Best Local Similarity 23.2%; Pred. No. 0.92;
Matches 33; Conservative 15; Mismatches 38; Indels 56; Gaps 8;

QY 28 SHPTASTP---RSE---PGPGGVCPEPRGSPSSGVPVRRLEKQFLGWLKKAHACSNLS 81
DB 182 SHKKAAGPPEARSEKRGSGPGRHRRHRSPEEAAREP-----RRH----- 227
QY 82 FLYLDQWRAWMOKSHKTRNOVGKLGACVGGK-----AEEERDPCEOPPOHR 129
DB 227 -----RAHRHQP-----SKCAKANGERARRHRRGPRAGPRAEAGEEPAR-- 269
QY 130 TILSKHRTGSC-PRADGVRR 150
DB 269 ---RHRARRKQAPAEAVEKE 286

RESULT 3
US-08-455-543A-47
Sequence 47, Application US/08455543A
Patent No. 5792846
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert

TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 2339 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: 1linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-455-543A-47

Query Match 9.0%; Score 78; DB 2; Length 2339;
Best Local Similarity 23.2%; Pred. No. 7.2;
Matches 33; Conservative 15; Mismatches 38; Indels 56; Gaps 8;

QY 28 SHPTASTP---RSE---PGPGGVCPEPRGSPSSGVPVRRLEKQFLGWLKKAHACSNLS 81
DB 891 SHKKAAGPPEARSEKRGSGPGRHRRHRSPEEAAREP-----RRH----- 936
QY 82 FLYLDQWRAWMOKSHKTRNOVGKLGACVGGK-----AEEERDPCEOPPOHR 129
DB 936 -----RAHRHQP-----SKCAKANGERARRHRRGPRAGPRAEAGEEPAR-- 978
QY 130 TILSKHRTGSC-PRADGVRR 150

Db 978 ----RRARHKAQPAHEAVEKE 995

RESULT 4

US-08-455-543A-48
Sequence 48, Application US/08455543A
Patent No. 5792846

GENERAL INFORMATION:

APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/223,305

FILING DATE: April 4, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/868,354

FILING DATE: April 10, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/745,206

FILING DATE: 15-AUG-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/620,250

FILING DATE: 30-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/482,384

FILING DATE: 20-FEB-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/603,751

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US89/01408

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/176,899

FILING DATE: 04-APR-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 6362-52517

FILING DATE: 33,779

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 6362-52517

FILING DATE: 33,779

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 6362-52517

FILING DATE: 33,779

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 6362-52517

FILING DATE: 33,779

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 6362-52517

FILING DATE: 33,779

PRIOR APPLICATION DATA:

Query Match

9.0% Score 78; DB 2; Length 2237;
Best Local Similarity 23.2%; Pred. No. 6.8;
Matches 33; Conservative 15; Mismatches 39; Indels 56; Gaps 8;

QY 28 SHPTASTP---RSEF---PQGGGVCERGPSSGPPVRLKQFLGWLKRAYCSNLS 81

DB 891 SSKKAGPPEARSEGRGPGEGRRHRRGSPPEAAREP-----RRH----- 936

QY 82 FLYDQWRAMQKSHRTNRQVGLGPAVCYGGK-----AEEPRDGEOPPOHR 129

DB 936 -----RAHRHDP-----SRECGAGKERRARRRGPPRAGPRAESGEEDPAR-- 978

QY 130 TILSKHRTGSC-PRADGVRR 150

DB 978 ----RRARHKAQPAHEAVEKE 995

RESULT 5

US-08-223-305C-47
Sequence 47, Application US/08223305C
Patent No. 5851824

GENERAL INFORMATION:

APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:APPLICATION NUMBER: US/08/223,305C
FILING DATE: April 4, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/868,354

FILING DATE: April 10, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/745,206

FILING DATE: 15-AUG-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/620,250

FILING DATE: 30-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/482,384

FILING DATE: 20-FEB-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/603,751

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US89/01408

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/176,899

FILING DATE: 04-APR-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 6362-52517

FILING DATE: 33,779

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 6362-52517

FILING DATE: 33,779

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 6362-52517

FILING DATE: 33,779

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 2339 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-223-305C-47

Query Match 9.0%; Score 78; DB 2; Length 2339;
Best Local Similarity 23.2%; Pred. No. 7.2;
Matches 33; Conservative 15; Mismatches 38; Indels 56; Gaps 8;

QY 28 SHPTASTP---RSE---PGPGGVCPEPGSGSPVRELEKQFLGMLKKHAYCSNLS 81
DB 891 SHSEKAGPPEARSERGRGPGEGRRHHRGSPFEAAEREP-----RRH----- 936
QY 82 FRLYDQWRAMQKSHKTRNOVGKIGECVCGKG-----AAEERDPGEOPPOHR 139
DB 936 -----RAHRHQDP-----SKECAGAKGERARRHNGRPRAGPREAESGEPPAR-- 978
QY 130 TLSKHRTGSC-PRADGVARE 150
DB 978 ----RRARRKQAPAEAVEKE 995

RESULT 6
US-08-223-305C-48
Sequence 48, Application US/08223305C
Patent No. 5851824
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSO Version 1.5
CURRENT APPLICATION DATA:
FILING DATE: April 4, 1994
APPLICATION NUMBER: US/08/223,305C
PRIOR APPLICATION DATA:
FILING DATE: April 10, 1992
APPLICATION NUMBER: 07/868,354
PRIOR APPLICATION DATA:
FILING DATE: 15-AUG-1991
APPLICATION NUMBER: US 07/745,206
PRIOR APPLICATION DATA:
FILING DATE: 30-NOV-1990
APPLICATION NUMBER: US 07/620,250
PRIOR APPLICATION DATA: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 2237 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-223-305C-48

Query Match 9.0%; Score 78; DB 2; Length 2237;
Best Local Similarity 23.2%; Pred. No. 6.8;
Matches 33; Conservative 15; Mismatches 38; Indels 56; Gaps 8;

QY 28 SHPTASTP---RSE---PGPGGVCPEPGSGSPVRELEKQFLGMLKKHAYCSNLS 81
DB 891 SHSEKAGPPEARSERGRGPGEGRRHHRGSPFEAAEREP-----RRH----- 936
QY 82 FRLYDQWRAMQKSHKTRNOVGKIGECVCGKG-----AAEERDPGEOPPOHR 139
DB 936 -----RAHRHQDP-----SKECAGAKGERARRHNGRPRAGPREAESGEPPAR-- 978
QY 130 TLSKHRTGSC-PRADGVARE 150
DB 978 ----RRARRKQAPAEAVEKE 995

RESULT 7
US-08-438-439C-17
Sequence 17, Application US/08438439C
Patent No. 5876967
GENERAL INFORMATION:
APPLICANT: Nathans, Jeremy
APPLICANT: Smallwood, Phillip M.
APPLICANT: Macke, Jennifer P.
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
TITLE OF INVENTION: FACTOR-2 AND METHODS OF USE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: LA Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,439C
FILING DATE: May 12, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hallie, Lisa A.
REGISTRATION NUMBER: 38,347

37. RSEKPGGGVCEPRGGEPSSG

96

Db 4 NRSISGPGAG---PRGCEEEBGLRR-----EAAAEAKSH 37
QY 97 KTRNOVGKIGACVGGKGAERDGPQ 125
Db 38 SPVKPRRAQRLRYAVEGSDSEKGEAGP 66

RESULT 10
US-08-026-138E-3
; Sequence 3, Application US/08026138E
; Patent No. 5502166
; GENERAL INFORMATION:
; APPLICANT: Masayoshi MISHINA
; TITLE OF INVENTION: NOVEL PROTEINS AND GENES CODING THE SAME
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nishiohata Residence 1-107
; STREET: 5214, Nishiohata-machi
; CITY: Niigata-shi
; STATE: Niigata-ken
; COUNTRY: JAPAN
; ZIP: 951
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS v.5
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/026,138E
; FILING DATE: 26-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 39563/1992
; FILING DATE: 26-FEB-1992
; APPLICATION NUMBER: JP 173155/1992
; FILING DATE: 30-JUN-1992
; APPLICATION NUMBER: JP 215017/1992
; FILING DATE: 12-AUG-1992
; APPLICATION NUMBER: JP 303878/1992
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamburg, C. Bruce
; REGISTRATION NUMBER: 22,389
; REFERENCE/DOCKET NUMBER: F-4551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 986-2340
; TELEFAX: (212) 953-7733
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1239 amino acids
; TYPE: amino acid
; STRANDEDNESS: single strand
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: mouse
; TISSUE TYPE: brain
; PUBLICATION INFORMATION:
; AUTHORS: Masayoshi MISHINA
; TITLE: NOVEL PROTEINS AND GENES CODING THE SAME
; RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 1 to 1239
; US-08-026-138E-3

Query Match 8 2%; Score 70.5; DB 1; Length 1239;
Best Local Similarity 26.1%; Pred. No. 21;
Matches 35; Conservative 10; Mismatches 42; Indels 47; Gaps 7;

QY 30 PTAATPSEERPGGCGVEPRGEPSSG---PVREELKQFLGMLKHAACSNLSFRLYD 86
Db 932 PT-TSGPRSCGTPGPGQ-SPSGWRPPGCGRTPLARAP----- 969
QY 87 QMRAHQKSHKTRNOVGKIGEAC-----VGGKGAEE---RDPEQPPQ-----HRTL 131

Db 969 -----QPARPAPAGRLSPTCPEHPAGTLGNKGCGESGINDRTSRPPERRALPERSL 1022
QY 132 LSKHRTGSCPRAD 145
Db 1023 LHAHCYSSFPRAE 1036

RESULT 11
US-07-814-964-7
; Sequence 7, Application US/07814964
; Patent No. 5359047
; GENERAL INFORMATION:
; APPLICANT: Donahue, Brian A.
; APPLICANT: Toney, Jeffrey H.
; APPLICANT: Bruhn, Suzanne L.
; APPLICANT: Pili, Peter M.
; APPLICANT: Brown, Steven
; APPLICANT: Kellelt, Patil
; APPLICANT: Essigmann, John M.
; TITLE OF INVENTION: DNA Structure Specific Recognition
; TITLE OF INVENTION: Protein and Uses Therefor
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: 2 Millia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/814,964
; FILING DATE: 19911226
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/539,906
; FILING DATE: 18-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-4/87AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 709 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: human SSR (predicted)
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 440..496
; OTHER INFORMATION: /label= Acidic
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 512..534
; OTHER INFORMATION: /label= Basic I
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 539..614
; OTHER INFORMATION: /label= HMG-box
; FEATURE:
; NAME/KEY: Domain

LOCATION: 623..640
OTHER INFORMATION: /label- Basic II
FEATURE:
NAME/KEY: Domain
LOCATION: 661..709
OTHER INFORMATION: /label- Mixed Charge
US-07-814-964-7

Query Match
Best Local Similarity 21.98; Score 68.5; DB 1; Length 709;
Matches 28; Conservative 23; Mismatches 52; Indels 25; Gaps 6;

QY 37 RSEPPGGGVCPEPGEPSGPPVRELKOFGLM-----KKHAYCS--NLSFRLYD 86
DB 529 RKSRRKP-----VEVKKGKDNDAP-KRPMAYMLNLSREKISDHPGISTDLSKRAE 563
QY 87 QHRA-----WMQSHKTRNOVGKLGACVGGKGAEEERDPGEPPQHRILLSKHRT- 138
DB 584 IWGMSKEKEEEDRKADRDYERAMKEYEGGREGSSKRSKKKKYKVMKKKSTP 643
QY 138 -RGSCDRA 144
DB 644 SRGSSSKS 651

RESULT 12
US-07-745-206A-13
Sequence 13, Application US/07745206A
Patent No. 5429921

GENERAL INFORMATION:

APPLICANT: Harpold, Michael

APPLICANT: Ellis, Steven

APPLICANT: Williams, Mark

APPLICANT: Mogue, Ann

APPLICANT: Feldman, Daniel

TITLE OF INVENTION: Human Calcium Channel Compositions and

TITLE OF INVENTION: Methods

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fitch, Even, Tabin & Flannery

STREET: 135 S. LaSalle

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/745,206A

FILING DATE: 19910815

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Feder, Scott B

REFERENCE/DOCKET NUMBER: 51504

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-372-7842

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 1754 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-745-206A-13

Query Match

Best Local Similarity 22.08; Score 68.5; DB 1; Length 1754;
Matches 33; Conservative 13; Mismatches 45; Indels 59; Gaps 6;

QY 30 PTASTRSERPPGGGVCPEPGEPSG--PYRELKOFGLMKHAYCSNLSFRLYD 87
DB 816 PLYVELRGDAGRGVGGKAPPAEAAPGVDPPRRHR----- 854
QY 88 WRAMQSHKTRNOVGKLG-----ACVGGKGAEEERDPGE-----PQHRILL 131
DB 854 -----HRDKDTPAGQDRAEAPKAESEGPAGAEERPRADRSKXENAGPPPARTS 905

QY 132 LSKHR-----TRGSCPRADGVRRFVRS 154
DB 906 AAQAQAPRAAGCTTGAPR-----RRRPSGS 931

RESULT 13
US-08-258-442-7
Sequence 7, Application US/08258442
Patent No. 5670621

GENERAL INFORMATION:

APPLICANT: Donahue, Brian A.

APPLICANT: Toney, Jeffrey H.

APPLICANT: Bruhn, Suzanne L.

APPLICANT: Pili, Pieter M.

APPLICANT: Brown, Steven

APPLICANT: Kelleet, Patcl

APPLICANT: Essigmann, John M.

APPLICANT: Lippard, Stephen J.

TITLE OF INVENTION: DNA Structure Specific Recognition

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: 2 Militia Drive

CITY: Lexington

STATE: MA

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/258,442

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/539,906

FILING DATE: 18-JUN-1990

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: MIT-4787AAA

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 709 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

IMMEDIATE SOURCE:

CLONE: human SSRP (predicted)

FEATURE:

NAME/KEY: Domain

LOCATION: 440..496

OTHER INFORMATION: /label- Acidic

FEATURE:

NAME/KEY: Domain

LOCATION: 512..534

OTHER INFORMATION: /label- Basic I

FEATURE:
NAME/KEY: Domain
LOCATION: 539..614
OTHER INFORMATION: /label- HMG-box
FEATURE:
NAME/KEY: Domain
LOCATION: 623..640
OTHER INFORMATION: /label- Basic II
FEATURE:
NAME/KEY: Domain
LOCATION: 661..709
OTHER INFORMATION: /label- Mixed Charge
US-08-258-442-7

Query Match
Best Local Similarity 7.9%; Score 68.5; DB 1; Length 709;
Matches 28; Conservative 23; Mismatches 52; Indels 25; Gaps 6;

QY 37 RSEPPGGGVCPEPGEPSGVPRLKQFLGWL-----KKHAYCS--NLSERLYD 86
DB 529 RSRKKRP---VEYKKGKDPNAP-KRPMASVYMLNLSREKIKSDHFGISITDLSKAGE 583
QY 87 QWRA-----WMQSKHTRNOVGKLGACVGGKGAEEERDPGEGPPQHRTLLSKHRT- 138
DB 584 IMKGMSEKKEEMDRKADARRDYERKAMKEYEGGREGSSKRDSKKKKKVKYMEKSTP 643
QY 138 -RSCCPRA 144
DB 644 SRGSSSKS 651

RESULT 14
US-08-328-809-2
Sequence 2, Application US/08328809

GENERAL INFORMATION:

APPLICANT: Lippard, Stephen J.
APPLICANT: Essigmann, John M.
APPLICANT: Donahue, Brian A.
APPLICANT: Toney, Jeffrey H.
APPLICANT: Bruhn, Suzanne L.
APPLICANT: Pili, Peter M.
APPLICANT: Brown, Steven
APPLICANT: Kellett, Paul
TITLE OF INVENTION: Uses For DNA Structure-Specific
TITLE OF INVENTION: Recognition Proteins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Administrator, Testa, Hurwitz & Thibault
STREET: 53 State Street
CITY: Boston
STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,809
FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Fenton, Gillian M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: MIR-023 (5473/24)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7100
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 709 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: human SSRP (predicted)
FEATURE:
NAME/KEY: Domain
LOCATION: 440..496
OTHER INFORMATION: /label- Acidic
FEATURE:
NAME/KEY: Domain
LOCATION: 512..534
OTHER INFORMATION: /label- Basic I
FEATURE:
NAME/KEY: Domain
LOCATION: 539..614
OTHER INFORMATION: /label- HMG
FEATURE:
NAME/KEY: Domain
LOCATION: 623..640
OTHER INFORMATION: /label- Basic II
FEATURE:
NAME/KEY: Domain
LOCATION: 661..709
OTHER INFORMATION: /label- Mixed Charge
US-08-328-809-2

Query Match
Best Local Similarity 7.9%; Score 68.5; DB 1; Length 709;
Matches 28; Conservative 23; Mismatches 52; Indels 25; Gaps 6;

QY 37 RSEPPGGGVCPEPGEPSGVPRLKQFLGWL-----KKHAYCS--NLSERLYD 86
DB 529 RSRKKRP---VEYKKGKDPNAP-KRPMASVYMLNLSREKIKSDHFGISITDLSKAGE 583
QY 87 QWRA-----WMQSKHTRNOVGKLGACVGGKGAEEERDPGEGPPQHRTLLSKHRT- 138
DB 584 IMKGMSEKKEEMDRKADARRDYERKAMKEYEGGREGSSKRDSKKKKKVKYMEKSTP 643
QY 138 -RSCCPRA 144
DB 644 SRGSSSKS 651

RESULT 15
US-08-311-363-13
Sequence 13, Application US/08311363

GENERAL INFORMATION:

APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McGue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: Human Calcium Channel Compositions and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```

: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/311,363
: FILING DATE:
: PRIORITY DATE:
: APPLICATION NUMBER: US 07/745,206
: FILING DATE: 15-AUG-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Seidman, Stephanie L.
: REGISTRATION NUMBER: 33,779
: REFERENCE/DOCKET NUMBER: 6362-51506
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619)238-0999
: TELEFAX: (619)238-0062
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1754 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-311-363-13

```

```

Query Match 7.9%; Score 68.5; DB 2; Length 1754;
Best Local Similarity 22.0%; Pred. No. 52;
Matches 33; Conservative 13; Mismatches 45; Indels 59; Gaps 6;

QY 30 PTAATPSEPRPGCGGVCPEPRGEPSSG--PVRELKQFLGWLKKAHYCSNLSFRLYDQ 87
Db 816 PLVELGHDGARGPVGKARPEAAEAPGVDPDRHR----- 854
QY 88 WRAWMOKSHKTRNOVGKLG-----ACVGGKGAEEERDQEQ-----PQHRTL 131
Db 854 -----HRDKDTPAAGDDRAAPKAESGEPGAREPRPADSHSKAAGPPEATS 905
QY 132 LSKHR-----TRGSCPRADGVRRREVNGS 154
Db 906 AAFAQAPPAAGTGAAPR---RRRPSGS 931

```

Search completed: September 16, 1999, 20:41:08
Job time: 5437 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:42:07 ; Search time 49.27 Seconds

(without alignments)
126.043 Million cell updates/sec

Title: US-09-037-657-17
Perfect score: 864

Sequence: 1 GTVFVGVRCNPFQIGYSKK.....RTRGSCPRADGVREVRSRG 155

Scoring table: BLOSUM62

Searched: 122810 seqs, 40065486 residues

Database: 1: PIR60:*
2: PIR1:*
3: PIR2:*
4: PIR3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	94	10.9	416	2	S27198	homeotic protein H
2	92.5	10.7	533	2	A49364	59 protein, brain
3	84	9.7	577	2	A40220	cleavage stimulat
4	83	9.6	485	2	A40751	finger protein MZF
5	82.5	9.5	488	2	A25156	cellulase (EC 3.2.
6	80.5	9.3	816	2	S64439	hypothetical prote
7	78	9.0	1388	2	S74245	serine/threonine-s
8	78	9.0	2339	2	A42566	omega-conotoxin-se
9	78	9.0	1309	2	T00078	probable RNA-direc
10	78	9.0	593	2	B71323	conserved hypotet
11	77.5	9.0	174	1	BOICIT	Baldini ring-1 ch
12	77.5	8.9	554	2	A56730	card protein - Pod
13	76.5	8.9	1325	2	S16129	dynein-associated
14	76	8.8	691	2	A25704	synapsin I - rat
15	75	8.7	336	2	JC4102	hypothetical 36.9K
16	74.5	8.6	990	2	T02309	probable chromatin
17	74	8.6	303	2	S28147	UI snRNP 70K prote
18	74	8.6	756	2	T00367	immunodominant mic
19	73.5	8.5	712	2	A45638	U136 protein - hum
20	73	8.4	3164	1	KMBEH6	shufflon B' - Esch
21	72.5	8.4	444	2	D26421	myocerosic acid s
22	72.5	8.4	2111	2	A70668	endo-beta-1,4-glic
23	72.5	8.4	2110	2	JC4110	prolactin receptor
24	72.5	8.4	725	2	BC1300	homeotic protein H
25	72.5	8.4	630	2	A15086	collagen alpha cna
26	72.5	8.4	431	1	WJH26	hypothetical prote
27	72	8.3	433	2	S20963	DNA (cytosine-5)-
28	72	8.3	1027	2	S28774	BHFI protein - hu
29	72	8.3	437	2	S04020	ciliary neurotroph
30	71.5	8.3	1537	2	JC4172	homeotic protein H
31	71.5	8.3	660	1	OCHE3	collagen alpha cna
32	71.5	8.3	372	2	S18141	hypothetical prote
33	71.5	8.3	417	2	S47539	DNA (cytosine-5)-
34	71.5	8.3	411	2	S31664	BHFI protein - hu
35	71	8.2	1106	2	J00405	ciliary neurotroph
36	71	8.2	1872	2	S36152	homeotic protein H
37	71	8.2	1870	2	S37671	hypothetical 119.5
38	70.5	8.2	411	2	PC2061	bat2 protein - hum
39	70.5	8.2	1522	2	T00028	genome polypeptid

40 70.5 8.2 984 2 T00326
41 70.5 8.2 705 2 A35363
42 70.5 8.2 668 2 B35363
43 70.5 8.2 581 2 I45971
44 70.5 8.2 706 2 E30411
45 70.5 8.2 670 2 F30411

ALIGNMENTS

RESULT 1
S27198
homeotic protein Hox D3 - human
N/Alternate names: homeotic protein Hox 4A
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Sep-1997
C/Accession: S27198
R/Taniguchi, Y.; Fujii, A.; Morlucht, T.
Blochim. Biophys. Acta 1132, 332-334, 1992
A/Title: Cloning and sequencing of the human homeobox gene HOXA4.
A/Reference number: S27198; MUID:93041940
A/Accession: S27198
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-416 <TAN>
A/Cross-References: EMBL:D11117; NID:g219879; PID:d1002368; PID:g219880
C/Genetics: 1
A/Introns: 165/1
C/Superfamily: homeotic protein Hox B3; homeobox homology
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
F1179-235/Domain: homeobox homology <HOX>

Query Match 10.9%; Score 94; DB 2; Length 416;
Best Local Similarity 25.8%; Pred. No. 0.11;
Matches 31; Conservative 16; Mismatches 43; Indels 30; Gaps 4;

QY 17 GSKKAGIEMSHPTASTPSEEP-----GPGGV--CEPRGEPSSGPRRELKQFLGM 70
DB 88 GSGPELNEQGPQPPPPPTLPSCSPINPGGVPAKPKGPPAASSSATISQIFPM 147
QY 71 LKHAICSLTSLRFLIDQWRAWAKSHKTRNOYGLGKAGCVGKAEEERDPGQPHRT 130
DB 148 MKE-----SRNSKQNSCATAGESC-----EDKSPPAKGRVPT 183

QY Hoxb-Luv

RESULT 2
A49364
59 protein, brain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 18-Sep-1998
C/Accession: A49364
R/Shaw, D.J.; McCurrach, M.; Rundie, S.A.; Harley, H.G.; Crow, S.R.; Sohn, R.; Thirio
Genomics 18, 673-679, 1993
A/Title: Genomic organization and transcriptional units at the myotonic dystrophy loc
A/Reference number: A49364; MUID:94140369
A/Accession: A49364
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-553 <SHA>
A/Cross-References: GB:L19267; NID:g306711; PID:g306712

Query Match 10.7%; Score 92.5; DB 2; Length 553;
Best Local Similarity 25.8%; Pred. No. 0.21;
Matches 34; Conservative 17; Mismatches 48; Indels 33; Gaps 6;

QY 30 PTAATPSRSPRPGP-----GGVCEPRGEPSSGP-VARE-----LKQFLGWLK 73
DB 349 PPAASSSGGEPGPPLRLSRSLNSLPHPAGGKAGAGPVAALGCTFTSGRF----- 403
QY 74 HAYGSLTSLRFLIDQWRAWAKSHKTRNOYGLGKAGCVGKAEEERDPGQPHRTLLS 133

Db 403 -----ATLTIQERDRGAKEKHXSHISNIRSGSGSGSGGEPSPV---RSRLD 453
 Oy 134 KHRTRGS--CPR 143
 Db 454 PAKVLGTALCPR 465

RESULT 3

AA0220
 cleavage stimulation factor 64k chain - human
 N:Alternate names: 64k polyadenylation factor
 C:Species: Homo sapiens (man)
 C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 24-Sep-1998
 C:Accession: AA0220
 R:Takagaki, Y.; MacDonald, C.C.; Shenk, T.; Manley, J.L.
 Proc. Natl. Acad. Sci. U.S.A. 89, 1403-1407, 1992
 A:Title: The human 64-kDa polyadenylation factor contains a ribonucleoprotein-type RNA
 A:Reference number: AA0220; MUID:92159058
 A:Accession: AA0220
 A:Molecule type: mRNA
 A:Residues: 1-577 <TAK>
 A:Cross-references: GB:M85085; NID:9181138; PID:9181139
 A:Note: Sequence extracted from NCBI Backbone (NCBIN:82408, NCBI:82414)
 C:Genetics:
 A:Gene: GDB:CF22
 A:Cross-references: GDB:137080; OMIM:600368
 A:Map position: 21q22.3-21q22.3
 C:Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotein
 C:Keywords: heterotrimer; phosphoprotein; RNA binding
 F:17-84/Domain: ribonucleoprotein repeat homology <RBM>
 F:414-464/Region: 5-residue repeats (M-E-A-R-A/G)

Query Match 9.7%; Score 84; DB 2; Length 577;
 Best Local Similarity 27.2%; Pred. No. 1.4;
 Matches 41; Conservative 15; Mismatches 55; Indels 40; Gaps 8;

Oy 18 SKKAGIMSEMSHPTAATSRSPGCGVCEPRGEPSPGVRRELKQFLGMLKKHAYC 77
 Db 249 SMGGVPAAGOMPAVATGCGPSLAPGGM-OAOGMPSGVSNERG----- 297
 Oy 78 SNLSRLYDQWRAMQKSHKTRN---QVGLGEA-----CVGKGKLEER---DPG 122
 Db 297 ----VPMQDP-RAAMQRGSLPANVPRLGLGDAPNDPRGTLTAVTGEVERGTLGPRH 351
 Oy 123 EOPPOHRTLSKHKTRGSCPRADGVAREYRG 153
 Db 352 QGPPMH--VPGHESKGRPP-----HELRG 374

RESULT 4

AA0751
 finger protein MZF1 - human
 C:Species: Homo sapiens (man)
 C>Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 24-Sep-1998
 C:Accession: AA0751
 R:Hromas, R.; Collins, S.J.; Hlckstein, D.; Raskind, W.; Deaven, L.L.; O'Hara, P.; Hager
 J. Biol. Chem. 266, 14183-14187, 1991
 A:Title: A retinoid acid-responsive human zinc finger gene, MZF-1, preferentially expres
 A:Reference number: AA0751; MUID:91317761
 A:Accession: AA0751
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-485 <HRO>
 A:Cross-references: GB:M58297; NID:9189043; PID:9189044
 C:Genetics:
 A:Gene: GDB:ZNF42; MZF-1
 A:Cross-references: GDB:125898; OMIM:194550
 A:Map position: 19q13.2-19q13.4
 C:Keywords: DNA binding; transcription regulation; zinc finger

Query Match 9.6%; Score 83; DB 2; Length 485;
 Best Local Similarity 27.9%; Pred. No. 1.5;
 Matches 43; Conservative 8; Mismatches 63; Indels 40; Gaps 8;

Oy 17 GSKKAGIMSEMSHPTAATSRSPGCGVCEPRGEPSPGVRRELKQFLGMLKKHAYC 75
 Db 76 GVGPALITTRMSRPRGRS---RGRSTGGVY--RGGCDVCGKVFQSRNSNLTNRQKXHT 130
 Oy 76 -----YCSNLSRLYDQWRAMQKSHKTRNVO-----GRIGACVGGKGAEEER- 120
 Db 131 GERPPVCSGCG-----RFSRSRSHLRLHOLHTHERPFVCGDCGGFVSARLEHRR 183
 Oy 120 -DPGEP-----POHRTLSKHKTRSCPP 142
 Db 184 VHTGQPPRCALCCGSGFQSRNSNLTNRQKXHT 217

RESULT 5

A25156
 cellulase (EC 3.2.1.4) 1 - Bacillus sp.
 N:Alternate names: endo-1,4-beta-glucanase
 C:Species: Bacillus sp.
 C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 20-Mar-1998
 C:Accession: A25156
 R:Fukumori, F.; Sashihara, N.; Kudo, T.; Horikoshi, K.
 J. Bacteriol. 168, 479-485, 1986
 A:Title: Nucleotide sequences of two cellulase genes from alkalophilic Bacillus sp.
 A:Reference number: A91825; MUID:87056924
 A:Accession: A25156
 A:Molecule type: DNA
 A:Residues: 1-488 <FRK>
 A:Cross-references: GB:M14781; GB:X53449; NID:9142659; PID:9142660
 A:Experimental source: strain N-4, plasmid pNK1
 C:Function:
 A:Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such a
 A:Pathway: cellulose degradation
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 9.5%; Score 82.5; DB 2; Length 488;
 Best Local Similarity 22.8%; Pred. No. 1.7;
 Matches 34; Conservative 14; Mismatches 50; Indels 51; Gaps 7;

Oy 24 MSEMS-----HPT-----AATPRSEPRGPGCV 47
 Db 283 WANMSLTKDESSAALMPGANPTGWTAAELSPSGAFVREKIRRSASIPSPDPTPPS--- 340
 Oy 48 CEPKGGEPSSGPVREKQFLGMLKKHAYCSNLSRLYDQWR--WMQKSHKTRNOV-- 104
 Db 340 -DPDGPEDPTFP-PSDGEIYFAMDPNOITTEIYHNGQLMOKAWTQNOEPGANQIGPW 397

Oy 104 -KIGACVCGK-----AEEERDPGEOPP 126
 Db 398 EPLGDAPPSPSPDPPEPEPPDPGEPPD 426

RESULT 6

S64439
 hypothetical protein YGR130C - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein G6382
 C:Species: Saccharomyces cerevisiae
 C>Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 14-Nov-1997
 R:Van Dyck, L.; Skala, J.; de Wergifosse, P.; Purnelle, B.; Talia, E.; Nawrocki, A.;
 submitted to the Protein Sequence Database, May 1996
 A:Reference number: S64428
 A:Accession: S64439
 A:Molecule type: DNA
 A:Residues: 1-816 <VAN>
 A:Cross-references: EMBL:Z72915; NID:91323214; PID:e243523; PID:91323215; MFS:YGR13
 A:Experimental source: strain S288C
 C:Genetics:
 A:Map position: 7R

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OW protein - protein search, using sw model

Run on: September 17, 1999, 03:10:12 ; Search time 35.09 Seconds

(without alignments)
124.867 Million cell updates/sec

Title: US-09-037-657-17

Sequence: 1 GVVYFQVQNCNPGITGSKK.....RTGSGPADGVREVRGSG 155

Scoring table: BLOSUM62

Searched: 77977 seqs, 28268293 residues

Database: SwissProt_37.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	10.9	416	1	HXD3_HUMAN
2	92.5	10.7	553	1	DMR9_HUMAN
3	84	9.7	577	1	CST2_HUMAN
4	83	9.6	485	1	ZN42_HUMAN
5	82.5	9.5	488	1	GUN1_BAC54
6	81	9.4	181	1	HAIR_RAT
7	80.5	9.3	816	1	YGA3_YEAST
8	79	9.1	1027	1	CAFE_RIFPA
9	78	9.0	2339	1	CIC5_HUMAN
10	77.5	9.0	174	1	BAR1_CHITE
11	77	8.9	554	1	PEX2_PODAN
12	73	8.4	3164	1	TEGU_HSV11
13	72.5	8.4	725	1	GUNG_CLOCE
14	72.5	8.4	2110	1	MCAS_MYCBO
15	72.5	8.4	630	1	PRLR_ORENI
16	72.5	8.4	444	1	SHU4_ECOLI
17	72	8.3	431	1	HXB3_HUMAN
18	72	8.3	437	1	NBR3_STRCY
19	71.5	8.3	372	1	CNTR_RAT
20	71.5	8.3	417	1	HXD3_MOUSE
21	71.5	8.3	581	1	PRLR_CEREL
22	71.5	8.3	660	1	YHL1_EBV
23	71	8.2	461	1	NNP1_HUMAN
24	70.5	8.2	1043	1	CSH2_PARRR
25	70.5	8.2	2547	1	FAFX_HUMAN
26	70.5	8.2	2547	1	FAFX_HUMAN
27	70.5	8.2	581	1	FAFX_MOUSE
28	70.5	8.2	706	1	PRLR_BOVIN
29	70.5	8.2	705	1	SYN1_BOVIN
30	70.5	8.2	238	1	SYN1_HUMAN
31	70	8.1	2142	1	YW15_MYCTU
32	70	8.1	1919	1	BAV2_HUMAN
33	70	8.1	431	1	KARI_RAT
34	69.5	8.0	372	1	UL61_HCMVA
35	69.5	8.0	2555	1	CNTR_HUMAN
36	69.5	8.0	199	1	FAFY_HUMAN
37	69.5	8.0	708	1	SRP_MOUSE
38	69.5	8.0	514	1	VE2_HPV05
39	69	8.0	860	1	AREA_PENRO
40	69	8.0	1182	1	HAIR_MOUSE
41	69	8.0	252	1	ICP3_HSV1D
42	69	8.0	1227	1	LAF4_HUMAN
43	69	8.0	128	1	YPRR_ECOLI

ALIGNMENTS

44 68.5 7.9 436 1 GDF6_BOVIN P55106 bos taurus
45 68.5 7.9 865 1 NRFA_PENRO Q92269 penicillium

RESULT 1

HXD3_HUMAN STANDARD; PRT; 416 AA.

AC P31249;
DT 01-JUL-1993 (REL. 26, CREATED)
DE 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DE 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE HOMEBOX PROTEIN HOX-D3 (HOX-4A).
GN HOXD3 OR HOX4A.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93041940.
RA TANIGUCHI Y., FUJII A., MORIUCHI T.;
RT Cloning and sequencing of the human homebox gene HOX4A.;
RL BIOCHIM. BIOPHYS. ACTA 1132:332-334(1992).
RN [2]
RP SEQUENCE OF 178-243 FROM N.A.
RX MEDLINE; 90215256.
RA BONCINELLI E., ACAMPORA D., PANNONE M., D'ESPOSITO M., SOMMA R.,
RA GAUDINO G., STORNIATOLO A., CARIERO M., FAIELLA A., SIMONE A.;
RT Organization of human class I homeobox genes.;
RL GENOME 31:745-756(1989).

CC - FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
A SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.

CC - SUBCELLULAR LOCATION: NUCLEAR.
CC - SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEBOX PROTEINS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
or send an email to license@sib-sib.ch).

DR EMBL, D11117; G219880;
DR PIR, S27198; S27198.
DR PIR, S15548; S15548.
DR MIN, 142980;

DR PROSITE, PS00027; HOMEBOX_1; 1.
DR PROSITE, PS00032; ANTENNAPEDIA_1.
DR PROSITE, PS00071; HOMEBOX_2; 1.
DR PFM: PF00046; homebox; 1.
DR HSSP: P02833; 15AN.

KW HOMEBOX; DNA-BINDING; DEVELOPMENTAL PROTEIN; NUCLEAR PROTEIN;
KW TRANSCRIPTION REGULATION.

FT DOMAIN 84 88 POLY-GLY.
FT DOMAIN 100 108 POLY-PRO.
FT DOMAIN 134 137 POLY-SER.
FT DOMAIN 144 149 ANTP-TYPE HEXAPEPTIDE.
FT DNABIND 178 237 HOMEBOX.
FT CONFLICT 241 241 G -> A (IN REF. 2).
SQ SEQUENCE 416 AA; 43927 MW; 6FD1F6B2 CRC32;

Query Match 10.94; Score 94; DB 1; Length 416;
Best Local Similarity 25.84; Pred. No. 0.09;
Matches 31; Conservative 16; Mismatches 43; Indels 30; Gaps 4;

QY 17 GSKRAGIWEWSHPTASTRSERP-----GPGGV--CEPRGEPSSGVPVRELKQFLGW 70
DB 88 GSQPGANSEQPPPPPTLPSCPTNPGGVPKPKRGKGNASSSATISKQIFPW 147

QY 71 LKHAACSLSTFLYDQWAMAKSHKTRNOVGLGEACVGGKAEERDPEQPOHRT 130
 DB 148 MKE-----SRONSKOKNSCATAGESC-----EDKSPPPAKRVRT 183

RESULT 2

DMR9_HUMAN STANDARD: PRT; 553 AA.

AC 009019;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE DMR-N9 PROTEIN (PROTEIN 59) (FRAGMENT).

GN DM9.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.

RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN;
 RX MEDLINE; 94140369.
 RA SHAW D.J., MCCURRACH M., RUNDLE S.A., HARLEY H.G., CROW S.R.,
 RA SOHN R., THIRION J.-P., HAMSHIRE M.G., BUCKLER A.J., HARPER P.S.,
 RA HOUSMAN D.E., BROOK J.D.,
 RT "Genomic organization and transcriptional units at the myotonic
 dystrophy locus".
 RL GENOMICS 18:673-679(1993).

RM [2]
 RP SEQUENCE OF 539-553 FROM N.A.

RA MAHADEVAN M.S., AMENIYA C., JANSEN G., SABOURIN L., BAIRD S.,
 RA NEVILLE C.E., WORMSKAMP N., SEGERS B., BATZER M., LAMERDIN J.,
 RA DE JONG P.J., WIERINGA B., KORNEELUK R.G.;
 RT "Structure and genomic sequence of the myotonic dystrophy (DM kinase)
 gene".

RL HUM. MOL. GENET. 2:299-304(1993).

CC -1- FUNCTION: COULD HAVE A REGULATORY FUNCTION IN MEIOSIS.

CC -1- TISSUE SPECIFICITY: STRONGEST EXPRESSION IN BRAIN, LIVER, AND
 TESTIS. ALSO EXPRESSED IN KIDNEY AND SPLEEN.

CC -1- DISEASE: MAY HAVE A ROLE IN THE DEVELOPMENT OF MENTAL SYMPTOMS IN
 SEVERE CASES OF MYOTONIC DYSTROPHY

CC -1- SIMILARITY: TO S.POMBE SPAC1B10.03 AND TO C.ELEGANS C08B6.7.

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CC EMBL; L19267; G306712;
 CC EMBL; L08835; G181602;
 CC PFM; PF00400; G-beta; 1.
 FT NON_TER 1
 FT SEQUENCE 553 AA; 59236 MM; 722D54A8 CRC32;

Query Match 10.7%; Score 92.5; DB 1; Length 553;

Best Local Similarity 25.8%; Pred. No. 0.17; Mismatches 48; Indels 33; Gaps 6;

Matches 34; Conservative 17; Mismatches 48; Indels 33; Gaps 6;

QY 30 PTAATSPSRPSPG-----GGVCEPRGSPSSGP-VRR-----LKOFGLMK 73

DB 349 PPAASSSGGEPGPRLRLSLRSNSLPHRAGGKAGAPVGALEGTFTSGRF----- 403

QY 74 HAYCNLSFLYDQWAMAKSHKTRNOVGLGEACVGGKAEERDPEQPOHRTLLS 133

DB 403 -----ATLTQERDRDRAKEHKKRYHSLGNISRGSGSGSGGKPGPVP---RSLD 453

QY 134 KHRTRGS--CPR 143

DB 454 PAKVLGALCPR 465

RESULT 3

CST2_HUMAN STANDARD: PRT; 577 AA.

AC P33240;
 DT 01-FEB-1994 (REL. 28, CREATED)
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1
 DE 64 KD SUBUNIT).

GN CSTF2.

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

CC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.

RN [1]
 RP SEQUENCE FROM N.A.

RA TAKAGAKI Y., MACDONALD C.C., SHENK T., MANLEY J.L.;
 RT "The human 64-kDa polyadenylation factor contains a
 ribonucleoprotein type RNA binding domain and unusual auxiliary
 motifs".
 RL PROC. NATL. ACADE. SCI. U.S.A. 89:1403-1407(1992).

CC -1- FUNCTION: ONE OF THE MULTIPLE FACTORS REQUIRED FOR POLYADENYLATION
 AND 3'-END CLEAVAGE OF MAMMALIAN PRE-MRNAs. THIS SUBUNIT IS
 DIRECTLY INVOLVED IN THE BINDING TO PRE-MRNAs. MAY INTERACT WITH
 THE CLEAVAGE-POLYADENYLATION SPECIFICITY FACTOR.

CC -1- SUBUNIT: COMPOSED OF THREE DISTINCT SUBUNITS OF 77, 64, AND 50 KD.

CC -1- PTM: KNOWN TO BE PHOSPHORYLATED.

CC -1- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RNP).

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 or send an email to license@sib-sib.ch).

CC EMBL; M85085; G181139;
 CC DR PIR; A40220; A40220.
 CC DR MIM; 600368;
 CC DR PROSITE; PS00030; RNP_1; FALSE_NEG.

CC DR PFM; PF00076; RTM_1; PHOSPHORYLATION; NUCLEAR PROTEIN.

CC KM RNA-BINDING; REPEAT; PHOSPHORYLATION; NUCLEAR PROTEIN.

CC FT DOMAIN 18 23 RNA-BINDING (RNP2) (BY SIMILARITY).

CC FT DOMAIN 57 64 RNA-BINDING (RNP1) (BY SIMILARITY).

CC FT DOMAIN 198 409 GLY/PRO-RICH.

CC FT DOMAIN 410 469 12 X 5 AA TANDEM REPEATS OF M-E-A-R-[AG].

CC FT REPEAT 410 414 1 (APPROXIMATE).

CC FT REPEAT 415 419 2.

CC FT REPEAT 420 424 3.

CC FT REPEAT 425 429 4 (APPROXIMATE).

CC FT REPEAT 430 434 5 (APPROXIMATE).

CC FT REPEAT 435 439 6.

CC FT REPEAT 440 444 7.

CC FT REPEAT 445 449 8.

CC FT REPEAT 450 454 9.

CC FT REPEAT 455 459 10 (APPROXIMATE).

CC FT REPEAT 460 464 11.

CC FT REPEAT 465 469 12 (APPROXIMATE).

CC FT MOD_RES 83 83 GLY/PRO-RICH.

CC FT MOD_RES 364 364 PHOSPHORYLATION (BY CGPK) (POTENTIAL).

CC FT MOD_RES 498 498 PHOSPHORYLATION (BY CGPK) (POTENTIAL).

CC SEQUENCE 577 AA; 60959 MM; 9868DCD CRC32;

Query Match

Best Local Similarity 9.7%; Score 84; DB 1; Length 577;

Matches 41; Conservative 15; Mismatches 55; Indels 40; Gaps 8;

FT	2N_FING	404	426	C2H2-TYPE.
FT	2N_FING	432	454	C2H2-TYPE.
FT	2N_FING	460	482	C2H2-TYPE.
SQ	SEQUENCE	485 AA;	54463 MW;	908B33F1 CRC32;
Query Match				
Best Local Similarity		9.6%;	Score 83;	DB 1;
Matches 43;		Conservative	27.9%;	Pred. No. 1.1;
		8;	Mismatches	63;
			Indels	40;
			Gaps	8
OY	17	GSKKAGIMSEWHFPAASTPRERERPGGCGVCEPGE	-PSSGPVPRREIKOTLGWIKKA	75
Db	76	GVGPAALITTRMRSPGRS	--KGRPSTGGGV--RGGRCDCGKVFOSQSNLIRHQIKIT	130
OY	76	-----YCSNLSFRLYDQWRAMQKSHKTRNRY	-----GKIGEACVCGKGAEEER	120
Db	131	GERPVCSECG	-----RSFSRSSHLIRHOLHTHEMRPVCDCGQGVRRARLEENHR	183
OY	120	-DPGEOP	-----POHRTLSKHRTGSCP	142
Db	184	VHTGQPPRCACGCGSFQORSNLIHQRIHGGPP	217	

OY 48 CEPGESESSGPVRELKOFGLMKHAYCSNLSRLYDQWRA--WMOKSHTRNOVG-- 104
 DB 340 -DPDGEEDPTP-PSPDEYFAMDPNQIYNEIYVHNGOLWQAKWMTNOBEGANQYCPW 397
 OY 104 -KLGACVGGK-----AEENDPGEOP 126
 DB 398 EPLGADPSEPSDPPPEPEPDGEPDP 426

RESULT 6

HAIR-RAT
 ID HAIR-RAT STANDARD; PRT; 1181 AA.
 AC P97609;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE HAIRLESS PROTEIN.

CS RATVUS NORVEGICUS (RAT).
 CC EURAROTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATVUS.
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-SPRAGUE-DAWLEY;
 RX MEDLINE; 97141510.

RA THOMPSON C.C.;
 RT "thyroid hormone-responsive genes in developing cerebellum include a novel synaptotagmin and a hairless homolog.";
 RL J. NEUROSCI. 16:7832-7840(1996).

CC -1- FUNCTION: MAY ACT AS A TRANSCRIPTION FACTOR.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.

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CC
 DR EMBL; U71293; G172656; ALT_INIT
 KW ZINC-FINGER; DNA-BINDING; NUCLEAR PROTEIN; TRANSCRIPTION REGULATION;
 FT ZN-FING 594 C6-TYPE.
 FT SEQUENCE 1181 AA; 127307 MW; E4011E24 CRC32;

Query Match 9.48; Score 81; DB 1; Length 1181;
 Best Local Similarity 23.48; Pred. No. 4.4;
 Matches 39; Conservative 15; Mismatches 35; Indels 78; Gaps 10;

OY 27 WSHPTAAS-----TPRSEPG-----PGGVC-----PRGSESSGPVRELKOFGLW 70
 DB 294 WAGSGSNFGLQGPVTPKPPSPPPPGCCSHLPABGDP--GPCRK----- 344
 OY 71 LKHAYCSNLSRLYDQWRAWMOKSHKTRNOVGKLGACVGGKAEERDGEQ--PROH 128
 DB 344 -----C-----QDSEPGSSSGGSESEENKAGSASPSH 374
 OY 129 -----RTLSKHTRTGSCP-----RADGVR-----EVRGS 154
 DB 375 HTKLKTKWLTTRHSEOFECPCGCGKSPATGLRLKRAKSGPEVOGA 421

RESULT 7

YGA3-YEAST STANDARD; PRT; 816 AA.
 AC P53278;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE HYPOTHELICAL 92.7 KD PROTEIN IN ASN2-PHBI INTERGENIC REGION.

GN YGR130C.
 OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 CC EURAROTA; FUNGI; ASCOMYCOTA; HEMIASCOCYCETES; SACCCHAROMYCETALES;
 CC SACCCHAROMYCETACEAE; SACCCHAROMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.

RA VAN DYCK L., SKALA J., DE WERGIOSSE P., PURNELLE B., TALLA E.,
 RA NAMROCKI A., DEL BINO S., GOFFEAU A.;
 RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.

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CC
 DR EMBL; Z72915; E243523;
 DR HSSP; P56255; IPJR.
 KW HYPOTHELICAL PROTEIN.
 FT DOMAIN 164 185 POLY-SR.
 FT DOMAIN 205 218 POLY-THR.
 FT SEQUENCE 816 AA; 92698 MW; 05E85671 CRC32;

Query Match 9.38; Score 80.5; DB 1; Length 816;
 Best Local Similarity 22.78; Pred. No. 3.4;
 Matches 20; Conservative 17; Mismatches 32; Indels 19; Gaps 2;

OY 19 KKAGIWEWSHPTAASPRSEPGGVCPEPRGSESSGPVRELKOFGLMKHAYCS 78
 DB 371 ERTGIFLMSPTSSSTSGKSTAPSNVATP-----ENELIYKTEHGILS 418
 OY 79 -----NLSRLYDQWRAWMOKSHKTR 99
 DB 419 KAVYDKINTDEKIHAWLADLAREKDK 446

RESULT 8

CAEP_RIFPA STANDARD; PRT; 1027 AA.
 AC P30754;
 DT 01-JUL-1993 (REL. 26, CREATED)
 DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE FIBRIL-FORMING COLLAGEN ALPHA CHAIN.
 OS EUKARYOTA; METAZOA; VESTIMENTIFERA; AXONOBANCHIA; RIFTIDA;
 CC RIFTIDAE; RIFTIA.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 93130909.
 RA MANN K., GALL F., TIMPL R.;
 RT "Amino-acid sequence and cell-adhesion activity of a fibril-forming collagen from the tube worm Riftia pachyptila living at deep sea hydrothermal vents.";
 RL EDR. J. BIOCHEM. 210:839-847(1992).
 RN [2]
 RP SEQUENCE OF 8-45; 525-618 AND 810-882.
 RC TISSUE-CUTICLE;
 RX MEDLINE; 92015209.
 RA GALL F., WIEDMANN H., MANN K., KUHN K., TIMPL R., ENGEL J.;
 RT "Molecular characterization of cuticle and interstitial collagens from worms collected at deep sea hydrothermal vents.";
 RL J. MOL. BIOL. 221:209-223(1991).
 CC -1- FUNCTION: FIBRIL-FORMING COLLAGEN.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- PTM: ALL THE "X" ARE PROBABLY GLYCOSYLATED HYDROXYLYSINES.
 DR PIR; S22915; S22915.
 KW EXTRACELLULAR MATRIX; CONNECTIVE TISSUE; REPEAT; HYDROXYLATION; GLYCOPROTEIN; COLLAGEN.
 FT DOMAIN 1 12 NONHELICAL REGION (N-TERMINAL).

FT	DOMAIN	13	1023	TRIPLE-HELICAL REGION
FT	MOD_RES	1024	1027	NONHELICAL REGION (C-TERMINAL)
FT	MOD_RES	21	21	HYDROXYLATION (PARTIAL).
FT	MOD_RES	24	24	HYDROXYLATION (PARTIAL).
FT	MOD_RES	27	27	HYDROXYLATION (PARTIAL).
FT	MOD_RES	39	39	HYDROXYLATION.
FT	MOD_RES	53	53	HYDROXYLATION (PARTIAL).
FT	MOD_RES	54	54	HYDROXYLATION.
FT	MOD_RES	72	72	HYDROXYLATION (PARTIAL).
FT	MOD_RES	90	90	HYDROXYLATION.
FT	MOD_RES	93	93	HYDROXYLATION.
FT	MOD_RES	123	123	HYDROXYLATION (PARTIAL).
FT	MOD_RES	128	128	HYDROXYLATION (PARTIAL).
FT	MOD_RES	150	150	HYDROXYLATION.
FT	MOD_RES	161	161	HYDROXYLATION.
FT	MOD_RES	162	162	HYDROXYLATION (PARTIAL).
FT	MOD_RES	164	164	HYDROXYLATION.
FT	MOD_RES	165	165	HYDROXYLATION.
FT	MOD_RES	174	174	HYDROXYLATION (PARTIAL).
FT	MOD_RES	177	177	HYDROXYLATION.
FT	MOD_RES	180	180	HYDROXYLATION.
FT	MOD_RES	183	183	HYDROXYLATION.
FT	MOD_RES	207	207	HYDROXYLATION.
FT	MOD_RES	216	216	HYDROXYLATION.
FT	MOD_RES	219	219	HYDROXYLATION.
FT	MOD_RES	228	228	HYDROXYLATION.
FT	MOD_RES	237	237	HYDROXYLATION.
FT	MOD_RES	243	243	HYDROXYLATION (PARTIAL).
FT	MOD_RES	291	291	HYDROXYLATION (PARTIAL).
FT	MOD_RES	303	303	HYDROXYLATION (PARTIAL).
FT	MOD_RES	306	306	HYDROXYLATION (PARTIAL).
FT	MOD_RES	312	312	HYDROXYLATION.
FT	MOD_RES	321	321	HYDROXYLATION.
FT	MOD_RES	327	327	HYDROXYLATION.
FT	MOD_RES	339	339	HYDROXYLATION.
FT	MOD_RES	342	342	HYDROXYLATION.
FT	MOD_RES	348	348	HYDROXYLATION (PARTIAL).
FT	MOD_RES	351	351	HYDROXYLATION (PARTIAL).
FT	MOD_RES	366	366	HYDROXYLATION.
FT	MOD_RES	372	372	HYDROXYLATION.
FT	MOD_RES	375	375	HYDROXYLATION.
FT	MOD_RES	381	381	HYDROXYLATION.
FT	MOD_RES	387	387	HYDROXYLATION (PARTIAL).
FT	MOD_RES	416	416	HYDROXYLATION (PARTIAL).
FT	MOD_RES	417	417	HYDROXYLATION.
FT	MOD_RES	423	423	HYDROXYLATION.
FT	MOD_RES	429	429	HYDROXYLATION.
FT	MOD_RES	432	432	HYDROXYLATION.
FT	MOD_RES	453	453	HYDROXYLATION.
FT	MOD_RES	465	465	HYDROXYLATION.
FT	MOD_RES	483	483	HYDROXYLATION.
FT	MOD_RES	500	500	HYDROXYLATION (PARTIAL).
FT	MOD_RES	503	503	HYDROXYLATION (PARTIAL).
FT	MOD_RES	506	506	HYDROXYLATION (PARTIAL).
FT	MOD_RES	513	513	HYDROXYLATION.
FT	MOD_RES	525	525	HYDROXYLATION.
FT	MOD_RES	533	533	HYDROXYLATION (PARTIAL).
FT	MOD_RES	536	536	HYDROXYLATION (PARTIAL).
FT	MOD_RES	540	540	HYDROXYLATION.
FT	MOD_RES	546	546	HYDROXYLATION.
FT	MOD_RES	551	551	HYDROXYLATION (PARTIAL).
FT	MOD_RES	552	552	HYDROXYLATION.
FT	MOD_RES	561	561	HYDROXYLATION.
FT	MOD_RES	603	603	HYDROXYLATION.
FT	MOD_RES	610	610	IMPERFECTION IN THE GAA REPEAT.
FT	MOD_RES	621	621	HYDROXYLATION (PARTIAL).
FT	MOD_RES	627	627	HYDROXYLATION.
FT	MOD_RES	645	645	HYDROXYLATION (PARTIAL).

FT	MOD_RES	647	647	HYDROXYLATION (PARTIAL).
FT	MOD_RES	648	648	HYDROXYLATION.
FT	MOD_RES	663	663	HYDROXYLATION.
FT	MOD_RES	708	708	HYDROXYLATION.
FT	MOD_RES	711	711	HYDROXYLATION.
FT	MOD_RES	714	714	HYDROXYLATION.
FT	MOD_RES	717	717	HYDROXYLATION.
FT	MOD_RES	723	723	HYDROXYLATION.
FT	MOD_RES	744	744	HYDROXYLATION.
FT	MOD_RES	759	759	HYDROXYLATION.
FT	MOD_RES	773	773	HYDROXYLATION.
FT	MOD_RES	774	774	HYDROXYLATION.
FT	MOD_RES	783	783	HYDROXYLATION.
FT	MOD_RES	792	792	HYDROXYLATION.
FT	MOD_RES	815	815	HYDROXYLATION.
FT	MOD_RES	816	816	HYDROXYLATION (PARTIAL).
FT	MOD_RES	843	843	HYDROXYLATION.
FT	MOD_RES	849	849	HYDROXYLATION.
FT	MOD_RES	855	855	HYDROXYLATION.
FT	MOD_RES	861	861	HYDROXYLATION.
FT	MOD_RES	867	867	HYDROXYLATION.
FT	MOD_RES	888	888	HYDROXYLATION.
FT	MOD_RES	894	894	HYDROXYLATION.
FT	MOD_RES	903	903	HYDROXYLATION.
FT	MOD_RES	903	903	HYDROXYLATION.
FT	MOD_RES	915	915	HYDROXYLATION.
FT	MOD_RES	933	933	HYDROXYLATION (PARTIAL).
FT	MOD_RES	939	939	HYDROXYLATION.
FT	MOD_RES	945	945	HYDROXYLATION.
FT	MOD_RES	954	954	HYDROXYLATION.
FT	MOD_RES	963	963	HYDROXYLATION (PARTIAL).
FT	MOD_RES	966	966	HYDROXYLATION.
FT	MOD_RES	984	984	HYDROXYLATION.
FT	MOD_RES	990	990	HYDROXYLATION.
FT	MOD_RES	1010	1010	HYDROXYLATION (PARTIAL).
FT	MOD_RES	1011	1011	HYDROXYLATION.
FT	MOD_RES	1013	1013	HYDROXYLATION (PARTIAL).
FT	MOD_RES	1014	1014	HYDROXYLATION.
FT	MOD_RES	1016	1016	HYDROXYLATION (PARTIAL).
FT	MOD_RES	1017	1017	HYDROXYLATION.
FT	MOD_RES	1019	1019	HYDROXYLATION (PARTIAL).
FT	MOD_RES	1020	1020	HYDROXYLATION.
SO	SEQUENCE	1027	AA: 96353 MW: 9F940A4 CRC32;	

Query Match	9.18;	Score 79;	DB 1;	Length 1027
Best local similarity	37.58;	pred	no	5.0.

Matches	39;	Conservative	5;	Mismatches	50;	Indels	48;	Gaps	5;
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[illegible]

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RESULT 9
CIC5_HUMAN
ID CIC5_HUMAN STANDARD; PRT: 2339 AA.
AC 000975;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (OMEGA-CONOTOXIN-SENSITIVE N-
DE TYPE, BRAIN CALCIUM CHANNEL ALPHA-1 SUBUNIT).
GN CACNL1A5
OS HOMO SAPIENS (HUMAN).

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DR EMBL; K00447; G156531; -
DR EMBL; J01055; G552075; -
DR PIR; A03339; BQICIT.
REPEAT.
NON_TER
FT DOMAIN 1 1
FT REPEAT 42 85 4 X 11 AA TANDEM REPEATS.
FT REPEAT 42 52 1-1.
FT REPEAT 53 63 1-2.
FT REPEAT 64 74 1-3.
FT REPEAT 75 85 1-4.
FT DOMAIN 124 167 4 X 11 AA TANDEM REPEATS.
FT REPEAT 124 134 2-1.
FT REPEAT 135 145 2-2.
FT REPEAT 146 156 2-3.
FT REPEAT 157 167 2-4.
FT VARIANT 40 40 N -> K (IN CLONE PCT21).
FT VARIANT 57 57 G -> E (IN CLONE PCT21).
FT VARIANT 72 72 K -> R (IN CLONE PCT21).
FT VARIANT 86 86 R -> G (IN CLONE PCT21).
NON_TER 174 174
SEQUENCE 174 AA; 18920 MW; E9720893 CRC32;

Query Match 9.0%; Score 77.5; DB 1; Length 174;
Best Local Similarity 23.9%; Pred. No. 1.3; Matches 37; Conservative 20; Mismatches 61; Indels 37; Gaps 6;

21 AGTWSMHTAATPRSERPPGCGVCEPRGSGPYRRELKQFLGMLKHAACSNL 80
34 AGPFSHNSPEKSKSRPEKSKGS--KPRPEKSGSKPKPEKSKPRERKSGA 90
81 SFLYDQWRAWMOK--SHKTRNOVGKIGEA-----CVGGAEEERPGSOP-PQHTLL 132
91 -----MKRAEKECARNGRNMASKRCTSGAKSPKSEPSKSKPRPEKSKPE 139
133 SKHR-----TRGSCPRADGVREVR 152
140 SKRPEKPSKSGKPRPEKSKSGKPRPEGCGSAMR 174

RESULT 11
EX2_PODAN
D PEX2_PODAN STANDARD; PRT; 554 AA.
C P51021.
T 01-OCT-1996 (REL. 34, CREATED)
T 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
T 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
T PEROXISOME ASSEMBLY PROTEIN CARL (PEROXIN-2).
T PEX2 OR CARL
T PODOSPORA ANSERINA.
T EURAKIOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PYRENOMYCETES;
T SORDARIALES; SORDARIACEAE; PODOSPORA.
T [1]
T SEQUENCE FROM N.A.
T STRAIN-S:
T MEDLINE; 95323960.
T BERTEAUX-DECELLIER V., PICARD M., THOMSON-COFFE C., ZICKLER D.,
T PAVIER-ABOUE A., SIMONET J.-M.;
T "A nonmammalian homolog of the Pex1 gene (Zellweger syndrome)
T discovered as a gene involved in caryogamy in the fungus Podospora
T anserina";
T CELL 81:1043-1051(1995).
T -1- FUNCTION: INVOLVED IN CARYOGAMY (NUCLEAR FUSION), A PROCESS
T REQUIRED FOR SEXUAL SPOROGATION.
T -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PEROXISOMAL.
T -1- SIMILARITY: CONTAINS A CHHC4-CLASS ZINC FINGER.
T
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DR EMBL; X87329; E246075; -
DR PROSITE; PS00518; ZINC_FINGER_C3HC4; FALSE_NEG.
KM TRANSMEMBRANE; PEROXISOME; ZINC-FINGER.
FT TRANSMEM 256 271
FT TRANSMEM 307 325 POTENTIAL.
FT ZN_FING 366 435
FT DOMAIN 466 554 C3HC4-TYPE (ATYPICAL).
FT DOMAIN 21 25 ASP/GLU-RICH (HIGHLY ACIDIC).
FT DOMAIN 145 150 POLY-ALA.
FT DOMAIN 501 508 POLY-GLY.
FT DOMAIN 541 546 POLY-GLU.
SEQUENCE 554 AA; 61533 MW; 7F9A6748 CRC32;

Query Match 8.9%; Score 77; DB 1; Length 554;
Best Local Similarity 21.4%; Pred. No. 4.8; Matches 33; Conservative 20; Mismatches 45; Indels 56; Gaps 7;

14 GYGSKKAG--TWSESHPTAATPRSERPPG-----
210 GLTGLMTVGGRYMSKKNENLRDODGDEPSPVORLSMTDRSLTHAASFAFLVF 269
45 -----GGVCEPPGEGSSGPVRE-----LQFLGMLKHAACSNL-----Y 85
270 LQGRVYTLDRVLRRLAPPTIS-QVSKREVSFEYLNQOLW--HAFTEFLVLPVGI 325
86 DQWPAWMOKSHKTRNOVGKIGEAQVCGAKAEER 119
326 NWRWRLAATWRTKTKI-----NSTGTGGAEEKK 355

RESULT 12
TECU_HSV11
ID TECU_HSV11 STANDARD; PRT; 3164 AA.
AC P10220;
DT 01-MAR-1989 (REL. 10, CREATED)
DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE LARGE TEGUMENT PROTEIN (VIRION PROTEIN UL36).
GN UL36.
OS HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
OC VIRUSES; DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE;
OC ALPHAHERPESVIRINAE; SIMPLEXVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88274327.
RA MCGEOCH D.J., DALRYMPLE M.A., DAVISON A.J., DOLAN A., FRAME M.C.,
RT MCNAB D., PERRY L.J., SCOTT J.E., TAYLOR P.;
RT "The complete DNA sequence of the long unique region in the genome of
RT herpes simplex virus type 1";
RT J. GEN. VIROL. 69:1531-1574(1988).
CC -1- FUNCTION: TEGUMENT PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
CC HSV-1 24, EBV BFLF1, HSV-1 64, VZV 22, AND HCMV UL48.
CC
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).

DR EMBL; X14112; G59536; -
DR EMBL; X14112; E312351; -
DR PIR; I30085; WMBEH6.

KW REPEAT 2911 2980 35 x 2 AA TANDEN REPEATS OF P-Q.
 SQ SEQUENCE 3164 AA; 335857 MW; 6B3C2958 CRC32;

Query Match 8.4%; Score 73; DB 1; Length 3164;
 Best Local Similarity 23.5%; Pred No. 70;
 Matches 27; Conservative 10; Mismatches 42; Indels 36; Gaps 3;

OY 50 PRGGEPSGPRRELKQFLGWLKHAACNSLFRDYDQWRAVQK-----SHKTR 99
 DB 242 PGGPEPAA-----PADLTAALHLTGASETYLDQDAFSERRVATHTPLR 285
 OY 100 NQVGRKGACVCGKGAEEERDPECPPOHTLSKRTGSCPRADGVRRVRS 154
 DB 286 GELAGGEPCVGVGPREGVGPGPP-----TAASPPPTARRDRAS 330

RESULT 13
 GUNG_CLOCE STANDARD; PRT; 725 AA.

AC P37700;
 DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
 DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
 DE 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE ENDOGLUCANASE G PRECURSOR (EC 3.2.1.4) (ENDO-1,4-BETA-GLUCANASE G)
 GN (CELLULOSE G) (EGCG).
 OS CLOSTRIDIUM CELLULOLYTICUM.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; CLOSTRIDIACEAE;
 RN CLOSTRIDIUM.
 RP [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN-ATCC 35319;
 RX MEDLINE; 93012971.
 RA BAGNARA-TARDIF C., GAUDIN C., BELAICH A., HOEST P., CITARD T.,
 RA BELAICH J.-P.;
 RT "Sequence analysis of a gene cluster encoding cellulases from
 RT Clostridium cellulolyticum.";
 RL GENE 119:17-28(1992).

-1- FUNCTION: THE BIOLOGICAL CONVERSION OF CELLULOSE TO GLUCOSE
 GENERALLY REQUIRES THREE TYPES OF HYDROLYTIC ENZYMES:
 (1) ENDOGLUCANASES WHICH CUT INTERNAL BETA-1,4-GLUCOSIDIC BONDS;
 (2) EXOCELLULOHYDROLASES THAT CUT THE DISACCHARIDE CELLULOSE
 FROM THE NONREDUCING END OF THE CELLULOSE POLYMER CHAIN;
 (3) BETA-1,4-GLUCOSIDASES WHICH HYDROLYSE THE CELLULOSE AND OTHER
 SHORT CELLO-OLIGOSACCHARIDES TO GLUCOSE.
 -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-GLUCOSIDIC
 LINKAGES IN CELLULOSE.
 -1- PATHWAY: CELLULOSE DEGRADATION.
 -1- DOMAIN: A 24 RESIDUES DOMAIN IS REPEATED TWICE IN THIS ENZYME AS
 WELL AS IN OTHER C.THERMOCELLULUM CELLULOSE ENZYMES. THIS DOMAIN
 MAY FUNCTION AS THE BINDING LIGAND FOR THE SL COMPONENT.
 -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY E (FAMILY 9 OF GLYCOSYL
 HYDROLASES).

-1- SIMILARITY: CONTAINS 1 CELLULOSE-BINDING DOMAIN (CBD).
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CC EMBL; M87018; G531774;
 CC PIR; J01300; J01300;
 CC PROSITE; PS00018; EF_HAND; UNKNOWN 1;
 CC PROSITE; PS00448; CLOS_CELLULOSOME_PRT; 1;
 CC PROSITE; PS00592; GLYCOSYL_HYDROL_F9_1; 1;
 CC PROSITE; PS00698; GLYCOSYL_HYDROL_F9_2; 1;
 CC PFM; PF00371; GLYCOSYL_hydrol_1;
 CC PFM; PF00404; celcc_2;

PFAM; PF00759; glycosyl_hydrl2; 1.

DR HSSP; P26221; 3TR4.
 KW CELLULOSE DEGRADATION; HYDROLASE; GLYCOSIDASE; REPEAT; SIGNAL.

FT SIGNAL 1 35
 FT CHAIN 36 725
 FT DOMAIN 485 662
 FT ACT_SITE 408 408
 FT ACT_SITE 446 446
 FT ACT_SITE 455 455
 FT ACT_SITE 664 719
 FT DOMAIN 664 719
 FT REPEAT 664 687
 FT REPEAT 719 719
 SQ SEQUENCE 725 AA; 79686 MW; 61CEFC9E CRC32;

Query Match 8.4%; Score 72.5; DB 1; Length 725;
 Best Local Similarity 24.8%; Pred No. 17;
 Matches 39; Conservative 12; Mismatches 55; Indels 51; Gaps 11;

OY 4 YFVQVRCNPF-GIY-----GSKKAGINSEWSHPTASTPSEPRG-----PGGYCE 49
 DB 138 YF--IKNPTEGVYVYVGGDGKDSWVG-----PAEVMQERSEFYVDASKPSAYCA 189
 OY 50 PRGGE-----PSSGVRRNE-----LKQFLGWLKHAACNSLFRDYD 86
 DB 190 STASIASAAVVFKESSDPTVAEKCSHAKNLFDMADKAKSDGATYAAAGYSSSF--YD 247
 OY 87 --QWRA--WQKSHKTRNVOYKLGACVCGKGAEEERD 120
 DB 248 DISMAVWLYLATINDSTYLDR-AESYVPMWKEQOTD 283

RESULT 14
 MCAS_MYCBO STANDARD; PRT; 2110 AA.

AC Q02231;
 DT 01-JUN-1994 (REL. 29, CREATED)
 DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE MYCOCEROSIC ACID SYNTHASE.
 GN MAS.
 OS MYCOBACTERIUM BOVIS.
 OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIACEAE;
 OC ACTINOMYCETALES; CORYNEBACTERIAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
 RN [1]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.

RX MEDLINE; 92406887.
 RA MATHUR M., KOLATTURUDY P.E.;
 RT "Molecular cloning and sequencing of the gene for mycrocercosic acid
 RT synthase, a novel fatty acid elongating multifunctional enzyme, from
 RT Mycobacterium tuberculosis var. bovis Bacillus Calmette-Guérin.";
 RL J. Biol. Chem. 267:19388-19395(1992).

-1- FUNCTION: CATALYZES THE ELONGATION OF N-FATTY ACYL-COA WITH
 METHYLMALONYL-COA (NOT MALONYL-COA) AS THE ELONGATING AGENT TO
 FORM MYCOCEROSYL LIPIDS.
 -1- COFACTOR: CONTAINS ONE COVALENTLY BOUND PHOSPHOPANTHETHEINE
 ARRANGEMENT.
 -1- SUBUNIT: HOMODIMER WHOSE MONOMERS PROBABLY HAVE A HEAD TO TAIL
 4, AND TO VERTIBRATE FATTY ACID SYNTHASES.

-1- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.
 -1- SIMILARITY: PARTIAL TO S.ERYTHRAEA ERYTHRONOLIDE SYNTHASE, MODULE
 4, AND TO VERTIBRATE FATTY ACID SYNTHASES.

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CC EMBL; M95808; G149980;
 CC PIR; B44110; B44110;
 CC PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:40:05 ; Search time 68.96 Seconds

(Without alignments) 138.330 Million cell updates/sec

Title: US-09-037-657-17

Perfect score: 864

Sequence: 1 GVTYFVQVNCNPFQYGSRRK.....RTRGSCPADGVREVRSRG 155

Scoring table: BLOSUM62

Searched: 201082 seqs, 61543640 residues

Database:

- 1: SP_ARCHAEA:*
- 2: SP_BACTERIA:*
- 3: SP_FUNGI:*
- 4: SP_HUMAN:*
- 5: SP_INVERTEBRATE:*
- 6: SP_MAMMAL:*
- 7: SP_MHC:*
- 8: SP_ORGANELLE:*
- 9: SP_PHAGE:*
- 10: SP_PLANT:*
- 11: SP_PROTOZOA:*
- 12: SP_VIRUS:*
- 13: SP_VIRIDIA:*
- 14: SP_UNCLASSIFIED:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	569	65.9	422	4	075462
2	88	10.2	425	6	002661
3	79.5	9.2	294	4	095873
4	79.5	9.2	433	10	064807
5	78	9.0	593	2	083470
6	78	9.0	957	5	019204
7	78	9.0	1309	10	064428
8	78	9.0	1379	11	062868
9	78	9.0	1388	11	P70336
10	77.5	9.0	292	2	0928F5
11	76.5	8.9	790	10	080394
12	76.5	8.9	297	10	0920C7
13	76	8.8	481	6	097641
14	75.5	8.7	561	13	090711
15	75	8.7	336	2	044128
16	74.5	8.6	990	10	080770
17	74.5	8.6	435	10	081009
18	74	8.6	756	4	075154
19	74	8.6	712	11	070204
20	73.5	8.5	731	5	043981
21	73	8.4	264	3	042798
22	73	8.4	316	12	069088
23	72.5	8.4	211	2	093029
24	72.5	8.4	594	4	093404
25	72.5	8.4	346	13	093404
26	72	8.3	437	2	052205
27	72	8.3	312	4	093794
28	72	8.3	312	4	093794
29	72	8.3	431	4	095615

ALIGNMENTS

30	72	8.3	670	11	088935	088935 mus musculus
31	72	8.3	1537	13	092072	092072 gallus galli
32	71.5	8.3	457	4	013518	013518 homo sapien
33	71.5	8.3	1208	4	094761	094761 homo sapien
34	71.5	8.3	140	5	025212	025212 junonia coe
35	71.5	8.3	207	5	076587	076587 caenorhabdit
36	71.5	8.3	697	5	093645	093645 caenorhabdit
37	71.5	8.3	266	12	069118	069118 human herpe
38	71	8.2	629	2	092C17	092C17 streptomyc
39	71	8.2	736	6	018805	018805 cercopithe
40	71	8.2	1804	11	093101	093101 mesocricetu
41	70.5	8.2	448	4	015468	015468 homo sapien
42	70.5	8.2	1522	4	060242	060242 homo sapien
43	70.5	8.2	984	4	060297	060297 homo sapien
44	70.5	8.2	819	4	013443	013443 homo sapien
45	70.5	8.2	411	12	081813	081813 hepatitis C

RESULT 1						
ID 075462	PRELIMINARY	PRT	422 AA.			
AC 075462						
DT 01-NOV-1998 (TREMELREL. 08, Created)						
DT 01-NOV-1998 (TREMELREL. 08, Last sequence update)						
DT 01-MAY-1999 (TREMELREL. 10, Last annotation update)						
DE CYTOKINE-LIKE FACTOR-1 PRECURSOR.						
GN CLF-1.						
OS Homo sapiens (Human).						
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;						
NC Eutheria; Primates; Catarrhini; Hominoidea; Homo.						
NC [1]						
RP ELSON G.C.A., GRABER P., LOSBERGER P., HERRER S., GREYNER D.,						
RA MENOD L.N., WELLS T.N.C., ROSCO-VILBOIS M.H., GAUCHAT J.F.;						
RT "CLF-1, a Novel Soluble Protein Shares Homology with Members of the						
RT Cytokine Type-1 Receptor Family."						
RL J. Immunol. 0:0-0(1998).						
DR EMBL: AF059293; AAC28335.1; ..						
DR PRAM: PF00041; fn3; 2.						
KW Signal.						
FT SIGNAL	1	37	POTENTIAL.			
FT CHAIN	38	422	CYTOKINE-LIKE FACTOR-1.			
SC SEQUENCE	422 AA;	46301 MW;	877F9C9 CRC32;			

Query Match 65.9%; Score 569; DB 4; Length 422;
Best Local Similarity 99.0%; Pred. No. 1.9e-51;
Matches 100; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	GTVHVVQVNCNPFQYGSRRKAGIWSHSPPTAASPPGPGGVCBPPGSGSPGV	60
Db	304	GTVHVVQVNCNPFQYGSRRKAGIWSHSPPTAASPPGPGGVCBPPGSGSPGV	363
QY	61	RELKQFLGMLKKHAYCSNLSRLTDQWRAWQKSHKTRNQ	101
Db	364	RELKQFLGMLKKHAYCSNLSRLTDQWRAWQKSHKTRNQ	404
RESULT	2		
ID	002661		
AC	002661	PRELIMINARY;	PRT; 425 AA.
DT	01-JUL-1997 (TREMELREL. 04, Created)		
DT	01-JUL-1997 (TREMELREL. 04, Last sequence update)		
DT	01-NOV-1998 (TREMELREL. 08, Last annotation update)		
DE	SCO-SPONDIN (FRAGMENT).		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
NC	Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;		
CC	Bovinae; Bos.		

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SUBCOMMISSURAL ORGAN;
 RA GBRON S.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Y08551; CAA69868.1;
 PR: P00050; tsp-1; 3.
 FT NON-TER
 FT SEQUENCE 425 AA; 43721 MW; 20D06545 CRC32;
 SO
 Query Match 10.2%; Score 88; DB 6; Length 425;
 Best Local Similarity 28.6%; Pred. No. 0.17;
 Matches 34; Conservative 4; Mismatches 47; Indels 34; Gaps 6;
 QY 24 MSEMSEH-----PTASTPRSER---PGGGGVC---EPGGESSGPPVRELKQFLGWL 71
 DB 196 WAPMSACSGCLVPGGGPPALRSRLCPGPDJSCIGENTEEPCSPV----- 245
 QY 72 KHAAYCSNLSFRLYDQNRAMNOKSHKTRNOVGLGACVGGKGAEEERDPGEOPPOHRT 130
 DB 245 -----C-LGLGVWQWMAWMSACSPACNGGVQTRGRRC-----SASAPGDGCGGPHSGT 292
 RESULT 3
 ID 095873 PRELIMINARY; PRT; 294 AA.
 AC 095873;
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
 DE NG34.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA ROMEN L., MADAN A., QIN S., SHAFFER T., JAMES R., RATCIFFEE A.,
 RA ABBASI N., DICHOFF R., LORETZ C., MADAN A., DORS M., YOUNG J.,
 RA LASKY S., HOOD L.;
 RT "Sequence of the human major histocompatibility complex class III
 RT region";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A0129756; AAD18083.1;
 SO SEQUENCE 294 AA; 31809 MW; B0E58C83 CRC32;
 QY 27 MSHPTASTPRSERPG---PGGVCPEPRGEPSSGPPVRELKQFLGWL 72
 DB 117 WDHYDSGCT---RRPGVSPBGGLSVPGAPLEKPGRR--KLLGWLK 159
 Query Match 9.2%; Score 79.5; DB 4; Length 294;
 Best Local Similarity 41.7%; Pred. No. 0.85;
 Matches 20; Conservative 4; Mismatches 17; Indels 7; Gaps 3;
 QY 27 MSHPTASTPRSERPG---PGGVCPEPRGEPSSGPPVRELKQFLGWL 72
 DB 117 WDHYDSGCT---RRPGVSPBGGLSVPGAPLEKPGRR--KLLGWLK 159
 RESULT 4
 ID 064807 PRELIMINARY; PRT; 433 AA.
 AC 064807;
 DT 01-AUG-1998 (Tremblrel. 07, Created)
 DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
 DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
 DE PUTATIVE SERINE CARBOXYPEPTIDASE I.
 GN F11P24.3 OR T20K9.18
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
 OC Arabidopsis.
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-CV, COLUMBIA;
 RA ROUNSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
 RA SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
 RA SOMERVILLE C.R., VENTER J.C.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV, COLUMBIA;
 RA ROUNSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
 RA SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
 RA SOMERVILLE C.R., VENTER J.C.;
 RT "Arabidopsis thaliana chromosome II BAC T20K9 genomic sequence";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC004401; AAC17814.1;
 DR EMBL: AC004786; AAC32443.1;
 DR PFAM: PF00450; serine_carboxypeptidase.
 KW carboxypeptidase.
 SO SEQUENCE 433 AA; 49233 MW; 07D281C3 CRC32;
 QY 70 WTKHAAYCSNLSFRLYDQNRAMN---QKSHKTRNOVGLGACVGGKGAEEERDPGE 123
 DB 363 FLATQAMIKSLNYSIDENRPMIRDOITGYTRYSNKMTFATVKGSGHTAENKPE 419
 RESULT 5
 ID 083470 PRELIMINARY; PRT; 593 AA.
 AC 083470;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE CONSERVED HYPOTHETICAL PROTEIN.
 GN TP0457.
 OS Treponema pallidum.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96332770.
 RA FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
 RA DODSON R., GWINN M., HICKEY E.R., CLAYTON R., KETCHUM K.A.,
 RA SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
 RA KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTERBACK T.,
 RA MCDONALD L., ARTACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
 RA HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
 RA VENTER J.C.;
 RT "Complete genome sequence of Treponema pallidum, the syphilis
 RT spirochete";
 RL Science 281:375-388(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
 RA DODSON R., GWINN M., HICKEY E.R., CLAYTON R., KETCHUM K.A.,
 RA SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
 RA KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTERBACK T.,
 RA MCDONALD L., ARTACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
 RA HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
 RA VENTER J.C.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE001222; AAC65441.1;
 SO SEQUENCE 593 AA; 65567 MW; 16898991 CRC32;
 QY 2 TYT-----FVQVKNPFGTIGSKKAGIWSMSHTPA--STPRSERPGGVCPEPR--GG 53
 Query Match 9.0%; Score 78; DB 2; Length 593;
 Best Local Similarity 32.0%; Pred. No. 2.6;
 Matches 33; Conservative 9; Mismatches 39; Indels 22; Gaps 6;

Page 3

DT 01-NOV-1998 (TREMBLrel 07, last sequence update)
DT 01-MAY-1999 (TREMBLrel 10, last annotation update)
DE REVERSE TRANSCRIPTASE.
OS *Chlorella vulgaris*.
OC Eukaryota, Viridiplantae; Chlorophyta; Chlorophyceae; Chlorellales

RC TRANSPOSON-ZEP;
RC MEDLINE; 97361851.
RA HIGASHIYAMA T., NOTOSHI Y., FUJIE M., YAMADA T.;
RT "Zep", a LINE-like retrotransposon accumulated in the telomeric region.";
RT telomeric region.";
DL Expo J. 16:3715-3723(1997).
DR EMBL; AB008896; BAA25763.1.

DR PFAM: PF00078; rvt; 1.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 1309 AA; 141659 MW; C87AE321 CRC32

```

Query Match          9.0%; Score 78; DB 10; Length 1309;
Best Local Similarity 24.2%; Pred. No. 6.1;
Matches 36; Conservative 19; Mismatches 46; Indels 48; Gaps 10

QY 17 GSKKKGIVSEWHPAAAPSRSERP-----GGGGVCEPGRGEPSSGPV----REELKQF 67
      | : : : : : | : : : : : | : : : : : | : : : : : |
DB 973 GSGTSGSMED-----SCSSPSPQSRKMRPRSAIYGTCLMPT---SCGPIPTGSKRRKSATV 1024

QY 68 LGWLKHAHYCSLISFRLYDQWRAMQKSHKTRNQYQKLGECACVGGKGADEERDPG--EOPF 126
      | : : : : : | : : : : : | : : : : : | : : : : : |
DB 1025 QSWV---SHCS-----TGSMMQSAAL---CLGLLG---QAMPGDQDP 1060

QY 127 QHRTLLSKHRTGSCPRADGVAREYRGSG 155
      | : : : : : | : : : : : | : : : : : | : : : : : |
DB 1061 -----ARCRARPGASGSDGARARAHPSG 1083

```

RESULT	8	
Q62868		
ID	Q62868	
AC	Q62868	
DT	01-NOV-1996	(TREMblrel. 01, Created)
DT	01-NOV-1996	(TREMblrel. 01, Last sequence update)
DT	01-MAY-1999	(TREMblrel. 10, Last annotation update)
DE	ROR-ALPHA.	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia	
OC	Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Rattus.	
NC	[1]	

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RP SEQUENCE FROM N.A.
RX MEDLINE; 96094284.
RA LEUNG T., MANSER E., TAN L., LIM L.;
RT "A novel serine/threonine kinase binding the Ras-related Rhox GTPase
RT which translocates the kinase to peripheral membranes.";
RL J. Biol. Chem. 270:29051-29054(1995).
DR EMBL; U38481; AB37540.1; -.
DR PFAM; PF00130; DAG_PE-bind; 1.
DR DR PROSITE; PS00108; PROTEIN_KINASE_ST. 1.
SQ SEQUENCE 1379 AA; 159434 MW; 98CEBCFC CRC32;

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[illegible]

ID P70336 PRELIMINARY; PRT; 1388 AA.
AC P70336;
DT 01-FEB-1997 (Tremblrel. 02, Created)
DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
DE 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE RHO-ASSOCIATED COILED-COIL FORMING KINASE 2
DE (RHO-ASSOCIATED, COILED-COIL FORMING PROTEIN KINASE P160 ROCK-2).
GN ROCK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96368048.
RA NAKAGAWA O., FUJISAWA K., ISHIZAKI T., SAITO Y., NAKAO K.,
RA NAKAMURA S.;
RT "ROCK-I and ROCK-II, two isoforms of Rho-associated coiled-coil
RT forming protein serine/threonine kinase in mice.";
RL FEBS Lett. 392:189-193(1996).
DR EMBL; U58513; AAC53133.1; -
DR MGD; MGI:107926; ROCK2.
DR PFM: PFM0130; DAG-PE-Blind. 1.
DR PFM: PFM0069; Pkinase; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST. 1.
SQ SEQUENCE 1388 AA; 160584 MW; FCB26B88 CRC32;

Query Match 9.0%; Score 78; DB 11; Length 1388;
Best Local Similarity 38.5%; Pred. No. 6.5;
Matches 20; Conservative 4; Mismatches 20; Indels 8; Gaps 2;

QY 42 GPGGVCCEPRGEPSSG-----PVRELEKQFLGMLKNAKCSNLSRLTD 86
Db 1136 GSGPDADPDGPFESRLEGWLSLPVNRNKKF-GWVKYIVYSKRLFLPD 1186

RESULT 10
092BF5 PRELIMINARY; PRT; 292 AA.
AC 092BF5;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE HYPOTHETICAL 32.4 KD PROTEIN.
GN SC9B5.25.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA SEGER K.J., HARRIS D.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA BENTLEY S.D., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA REIDENBACH M., KIESER H.M., DENAPAITE D., EICHNER A., CULLUM J.,
RA KINASHI H., HOPWOOD D.A.;
RT "A set of ordered cosmid and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Molec. Microbiol. 21:77-86(1996).
DR EMBL; AL035206; CAA22767.1; -
DR Hypothetical protein.
SQ SEQUENCE 292 AA; 32399 MW; 61D7FCEE CRC32;

Query Match 9.0%; Score 77.5; DB 2; Length 292;
Best Local Similarity 23.5%; Pred. No. 1.4;

Matches 40; Conservative 20; Mismatches 57; Indels 53; Gaps 9;
QY 6 VOVRONCPGIGYSKKAGIMSE-----WSHPT-AASRP---RSRRP-- 44
Db 43 VVDAGATYAPSRNSLSLWERTPPDGRPDYKAFSLTGHPTRESLPADLRGTDPPLR 102
QY 44 -GGGVCCEPRGEPSSG--PVARE-----LKQFLGM-----LKKHAY 76
Db 103 RGRAGEGLDENVGRFAPGEPLEPLRKAGRLGTIVLFQFPNFAPOGPATLEACLLRTOGW 162
QY 77 CNSLSEFLYQWRAMMOKSHKTRNOYGLCEACVGGKAEERDPGPOPP 126
Db 163 PLAVEFRHPGWMP--ERAETRASLSALGASAVGTDMA--ORLPGLPLP 208

RESULT 11
080394 PRELIMINARY; PRT; 790 AA.
AC 080394;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE TRANSCRIPTION FACTOR VPL.
GN MCVPL.
OS Mesembryanthemum crystallinum (Common Ice plant).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Caryophyllidae; Caryophyllales; Alzooceae;
OC Mesembryanthemum.
RN [1]
RP SEQUENCE FROM N.A.
RA FUKUHARA T., BOHNERT H.J.;
RT "Expression of Vpl and water channel proteins during seed
RT germination.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB015183; BAA28779.1; -
SQ SEQUENCE 790 AA; 86467 MW; 6FFE0075 CRC32;

Query Match 8.9%; Score 76.5; DB 10; Length 790;
Best Local Similarity 33.9%; Pred. No. 5;
Matches 39; Conservative 8; Mismatches 37; Indels 31; Gaps 9;

QY 21 AGISEWSHPTASTPSERP--GPGGVCCEPRGCE--PSSGPVR--ELKQFLGWL 71
Db 580 AGNWTYSHPPPL-PPVYSHVPGPPVGMQGLERAAFGKCFQNGVYEKKQ--GWK 636
QY 72 KHAVCNLSFRLYDWRAMMOKSHKTRNOYGLCEACVGGKGAE-----EERD 120
Db 637 SE-----KNLRL-----QKYLK-QSDVGNLGRIVLPKKEATHLPLEARD 678

RESULT 12
092OC7 PRELIMINARY; PRT; 297 AA.
AC 092OC7;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE T2N18.14 PROTEIN.
GN T2N18.14.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, COLUMBIA;
RA LIN X., KAUL S., SHEA T.P., FUJII C.Y., SHEN M., VANAKEN S.E.,
RA BARNSTEAD M.E., MASON T.M., BOWMAN C.L., RONNING C.M., BENTO M.,
RA CARREIRA A.J., CREASY T.H., BOELL C.R., TOWN C.D., NIERMAN W.C.,
RA FRASER C.M., VENTER J.C.;

RT "Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence."
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC006260; AAD18149.1;
 SQ SEQUENCE 297 AA; 33756 MW; 0921E56E CRC32;

Query Match 8.9%; Score 76.5; DB 10; Length 297;
 Best Local Similarity 20.5%; Pred. No. 1.8;
 Matches 33; Conservative 20; Mismatches 55; Indels 53; Gaps 7;

19 KRAGIWSHSPFAASTP-----RSEPRP-----GGVCEPRGSGSPVRELK 65
 46 KNAASAEEOFTSPVTCGVNRKSKKPEETARVSGATE-----RRROS 94
 66 QFLGWLK---HAYCSNLSFRLYDQ-WRAMQKSH-----KTRNOYKLGACVCGKA 115
 95 RRCGWKNAFPCHSFGILKPCFSPVWRKMSFSAFSKSEKSSSRSEPTIGRST 154
 116 EERDPGE-----OPPHRTLLSKHRT 137
 155 VEPEEPETRKEENOEEASCKSFATPPRNALFLTRCS 195

RESULT 13
 097641 PRELIMINARY; PRT; 481 AA.

01-MAY-1999 (TREMBLrel. 10; Created)
 01-MAY-1999 (TREMBLrel. 10; Last sequence update)
 01-MAY-1999 (TREMBLrel. 10; Last annotation update)
 FIRINGEN A-ALPHA CHAIN (FRAGMENT).
 Equus caballus (Horse).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Perissodactyla; Equidae; Equus.
 [1]
 P SEQUENCE FROM N.A.
 MORAKAWA M.;
 Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 EMBL: AF095462; AAC67561.1;
 NON_TER 1
 NON_TER 1
 SEQUENCE 481 AA; 49506 MW; 5B5EFF36 CRC32;

Query Match 8.8%; Score 76; DB 6; Length 481;
 Best Local Similarity 25.6%; Pred. No. 3.3;
 Matches 42; Conservative 10; Mismatches 56; Indels 56; Gaps 9;

17 GSKRAGIWSHSPFAAST--PRSEPRGPG-----GVCEPRGSGSPV 60
 120 GSGSASTWTSGSYGSGASTWNPSSGSSGSLGASASTWNPSSSEPSDGP- 179
 61 RRELKQFLGKKAHAYCSNLSFRLYDQWRAMQKSHKTRNOYKLGACVCGKAEEERD 120
 179 -----RKPGSSGCTLSAST--WTSGS-----SGLSASTWNPSSSEPSGS 214
 121 PGEOPP-OHRTLLSKHRTGSG-----PRADGVR 149
 215 DGPQKPGSSGCTLSITWTSGSSGPGSASTRHPGSSSEPSDGP 258

RESULT 14
 090711 PRELIMINARY; PRT; 561 AA.

01-NOV-1996 (TREMBLrel. 01; Created)
 01-NOV-1996 (TREMBLrel. 01; Last sequence update)
 01-NOV-1998 (TREMBLrel. 08; Last annotation update)
 AE2-2 ANION EXCHANGER (FRAGMENT).
 AE2.
 Gallus gallus (Chicken).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
 Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PROVENTRICULUS (FORESTOMACH);
 RX MEDLINE; 96224107.
 RA COX K.H., ADAIR-KIRK T.L., COX J.V.;
 RT "Variant AE2 anion exchanger transcripts accumulate in multiple cell
 RL types in the chicken gastric epithelium."
 DR EMBL: U48890; AAC59882.1;
 FT NON_TER 561
 FT SEQUENCE 561 AA; 61186 MW; D1452E16 CRC32;

Query Match 8.7%; Score 75.5; DB 13; Length 561;
 Best Local Similarity 23.6%; Pred. No. 4.4;
 Matches 45; Conservative 17; Mismatches 66; Indels 63; Gaps 9;

9 RCNPFYISGSKKAGIWSHSP-----ASTPSEPRGSGVCEPRGSGSPV----- 61
 22 RVPQSSGGVRIA--IRGAPAPSPAPSPQPEPPAPG-----PASPPAEE 69
 61 RRELKQFLG-----WLKKAHAYCSNLSFRLYDQWRAMQKSHK 97
 70 EKDLNALGVERREELISDAHPSVPERITGEEDFEYHROSLSLHHPALAPDAR 129
 98 TRNOYKLGACVCGKAEEERDPGEP-----OHRTLLSKHRTGSGCPAD 145
 130 RKKGVKKRKKRGRALA-----PGENPPIEGEEDDEACCTERSAELRGC--PAE 182
 146 GVR-REVRGSG 155
 183 GVQVGEARAG 193

RESULT 15
 044128 PRELIMINARY; PRT; 336 AA.

01-NOV-1996 (TREMBLrel. 01; Created)
 01-NOV-1996 (TREMBLrel. 01; Last sequence update)
 01-NOV-1998 (TREMBLrel. 08; Last annotation update)
 PROTEIN A.
 Acetobacter pasteurianus.
 Plasmid pAP12875.
 OC Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
 AC Acetobacter.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 95309714.
 RA FOMENKOV A., XIAO J.P., XU S.Y.;
 RT "Nucleotide sequence of a small plasmid isolated from Acetobacter
 RL pasteurianus."
 DR EMBL: U20550; AAA86883.1;
 KW Plasmid.
 SQ SEQUENCE 336 AA; 36948 MW; CF24DEA4 CRC32;

Query Match 8.7%; Score 75; DB 2; Length 336;
 Best Local Similarity 25.0%; Pred. No. 2.9;
 Matches 49; Conservative 17; Mismatches 82; Indels 48; Gaps 10;

1 GTVFVQVRCNPF-----IYSGKAGIWSF-----WSHPTA 32
 95 GAYFADEAYEAAGPSPAMEHRLVAVTHLAISTGSK--WSQTVKHITDALGWSQYA 151
 33 ASTPSEPRGSGVCEPRGSGP-----PRRELKQFLGKKAHAYCSNLSFR 83
 152 KHARGARHIORSCHCPSGMOGOTGMNDKSGVPAEALKEFGMAAYAPRL-MR 210
 84 LYDQWRAMQKSHKTRNOYKLGACVCGKAEEERDPGEP--POHRTLLSKHRT--GSC 141
 211 SYSKAARVEENNAARSALVQAQQA--GGTARPTHTSLPSSPNAKRTMVRERAGGSA 269

OY 142 ---PRA-DGVREVG 153
|:| | | |
Db 270 VGOFRKVSRSVRSAAAG 285

Search completed: September 16, 1999, 20:40:08
Job time: 5559 sec

GenCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 17, 1999, 03:08:14 ; Search time 64.1 Seconds

(without alignments)
102.726 Million cell updates/sec

Title: US-09-037-657-19

Sequence: 1 PTLIGSSLIATCSIHGDRP.....VFQVACNPFQIGSKKAG 278

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database: A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1505	100.0	413	1 M55011	Novel haemopoietin
2	1505	100.0	425	1 M55012	Novel haemopoietin
3	1501	99.7	278	1 M55014	Protein sequence o
4	1501	99.7	425	1 M59804	Nucleotide sequenc
5	1500	99.7	425	1 W70841	Human zcyto5 vari
6	1500	99.7	425	1 W70862	Human zcyto5 vari
7	1464	97.3	389	1 W70850	Human zcyto5 vari
8	1463	97.2	408	1 M59805	Human zcyto5 vari
9	1463	97.2	382	1 W70840	Human zcyto5 vari
10	1463	97.2	389	1 W70844	Human zcyto5 vari
11	1463	97.2	303	1 W70845	Human zcyto5 vari
12	1463	97.2	425	1 W70861	Human zcyto5 vari
13	1462	97.1	389	1 W70851	Human zcyto5 vari
14	1461	97.1	389	1 W70852	Human zcyto5 vari
15	1460	97.0	389	1 W70846	Human zcyto5 vari
16	1460	97.0	389	1 W70847	Human zcyto5 vari
17	1460	97.0	389	1 W70849	Human zcyto5 vari
18	1459	96.9	389	1 W70848	Human zcyto5 vari
19	1459	96.9	303	1 W70843	Human zcyto5 vari
20	1459	96.9	422	1 W70860	Human zcyto5 vari
21	1458	96.9	389	1 W70853	Human zcyto5 vari
22	1452	96.5	388	1 W70839	Human zcyto5 vari
23	1452	96.5	385	1 W70842	Human zcyto5 vari
24	1330	87.7	350	1 M55015	Human zcyto5 vari
25	690	45.8	186	1 M55016	Amino acid sequenc
26	308.5	20.5	622	1 R15075	Human prolactin re
27	304	20.2	211	1 R24273	Truncated human pr
28	302	20.1	211	1 R22228	Recombinant human
29	290	19.3	918	1 R10545	Human gp130 N-term
30	290	19.3	708	1 R37804	Human gp130 N-term
31	290	19.3	658	1 R46233	Human gp130 N-term
32	290	19.3	658	1 R46233	Human gp130 N-term
33	290	19.3	658	1 R46233	Human gp130 N-term
34	290	19.3	658	1 R46233	Human gp130 N-term
35	290	19.3	658	1 R46233	Human gp130 N-term
36	290	19.3	658	1 R46233	Human gp130 N-term
37	290	19.3	658	1 R46233	Human gp130 N-term
38	290	19.3	658	1 R46233	Human gp130 N-term
39	290	19.3	658	1 R46233	Human gp130 N-term
40	250.5	16.6	180	1 W00404	Human gp130-Fc-His
41	233	15.5	630	1 R93120	Human gp130-Fc-His
42	233	15.5	606	1 R93121	Human gp130-Fc-His
43	222	14.8	783	1 R11741	Human gp130-Fc-His

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	ID	Description
1	M55011	100.0%	Score 1505;	DB 1;	Length 413;	
2	M55012	100.0%	Score 1505;	DB 1;	Length 413;	
3	M55014	99.7%	Score 1501;	DB 1;	Length 278;	
4	M59804	99.7%	Score 1501;	DB 1;	Length 425;	
5	W70841	99.7%	Score 1500;	DB 1;	Length 425;	
6	W70862	99.7%	Score 1500;	DB 1;	Length 425;	
7	W70850	97.3%	Score 1464;	DB 1;	Length 389;	
8	M59805	97.2%	Score 1463;	DB 1;	Length 408;	
9	W70840	97.2%	Score 1463;	DB 1;	Length 382;	
10	W70844	97.2%	Score 1463;	DB 1;	Length 389;	
11	W70845	97.2%	Score 1463;	DB 1;	Length 303;	
12	W70861	97.2%	Score 1463;	DB 1;	Length 425;	
13	W70851	97.1%	Score 1462;	DB 1;	Length 389;	
14	W70852	97.1%	Score 1461;	DB 1;	Length 389;	
15	W70846	97.0%	Score 1460;	DB 1;	Length 389;	
16	W70847	97.0%	Score 1460;	DB 1;	Length 389;	
17	W70849	97.0%	Score 1460;	DB 1;	Length 389;	
18	W70848	96.9%	Score 1459;	DB 1;	Length 389;	
19	W70843	96.9%	Score 1459;	DB 1;	Length 303;	
20	W70860	96.9%	Score 1459;	DB 1;	Length 422;	
21	W70853	96.9%	Score 1458;	DB 1;	Length 389;	
22	W70839	96.5%	Score 1452;	DB 1;	Length 388;	
23	W70842	96.5%	Score 1452;	DB 1;	Length 385;	
24	M55015	87.7%	Score 1330;	DB 1;	Length 350;	
25	M55016	45.8%	Score 690;	DB 1;	Length 186;	
26	R15075	20.5%	Score 308.5;	DB 1;	Length 622;	
27	R24273	20.2%	Score 304;	DB 1;	Length 211;	
28	R22228	20.1%	Score 302;	DB 1;	Length 211;	
29	R10545	19.3%	Score 290;	DB 1;	Length 918;	
30	R37804	19.3%	Score 290;	DB 1;	Length 708;	
31	R46233	19.3%	Score 290;	DB 1;	Length 658;	
32	R46233	19.3%	Score 290;	DB 1;	Length 658;	
33	R46233	19.3%	Score 290;	DB 1;	Length 658;	
34	R46233	19.3%	Score 290;	DB 1;	Length 658;	
35	R46233	19.3%	Score 290;	DB 1;	Length 658;	
36	R46233	19.3%	Score 290;	DB 1;	Length 658;	
37	R46233	19.3%	Score 290;	DB 1;	Length 658;	
38	R46233	19.3%	Score 290;	DB 1;	Length 658;	
39	R46233	19.3%	Score 290;	DB 1;	Length 658;	
40	W00404	16.6%	Score 250.5;	DB 1;	Length 180;	
41	R93120	15.5%	Score 233;	DB 1;	Length 630;	
42	R93121	15.5%	Score 233;	DB 1;	Length 606;	
43	R11741	14.8%	Score 222;	DB 1;	Length 783;	

Query Match	Score	Query Match	Length	ID	Description
1	100.0%	Score 1505;	DB 1;	Length 413;	
2	100.0%	Score 1505;	DB 1;	Length 413;	
3	99.7%	Score 1501;	DB 1;	Length 278;	
4	99.7%	Score 1501;	DB 1;	Length 425;	
5	99.7%	Score 1500;	DB 1;	Length 425;	
6	99.7%	Score 1500;	DB 1;	Length 425;	
7	97.3%	Score 1464;	DB 1;	Length 389;	
8	97.2%	Score 1463;	DB 1;	Length 408;	
9	97.2%	Score 1463;	DB 1;	Length 382;	
10	97.2%	Score 1463;	DB 1;	Length 389;	
11	97.2%	Score 1463;	DB 1;	Length 303;	
12	97.2%	Score 1463;	DB 1;	Length 425;	
13	97.1%	Score 1462;	DB 1;	Length 389;	
14	97.1%	Score 1461;	DB 1;	Length 389;	
15	97.0%	Score 1460;	DB 1;	Length 389;	
16	97.0%	Score 1460;	DB 1;	Length 389;	
17	97.0%	Score 1460;	DB 1;	Length 389;	
18	96.9%	Score 1459;	DB 1;	Length 389;	
19	96.9%	Score 1459;	DB 1;	Length 303;	
20	96.9%	Score 1459;	DB 1;	Length 422;	
21	96.9%	Score 1458;	DB 1;	Length 389;	
22	96.5%	Score 1452;	DB 1;	Length 388;	
23	96.5%	Score 1452;	DB 1;	Length 385;	
24	87.7%	Score 1330;	DB 1;	Length 350;	
25	45.8%	Score 690;	DB 1;	Length 186;	
26	20.5%	Score 308.5;	DB 1;	Length 622;	
27	20.2%	Score 304;	DB 1;	Length 211;	
28	20.1%	Score 302;	DB 1;	Length 211;	
29	19.3%	Score 290;	DB 1;	Length 918;	
30	19.3%	Score 290;	DB 1;	Length 708;	
31	19.3%	Score 290;	DB 1;	Length 658;	
32	19.3%	Score 290;	DB 1;	Length 658;	
33	19.3%	Score 290;	DB 1;	Length 658;	
34	19.3%	Score 290;	DB 1;	Length 658;	
35	19.3%	Score 290;	DB 1;	Length 658;	
36	19.3%	Score 290;	DB 1;	Length 658;	
37	19.3%	Score 290;	DB 1;	Length 658;	
38	19.3%	Score 290;	DB 1;	Length 658;	
39	19.3%	Score 290;	DB 1;	Length 658;	
40	16.6%	Score 250.5;	DB 1;	Length 180;	
41	15.5%	Score 233;	DB 1;	Length 630;	
42	15.5%	Score 233;	DB 1;	Length 606;	
43	14.8%	Score 222;	DB 1;	Length 783;	

29-SEP-1998 (first entry)
 DE Novel haemopoietin receptor NR6.2 protein.
 KM Haemopoietin receptor: cell proliferation; cell differentiation; cancer;
 KM cell survival; therapeutic; neuronal proliferation; drug screening;
 KM Mouse.
 OS Mus sp.
 PN MO9811225-A2.
 PD 19-MAR-1998.
 PF 11-SEP-1997: G02479.
 PR 11-SEP-1996: AU-002246.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PA (DZIE/) DZIEGLEMSKA H E.
 PI Alexander W, Fabril L, Farley A, Hilton DJ, Kikuchi Y,
 PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willison T,
 PI Zhang J.
 DR WPI: 98-260970/23.
 DR N-PSDB: V27141.
 PT New isolated haemopoietin receptor - used for developing products
 PT for modulating proliferation, differentiation and survival of cells,
 PT e.g. neuronal cells
 PS Claim 15: Page 84-87: 182pp: English.
 CC The haemopoietin receptor (HR) NR6.2 is a form of the novel HR NR6.
 CC Interaction between the novel HR and a ligand facilitates proliferation,
 CC differentiation and survival of a wide variety of cells. The HR and its
 CC derivatives can be used for modulating the activity of the receptors e.g.
 CC to regulate development, maintenance or regeneration in an array of
 CC different cells and tissues in vitro and in vivo. They can be present in
 CC therapeutics used for modulating neuronal proliferation, differentiation
 CC and survival. The products can also be used for detection and diagnosis,
 CC e.g. for cancers or predisposition to cancers, or for drug screening.
 SQ Sequence 425 AA:

Query Match 100.0%; Score 1505; DB 1; Length 425;
 Best Local Similarity 100.0%; Pred. No. 9.2e-139;
 Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PTLIGSSLOATCSIHGDPGATAGLYTLNGRRLPSELRLNTSTALANLNGSR 60
 DB 51 PTLIGSSLOATCSIHGDPGATAGLYTLNGRRLPSELRLNTSTALANLNGSR 110
 QY 61 QOSGDNLYCHARDGSLIAGSCLYVGLPPEKPFNISCSNRMDLTCRMTPGAHEFTLHT 120
 DB 111 QOSGDNLYCHARDGSLIAGSCLYVGLPPEKPFNISCSNRMDLTCRMTPGAHEFTLHT 170
 QY 121 NYSLKTKLWYQODNCEEHYVGPSCHPKDLALFTPEIWEATNRLGARSVDYTL 180
 DB 171 NYSLKTKLWYQODNCEEHYVGPSCHPKDLALFTPEIWEATNRLGARSVDYTL 230
 QY 181 DVLADVTTDPPDVHVSRYVGLLEDOLSVRWVSPALKDLEFOAKYQIRRVEDSDVMKYV 240
 DB 231 DVLADVTTDPPDVHVSRYVGLLEDOLSVRWVSPALKDLEFOAKYQIRRVEDSDVMKYV 290
 QY 241 DVSNOTSCRLAGLKPGETYFVQVRCNPGIYGSKKAG 278
 DB 291 DVSNOTSCRLAGLKPGETYFVQVRCNPGIYGSKKAG 328

RESULT 3
 W55014
 ID W55014 standard; Protein; 278 AA.
 AC W55014;
 DT 02-OCT-1998 (first entry)
 DE Protein sequence of products generated by 5N race of brain CDNA.
 KM Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
 KM cell survival; therapeutic; neuronal proliferation; drug screening;
 KM Mouse.
 OS Mus sp.
 PN MO9811225-A2.
 PD 19-MAR-1998.
 PF 11-SEP-1997: G02479.
 PR 11-SEP-1996: AU-002246.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.

(DZIE/) DZIEGLEMSKA H E.
 PI Alexander W, Fabril L, Farley A, Hilton DJ, Kikuchi Y,
 PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willison T,
 PI Zhang J.
 DR WPI: 98-260970/23.
 DR N-PSDB: V27143.
 PT New isolated haemopoietin receptor - used for developing products
 PT for modulating proliferation, differentiation and survival of cells,
 PT e.g. neuronal cells
 PS Claim 17: Page 93-95: 182pp: English.
 CC The protein sequence was generated by a 5N RACE of brain CDNA using
 CC NR6 specific primers. NR6 is a novel Haemopoietin receptor (HR).
 CC Interaction between the novel HR and a ligand facilitates proliferation,
 CC differentiation and survival of a wide variety of cells. The HR and its
 CC derivatives can be used for modulating the activity of the receptors e.g.
 CC to regulate development, maintenance or regeneration in an array of
 CC different cells and tissues in vitro and in vivo. They can be present in
 CC therapeutics used for modulating neuronal proliferation, differentiation
 CC and survival. The products can also be used for detection and diagnosis,
 CC e.g. for cancers or predisposition to cancers, or for drug screening.
 SQ Sequence 278 AA:

Query Match 100.0%; Score 1505; DB 1; Length 278;
 Best Local Similarity 100.0%; Pred. No. 5e-139;
 Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PTLIGSSLOATCSIHGDPGATAGLYTLNGRRLPSELRLNTSTALANLNGSR 60
 DB 1 PTLIGSSLOATCSIHGDPGATAGLYTLNGRRLPSELRLNTSTALANLNGSR 60
 QY 61 QOSGDNLYCHARDGSLIAGSCLYVGLPPEKPFNISCSNRMDLTCRMTPGAHEFTLHT 120
 DB 121 NYSLKTKLWYQODNCEEHYVGPSCHPKDLALFTPEIWEATNRLGARSVDYTL 180
 QY 181 DVLADVTTDPPDVHVSRYVGLLEDOLSVRWVSPALKDLEFOAKYQIRRVEDSDVMKYV 240
 DB 181 DVLADVTTDPPDVHVSRYVGLLEDOLSVRWVSPALKDLEFOAKYQIRRVEDSDVMKYV 240
 QY 241 DVSNOTSCRLAGLKPGETYFVQVRCNPGIYGSKKAG 278
 DB 241 DVSNOTSCRLAGLKPGETYFVQVRCNPGIYGSKKAG 278

RESULT 4
 W59804
 ID W59804 standard; Protein; 425 AA.
 AC W59804;
 DT 26-OCT-1998 (first entry)
 DE Nucleotide sequence of the murine U4 protein.
 KM Murine U4 protein; haemopoietin receptor superfamily;
 KM cell proliferation; immune response; antibody; cell differentiation;
 KM autoimmune disease; cancer; allergy.
 OS Mus sp.
 PN MO9831811-A1.
 PD 23-JUL-1998.
 PF 15-JAN-1998: U00334.
 PR 16-JAN-1997: U5-784863.
 PA (GENY) GENETICS INST INC.
 PI Collins M, Donaldson DD, Neben T, Whitters M,
 DR WPI: 98-414109/35.
 DR N-PSDB: V41688.
 PT New nucleic acid encoding U4 haemopoietin receptor superfamily
 PT chain - potentially useful, e.g. for modulating cell proliferation
 PT or immune response, for treating cancer and auto-immune disease
 PS Claim 9: Pages 26-27: 38pp: English.
 CC This is the amino acid sequence of the murine U4 protein from the
 CC haemopoietin receptor superfamily, used in the method of the
 CC invention for the modulation of cell proliferation, or the immune

CC response. Transformed mammalian cells are used to produce recombinant
CC u4 protein. The u4 protein is used to screen for specific binding
CC agents, raise antibodies. It is also used as reagents for assays and
CC as tissue markers for isolation of cognate ligands and receptors and
CC in pharmaceutical compositions which may modulate cell proliferation,
CC cell differentiation, and the immune system (e.g. for treating immune
CC deficiency, inherited or the result of infection, autoimmune diseases,
CC cancer, and allergy).

CC Sequence 425 AA;

Query Match 99.7%; Score 1501; DB 1; Length 425;
Best Local Similarity 99.6%; Pred. No. 2.3e-138;
Matches 277; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PTLTSSLOATCSIHGDPGATAGELTYTLNRRRLPSELRLNLTALANLNGSR 60
DB 51 PTLTSSLOATCSIHGDPGATAGELTYTLNRRRLPSELRLNLTALANLNGSR 110
QY 61 QOSGDLVCHARGSLIAGSCLYVGLPPEKPFNISCNRMKDLTCRMTGAGETFLHT 120
DB 111 QOSGDLVCHARGSLIAGSCLYVGLPPEKPFNISCNRMKDLTCRMTGAGETFLHT 170
QY 121 NYSLKTKLRMYGQDNTCEXHTVGPSPCHIPKDLALFTPEIWEATNRLGARSVDLT 180
DB 171 NYSLKTKLRMYGQDNTCEXHTVGPSPCHIPKDLALFTPEIWEATNRLGARSVDLT 230
QY 181 DVLDVYTTDPPPPVHVSRRVGLDQLSVKWSPPALKDFLQAKYQIRRVEDSDVMKVV 240
DB 231 DVLDVYTTDPPPPVHVSRRVGLDQLSVKWSPPALKDFLQAKYQIRRVEDSDVMKVV 290
QY 241 DVVSNQTSCLAGLKPQTYEYFVQVRCNPFQIYGSRRAG 278
DB 291 DVVSNQTSCLAGLKPQTYEYFVQVRCNPFQIYGSRRAG 328

RESULT 5
W70841
W70841 standard; Protein: 385 AA.

AC W70841:
DT 17-MAR-1999 (first entry)
DE Human zcyto5 variant.
KM zcyto5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
OS cardiac pathology; heart enlargement; zcyto5 ligand; variant.
PN Homo sapiens.
PM WO9849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
PI Lok S, Pressnell SR, Whitmore TE;
DR WPI: 99-034662/03.
PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
PT down-regulating zcyto5 natural ligands or detecting cardiotoxin-1
PT in blood
PS Claim 1; Page 83-84; 55pp; English.
CC The present sequence represents a zcyto5 variant protein. zcyto5
CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC thyroid, heart, and skeletal muscle for example to lessen the effect
CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
CC enlargement. zcyto5 could be used to detect cardiotoxin-1 in the
CC blood, and to discover other possible zcyto5 ligands. A probe
CC comprising zcyto5 DNA or RNA can be used to determine the presence
CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify zcyto5 and
CC therapeutically to modify zcyto5 ligand effects.
SQ Sequence 385 AA;

Query Match 99.7%; Score 1500; DB 1; Length 385;
Best Local Similarity 99.6%; Pred. No. 2.5e-138;
Matches 277; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PTLTSSLOATCSIHGDPGATAGELTYTLNRRRLPSELRLNLTALANLNGSR 60
DB 11 PTLTSSLOATCSIHGDPGATAGELTYTLNRRRLPSELRLNLTALANLNGSR 70
QY 61 QOSGDLVCHARGSLIAGSCLYVGLPPEKPFNISCNRMKDLTCRMTGAGETFLHT 120
DB 71 QOSGDLVCHARGSLIAGSCLYVGLPPEKPFNISCNRMKDLTCRMTGAGETFLHT 130
QY 121 NYSLKTKLRMYGQDNTCEXHTVGPSPCHIPKDLALFTPEIWEATNRLGARSVDLT 180
DB 131 NYSLKTKLRMYGQDNTCEXHTVGPSPCHIPKDLALFTPEIWEATNRLGARSVDLT 190
QY 181 DVLDVYTTDPPPPVHVSRRVGLDQLSVKWSPPALKDFLQAKYQIRRVEDSDVMKVV 240
DB 191 DVLDVYTTDPPPPVHVSRRVGLDQLSVKWSPPALKDFLQAKYQIRRVEDSDVMKVV 250
QY 241 DVVSNQTSCLAGLKPQTYEYFVQVRCNPFQIYGSRRAG 278
DB 251 DVVSNQTSCLAGLKPQTYEYFVQVRCNPFQIYGSRRAG 288

RESULT 6
W70862
W70862 standard; Protein: 425 AA.

AC W70862:
DT 17-MAR-1999 (first entry)
DE Rat zcyto5 protein.
KM zcyto5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
OS cardiac pathology; heart enlargement; zcyto5 ligand.
PN Rattus sp.
PM WO9849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
PI Lok S, Pressnell SR, Whitmore TE;
DR WPI: 99-034662/03.
PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
PT down-regulating zcyto5 natural ligands or detecting cardiotoxin-1
PT in blood
PS Claim 1; Page 75-76; 55pp; English.

CC The present sequence represents a protein designated zcyto5, which is
CC a cytokinin-like receptor. Soluble zcyto5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC thyroid, heart, and skeletal muscle for example to lessen the effect
CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
CC enlargement. zcyto5 could be used to detect cardiotoxin-1 in the
CC blood, and to discover other possible zcyto5 ligands. A probe
CC comprising zcyto5 DNA or RNA can be used to determine the presence
CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify zcyto5 and
CC therapeutically to modify zcyto5 ligand effects.
SQ Sequence 425 AA;

Query Match 99.7%; Score 1500; DB 1; Length 425;
Best Local Similarity 99.6%; Pred. No. 2.8e-138;
Matches 277; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PTLTSSLOATCSIHGDPGATAGELTYTLNRRRLPSELRLNLTALANLNGSR 60
|||||

Db 51 PTLIGSSLATGCSIHGDPGATAGLYWTLNGRRLPSELRLNTSLALANLNGSR 110

QY 61 QOSGDNLYCHARDGSIAGSCLYVGLPEKPFNISCSRMKDLTCRMPGAGETFLHT 120

Db 111 QOSGDNLYCHARDGSIAGSCLYVGLPEKPFNISCSRMKDLTCRMPGAGETFLHT 170

QY 121 NYSLKTKLRMYGODNCEEHYHVGPHSCHIPKDLAFTPEIWEATNRLGARSVDLT 180

Db 171 NYSLKTKLRMYGODNCEEHYHVGPHSCHIPKDLAFTPEIWEATNRLGARSVDLT 230

QY 181 DVLAVYTTDPPDPVHVSRYVGLLEDQSVKRWSPALKDPLFOAKYQIRRVEDSDVMKVY 240

Db 231 DVLAVYTTDPPDPVHVSRYVGLLEDQSVKRWSPALKDPLFOAKYQIRRVEDSDVMKVY 290

QY 241 DVSNOTSCRLAGLKPRTYFVQVRCNPFGITGSKKAG 278

Db 291 DVSNOTSCRLAGLKPRTYFVQVRCNPFGITGSKKAG 328

RESULT 7

W70850 standard; Protein: 389 AA.

AC W70850:

DT 17-MAR-1999 (first entry)

DE Human zcyto5 variant.

KW zcyto5; cytokinin-like receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1; cardiac pathology; heart enlargement; zcyto5 ligand; variant.

OS Homo sapiens.

PN MO9849307-A1.

PD 05-NOV-1998.

PF 01-MAY-1998; 008865.

PR 13-FEB-1998; US-074721.

PR 01-MAY-1997; US-045287.

PR 01-MAY-1997; US-850030.

PR 13-FEB-1998; US-023890.

PA (ZYMO) ZYMOGENETICS INC.

PI Adams RL, Foster DC, Gilbert T, Jelnberg AC, Lehner JM, Lok S, Presnell SR, Whitmore TE.

DR WPI: 99-034662/03.

PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g. down-regulating zcyto5 natural ligands or detecting cardiostrophin-1 in blood.

PS Claim 1: Page 95-96; 55pp; English.

CC The present sequence represents a zcyto5 variant protein. zcyto5 is a cytokinin-like receptor. Soluble zcyto5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiostrophin-1 on cardiac pathologies, so preventing heart enlargement. zcyto5 could be used to detect cardiostrophin-1 in the blood, and to discover other possible zcyto5 ligands. A probe comprising zcyto5 DNA or RNA can be used to determine the presence and integrity of the zcyto5 gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify zcyto5 and therapeutically to modify zcyto5 ligand effects.

CC Sequence 389 AA;

Query Match 97.38; Score 1464; DB 1; Length 389; Best Local Similarity 96.88; Pred. No. 8.1e-135; Matches 268; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 PTLIGSSLATGCSIHGDPGATAGLYWTLNGRRLPSELRLNTSLALANLNGSR 60

Db 11 PTLIGSSLATGCSIHGDPGATAGLYWTLNGRRLPSELRLNTSLALANLNGSR 70

QY 61 QOSGDNLYCHARDGSIAGSCLYVGLPEKPFNISCSRMKDLTCRMPGAGETFLHT 120

Db 71 QOSGDNLYCHARDGSIAGSCLYVGLPEKPFNISCSRMKDLTCRMPGAGETFLHT 130

QY 121 NYSLKTKLRMYGODNCEEHYHVGPHSCHIPKDLAFTPEIWEATNRLGARSVDLT 180

Db 131 NYSLKTKLRMYGODNCEEHYHVGPHSCHIPKDLAFTPEIWEATNRLGARSVDLT 190

QY 181 DVLAVYTTDPPDPVHVSRYVGLLEDQSVKRWSPALKDPLFOAKYQIRRVEDSDVMKVY 240

Db 191 DVLAVYTTDPPDPVHVSRYVGLLEDQSVKRWSPALKDPLFOAKYQIRRVEDSDVMKVY 250

QY 241 DVSNOTSCRLAGLKPRTYFVQVRCNPFGITGSKKAG 278

Db 251 DVSNOTSCRLAGLKPRTYFVQVRCNPFGITGSKKAG 288

RESULT 8

W59805 standard; Protein: 408 AA.

AC W59805:

DT 26-OCT-1998 (first entry)

DE Amino acid sequence of the human U4 protein.

KW Human; U4 protein; haematopoietin receptor superfamily; cell proliferation; immune response; antibody; cell differentiation; autoimmune disease; cancer; allergy.

OS Homo sapiens.

PN MO9831811-A1.

PD 23-JUL-1998.

PF 15-JAN-1998; U00334.

PR 16-JAN-1997; US-784863.

PA (GENE) GENETICS INST INC.

PI Collins M, Donaldson DD, Neben T, Whitters M; WPI: 98-41409/35.

DR N-PSDB; V41689.

PT New nucleic acid encoding U4 haematopoietin receptor superfamily chain - potentially useful, e.g. for modulating cell proliferation or immune response, for treating cancer and autoimmune disease.

PS Claim 9; Pages 29-30; 38pp; English.

CC This is the amino acid sequence of the human U4 protein from the haematopoietin receptor superfamily, used in the method of the invention for the modulation of cell proliferation, or the immune response. Transformed mammalian cells are used to produce recombinant U4 protein. The U4 protein is used to screen for specific binding agents, raise antibodies. It is also used as reagents for assays and as tissue markers for isolation of cognate ligands and receptors, and in pharmaceutical compositions which may modulate cell proliferation, cell differentiation and the immune system (e.g. for treating immune deficiency, inherited or the result of infection, autoimmune diseases, cancer, and allergy).

CC Sequence 408 AA;

Query Match 97.28; Score 1463; DB 1; Length 408; Best Local Similarity 96.48; Pred. No. 1.1e-134; Matches 268; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 PTLIGSSLATGCSIHGDPGATAGLYWTLNGRRLPSELRLNTSLALANLNGSR 60

Db 34 PTLIGSSLATGCSIHGDPGATAGLYWTLNGRRLPSELRLNTSLALANLNGSR 93

QY 61 QOSGDNLYCHARDGSIAGSCLYVGLPEKPFNISCSRMKDLTCRMPGAGETFLHT 120

Db 94 QOSGDNLYCHARDGSIAGSCLYVGLPEKPFNISCSRMKDLTCRMPGAGETFLHT 153

QY 121 NYSLKTKLRMYGODNCEEHYHVGPHSCHIPKDLAFTPEIWEATNRLGARSVDLT 180

Db 154 NYSLKTKLRMYGODNCEEHYHVGPHSCHIPKDLAFTPEIWEATNRLGARSVDLT 213

QY 181 DVLAVYTTDPPDPVHVSRYVGLLEDQSVKRWSPALKDPLFOAKYQIRRVEDSDVMKVY 240

Db 214 DVLAVYTTDPPDPVHVSRYVGLLEDQSVKRWSPALKDPLFOAKYQIRRVEDSDVMKVY 273

QY 241 DVSNOTSCRLAGLKPRTYFVQVRCNPFGITGSKKAG 278

Db 274 DVSNOTSCRLAGLKPRTYFVQVRCNPFGITGSKKAG 311

RESULT 9

W70840

ID W70840 standard; Protein: 392 AA.
 AC W70840;
 DT 17-MAR-1999 (first entry)
 DE Human zcyto5 variant.
 KM zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 OS Homo sapiens.
 PN MO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; US-074721.
 PR 13-FEB-1998; US-045287.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI; 99-034662/03.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiostrophin-1
 in blood
 PS Claim 1: Page 81-82; 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. Zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcyto5 could be used to detect cardiostrophin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SO Sequence 392 AA:

Query Match 97.2%; Score 1463; DB 1; Length 392;
 Best Local Similarity 96.4%; Pred. No. 1e-134; Indels 0; Gaps 0;
 Matches 268; Conservative 5; Mismatches 5;

QY 1 PTLIGSSLATGCSIHGDPGATAGLWTLNRRRLPELSRLNTSTLALANLNGSR 60
 DB 14 PTLIGSSLATGCSVHDPGATAGLWTLNRRRLPELSRLNTSTLALANLNGSR 73
 QY 61 QOSGDNLYCHARGSTIAGSCLVGLPEKPFNISCMSRNMKDLTCRMTGAGETFLHT 120
 DB 74 QOSGDNLYCHARGSTIAGSCLVGLPEKPFNISCMSRNMKDLTCRMTGAGETFLHT 133
 QY 121 NYSIKYLRMYGDNCEEHVTPGHSCHIPKDLALFTPEIWEATNRLGARSADVLTL 180
 DB 134 NYSIKYLRMYGDNCEEHVTPGHSCHIPKDLALFTPEIWEATNRLGARSADVLTL 193
 QY 181 DVLAVYTPDPVHVSRRVSGLEDQLSVRWVSPALKDFLQAKYQIRYVEDSVDMKVY 240
 DB 194 DVLAVYTPDPVHVSRRVSGLEDQLSVRWVSPALKDFLQAKYQIRYVEDSVDMKVY 253
 QY 241 DDVSNOTSCLAGLKGFTVYFVVRCPNPGIYSGSKAG 278
 DB 254 DDVSNOTSCLAGLKGFTVYFVVRCPNPGIYSGSKAG 291

RESULT 10
 ID W70844
 AC W70844 standard; Protein: 389 AA.
 DT 17-MAR-1999 (first entry)
 DE Human zcyto5 variant.
 KM zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 OS Homo sapiens.
 PN MO9849307-A1.

PD 05-NOV-1998.
 PF 01-MAY-1998; US-074721.
 PR 13-FEB-1998; US-045287.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI; 99-034662/03.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiostrophin-1
 in blood
 PS Claim 1: Page 87-88; 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. Zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcyto5 could be used to detect cardiostrophin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SO Sequence 389 AA:

Query Match 97.2%; Score 1463; DB 1; Length 389;
 Best Local Similarity 96.4%; Pred. No. 1e-134; Indels 0; Gaps 0;
 Matches 268; Conservative 5; Mismatches 5;

QY 1 PTLIGSSLATGCSIHGDPGATAGLWTLNRRRLPELSRLNTSTLALANLNGSR 60
 DB 11 PTLIGSSLATGCSVHDPGATAGLWTLNRRRLPELSRLNTSTLALANLNGSR 70
 QY 61 QOSGDNLYCHARGSTIAGSCLVGLPEKPFNISCMSRNMKDLTCRMTGAGETFLHT 120
 DB 71 QOSGDNLYCHARGSTIAGSCLVGLPEKPFNISCMSRNMKDLTCRMTGAGETFLHT 130
 QY 121 NYSIKYLRMYGDNCEEHVTPGHSCHIPKDLALFTPEIWEATNRLGARSADVLTL 180
 DB 131 NYSIKYLRMYGDNCEEHVTPGHSCHIPKDLALFTPEIWEATNRLGARSADVLTL 190
 QY 181 DVLAVYTPDPVHVSRRVSGLEDQLSVRWVSPALKDFLQAKYQIRYVEDSVDMKVY 240
 DB 191 DVLAVYTPDPVHVSRRVSGLEDQLSVRWVSPALKDFLQAKYQIRYVEDSVDMKVY 250
 QY 241 DDVSNOTSCLAGLKGFTVYFVVRCPNPGIYSGSKAG 278
 DB 251 DDVSNOTSCLAGLKGFTVYFVVRCPNPGIYSGSKAG 288

RESULT 11
 ID W70845
 AC W70845 standard; Protein: 303 AA.
 DT 17-MAR-1999 (first entry)
 DE Human zcyto5 variant.
 KM zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 OS Homo sapiens.
 PN MO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; US-074721.
 PR 13-FEB-1998; US-045287.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;

Query Match	97.28;	Score 1463;	DB 1;	Length 303;
Best Local Similarity	96.48;	Pred. No. 7e-135;		
Matches 268; Conservative	5;	Mismatches 5;	Indels 0;	Gaps 0;

RESULT 12
W70861
ID W70861 standard; Protein; 425 AA.
AC W70861;
DT 17-MAR-1999 (first entry)
DE Allelic variant of human zcytor5.
KW zcytor5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
KW cardiac pathology; heart enlargement; zcytor5 ligand; allelic variant.
OS Homo sapiens.
PN M09849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
PI Lok S, Pressnell SR, Whitmore TE;
DR WPI: 99-034662/03.
DR N-PDB: V70895.
PT New mammalian cytokinin-like receptor zcytor5 - useful for, e.g.
PT down-regulating zcytor5 natural ligands or detecting cardiostrophin-1
PT in blood
PS Claim 1; Page 71-72; 55pp; English.
CC The present sequence represents an allelic variant of protein designated
CC zcytor5, which is a cytokinin-like receptor. Soluble zcytor5 may be
CC administered to down-regulate the effects of a growth and/or maintenance

Query Match	97.28;	Score 1463;	DB 1;	Length 425;
Best Local Similarity	96.48;	Pred. No. 1.1e-134;		
Matches 268;	Conservative 5;	Mismatches 5;	Indels 0;	Gaps 0

RESULT 13
W70851
ID W70851 standard; Protein; 389 AA.
AC W70851;
DT 17-MAR-1999 (first entry)
DE Human zcytor5 variant.
KW zcytor5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
KW cardiac pathology; heart enlargement; zcytor5 ligand; variant.
OS Homo sapiens.
PN M09849307-A1.
PD 05-NOV-1998.
PE 01-MAY-1998; U08865.
PR 13-FEB-1998; U8-074721.
PR 01-MAY-1997; U8-045287.
PR 01-MAY-1997; U8-850030.
PR 13-FEB-1998; U8-023890.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehnert JM,
PI Lok S, Presnell SR, Whitmore TE;
PI WPI; 99-034662/03.
PT New mammalian cytokinin-like receptor zcytor5 - useful for, e.g.,
PT down-regulating zcytor5 natural ligands or detecting cardiostrophin-1
PT in blood
PS Claim 1; Page 96-97; 55pp; English.
CC The present sequence represents a zcytor5 variant protein. zcytor5
CC is a cytokinin-like receptor. Soluble zcytor5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC thyroid, heart, and skeletal muscle for example to lessen the effect
CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
CC enlargement. zcytor5 could be used to detect cardiostrophin-1 in the
CC blood, and to discover other possible zcytor5 ligands. A probe
CC comprising zcytor5 DNA or RNA can be used to determine the presence
CC and integrity of the zcytor5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify zcytor5 and the
CC therapeutically to modify zcytor5 ligand effects.
CC Sequence 389 AA.

Query Match 97.1%; Score 1462; DB 1; Length 389;
 Best Local Similarity 96.0%; Pred. No. 1.3e-134;
 Matches 267; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 PTLIGSSLATCISIHGDPGATAGELTYLNGRLPSELRLNTSTLALANLNGSR 60
 DB 11 PTLIGSSLATCISVHGDPPGATAGELTYLNGRLPSELRLNTSTLALANLNGSR 70
 QY 61 QOSGDNLYCHARDGSIAGSCLTYGLPPEKPNISCSRNKMDLTCRMTPGAHEFTFLHT 120
 DB 71 QRSQDNLYCHARDGSIAGSCLTYGLPPEKPNISCSRNKMDLTCRMTPGAHEFTFLHT 130
 QY 121 NYSLKYLKRWYGODNCEEHHTVGPCHSHPKDLALFTPEIWEATNRLGARSADVLT 180
 DB 131 NYSLKYLKRWYGODNCEEHHTVGPCHSHPKDLALFTPEIWEATNRLGARSADVLT 190
 QY 181 DVLDTVTDPDPDVHVSRYGLEDOLSVRWSPPALKDFLFOAKYQIRYVEDSVDMKVV 240
 DB 191 DILDTVTDPDPDVHVSRYGLEDOLSVRWSPPALKDFLFOAKYQIRYVEDSVDMKVV 250
 QY 241 DVVSNQTSCLAGLKPQVTVYVQVRCNPNPGIYGSKKAG 278
 DB 251 DVVSNQTSCLAGLKPQVTVYVQVRCNPNPGIYGSKKAG 288

RESULT 14

W70852
 ID W70852 standard; Protein; 389 AA.
 AC W70852;
 DT 17-MAR-1999 (first entry)
 DE Human Zcytor5 variant.
 KW Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
 maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 cardiac pathology; heart enlargement; Zcytor5 ligand; variant.
 OS Homo sapiens.
 PN MO9849307-A1.
 PD 05-NOV-1998
 PR 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelnberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI; 99-034662/03.
 PT New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.,
 PT down-regulating Zcytor5 natural ligands or detecting cardiostrophin-1
 in blood
 PS Claim 1; Page 98-99; 55pp; English.
 CC The present sequence represents a Zcytor5 variant protein. Zcytor5
 is a cytokinin-like receptor. Soluble Zcytor5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytor5 could be used to detect cardiostrophin-1 in the
 CC blood, and to discover other possible Zcytor5 ligands. A probe
 CC comprising Zcytor5 DNA or RNA can be used to determine the presence
 CC and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcytor5 and the
 CC therapeutically to modify Zcytor5 ligand effects.
 SQ Sequence 389 AA;

Query Match 97.1%; Score 1461; DB 1; Length 389;
 Best Local Similarity 96.0%; Pred. No. 1.6e-134;
 Matches 267; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 QY 1 PTLIGSSLATCISIHGDPGATAGELTYLNGRLPSELRLNTSTLALANLNGSR 60
 DB 11 PTLIGSSLATCISVHGDPPGATAGELTYLNGRLPSELRLNTSTLALANLNGSR 70

QY 61 QOSGDNLYCHARDGSIAGSCLTYGLPPEKPNISCSRNKMDLTCRMTPGAHEFTFLHT 120
 DB 71 QRSQDNLYCHARDGSIAGSCLTYGLPPEKPNISCSRNKMDLTCRMTPGAHEFTFLHT 130
 QY 121 NYSLKYLKRWYGODNCEEHHTVGPCHSHPKDLALFTPEIWEATNRLGARSADVLT 180
 DB 131 NYSLKYLKRWYGODNCEEHHTVGPCHSHPKDLALFTPEIWEATNRLGARSADVLT 190
 QY 181 DVLDTVTDPDPDVHVSRYGLEDOLSVRWSPPALKDFLFOAKYQIRYVEDSVDMKVV 240
 DB 191 DILDTVTDPDPDVHVSRYGLEDOLSVRWSPPALKDFLFOAKYQIRYVEDSVDMKVV 250
 QY 241 DVVSNQTSCLAGLKPQVTVYVQVRCNPNPGIYGSKKAG 278
 DB 251 DVVSNQTSCLAGLKPQVTVYVQVRCNPNPGIYGSKKAG 288

RESULT 15

W70846
 ID W70846 standard; Protein; 389 AA.
 AC W70846;
 DT 17-MAR-1999 (first entry)
 DE Human Zcytor5 variant.
 KW Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
 maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 cardiac pathology; heart enlargement; Zcytor5 ligand; variant.
 OS Homo sapiens.
 PN MO9849307-A1.
 PD 05-NOV-1998
 PR 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelnberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI; 99-034662/03.
 PT New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.,
 PT down-regulating Zcytor5 natural ligands or detecting cardiostrophin-1
 in blood
 PS Claim 1; Page 89-90; 55pp; English.
 CC The present sequence represents a Zcytor5 variant protein. Zcytor5
 is a cytokinin-like receptor. Soluble Zcytor5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytor5 could be used to detect cardiostrophin-1 in the
 CC blood, and to discover other possible Zcytor5 ligands. A probe
 CC comprising Zcytor5 DNA or RNA can be used to determine the presence
 CC and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcytor5 and the
 CC therapeutically to modify Zcytor5 ligand effects.
 SQ Sequence 389 AA;

Query Match 97.0%; Score 1460; DB 1; Length 389;
 Best Local Similarity 96.0%; Pred. No. 2e-134;
 Matches 267; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 QY 1 PTLIGSSLATCISIHGDPGATAGELTYLNGRLPSELRLNTSTLALANLNGSR 60
 DB 11 PTLIGSSLATCISVHGDPPGATAGELTYLNGRLPSELRLNTSTLALANLNGSR 70
 QY 61 QOSGDNLYCHARDGSIAGSCLTYGLPPEKPNISCSRNKMDLTCRMTPGAHEFTFLHT 120
 DB 71 QRSQDNLYCHARDGSIAGSCLTYGLPPEKPNISCSRNKMDLTCRMTPGAHEFTFLHT 130
 QY 121 NYSLKYLKRWYGODNCEEHHTVGPCHSHPKDLALFTPEIWEATNRLGARSADVLT 180
 DB 131 NYSLKYLKRWYGODNCEEHHTVGPCHSHPKDLALFTPEIWEATNRLGARSADVLT 190

OY 181 DVLDTTDPDPDVHVSNGLELDOLSTRWVSPALNDLFOAKYQIRRVEDSVDMKVV 240
DB 191 DILDVTTDPDPDVHVSNGLELDOLSTRWVSPALNDLFOAKYQIRRVEDSVDMKVV 250
OY 241 DDVSNQTSCLAGLPGTVYFVQVRCNPFGIYSKKAG 278
DB 251 DDVSNQTSCLAGLPGTVYFVQVRCNPFGIYSKKAG 288

Search completed: September 17, 1999, 03:08:15
Job time: 306 sec

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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:41:08 ; Search time 53.94 seconds

(without alignments)
50.860 Million cell updates/sec

ALIGNMENTS

40	135.5	9.0	888	1	US-08-445-640-35	Sequence 35, Appl
41	134	8.9	229	2	US-08-684-687-2	Sequence 2, Appl1
42	133.5	8.9	719	1	US-07-943-843-4	Sequence 4, Appl1
43	133.5	8.9	719	2	US-08-347-003-4	Sequence 4, Appl1
44	133.5	8.9	1452	2	US-08-652-971-4	Sequence 4, Appl1
45	132	8.8	230	3	PCT-US93-09636-6	Sequence 6, Appl1

Title: US-09-037-657-19
Perfect score: 1505
Sequence: 1 PTLIGSSLOATCSIHGDP.....VFYVQVRCNPFQYSSKKAG 278

Scoring table: BLOSUM62
106577 segs, 9866381 residues

Database: Issued Patents:AA:*
1: /cg2.6/ptodata/2/1aa/5A.COMB.pep:*
2: /cg2.6/ptodata/2/1aa/5B.COMB.pep:*
3: /cg2.6/ptodata/2/1aa/PTUS9.COMB.pep:*
4: /cg2.6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	290	19.3	708	1	US-07-797-556-2
2	290	19.3	708	1	US-08-308-881-2
3	290	19.3	708	3	PCT-US95-06530-2
4	222	14.8	836	1	US-07-923-976-4
5	222	14.8	771	1	US-07-923-976-6
6	222	14.8	863	1	US-07-923-976-8
7	221.5	14.7	837	1	US-07-923-976-2
8	199	13.2	602	2	US-08-419-653-6
9	184	12.2	572	2	US-08-419-653-5
10	178	11.8	862	2	US-08-685-118-2
11	178	11.8	862	2	US-08-915-495-2
12	172.5	11.5	372	1	US-07-865-878A-4
13	172.5	11.5	372	1	US-07-676-647-2
14	172.5	11.5	372	1	US-08-449-329-2
15	172.5	11.5	372	2	US-08-445-073-2
16	172.5	11.5	372	3	PCT-US91-03866-2
17	166	11.0	635	1	US-08-184-327A-4
18	166	11.0	635	3	PCT-US95-00670-4
19	165.5	11.0	633	1	US-08-250-859-17
20	165.5	11.0	633	1	US-08-490-803-17
21	165.5	11.0	633	3	PCT-US94-08806-17
22	165.5	11.0	633	3	PCT-US95-01775-17
23	165.5	11.0	633	3	PCT-US95-16626-7
24	159.5	10.6	626	1	US-08-184-327A-2
25	159.5	10.6	482	1	PCT-US95-00670-2
26	159.5	10.6	482	3	PCT-US95-00670-8
27	159.5	10.6	482	3	US-07-797-556-6
28	147.5	9.8	1001	1	US-07-943-843-6
29	147.5	9.8	1001	1	US-07-943-843-6
30	147.5	9.8	1097	1	US-08-347-003-2
31	147.5	9.8	1097	2	US-08-347-003-6
32	147.5	9.8	1097	2	US-08-347-003-6
33	146	9.7	569	1	US-08-355-888A-8
34	146	9.7	569	2	US-08-693-697-33
35	146	9.7	569	2	US-08-693-697-33
36	146	9.7	569	2	US-08-693-697-33
37	146	9.7	569	2	US-08-693-697-33
38	145	9.6	908	2	US-08-588-526-3
39	141	9.4	960	2	US-08-588-190-3

RESULT 1
US-07-797-556-2
Sequence 2, Application US/07/797556

Patent No. 5262522
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
TITLE OF INVENTION: Inhibitory factor
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/797,556
FILING DATE: 19911122
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2607
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
TELEFAX: 206-587-0606

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-797-556-2

Query Match 19.3%, Score 290, DB 1, Length 708;
Best Local Similarity 28.38%, Pred. No. 1.2e-21;
Matches 77; Conservative 47; Mismatches 136; Indels 12; Gaps 6;

QY	1	PTLIGSSLOATCSIHGDP	19.3%	Score 290, DB 1, Length 708;	Sequence 2, Appl1
DB	36	PVVOHSHNFTAVCVLKEKCMDFHNNANTYWKTNHFTPEQITINRTASSVFTDIA	28.38%	Pred. No. 1.2e-21;	Sequence 2, Appl1
QY	58	GSROGSGNVLVCHADGSIILAGSCLYVGLPEPEKFNISCSWRNMKDLTCRTPGAHGETF	47%	Mismatches 136; Indels 12; Gaps 6;	Sequence 35, Appl1
DB	96	SLNIGLTCNLTFLFGLQENYGITIISLPEKPNKLSIYNEGKMKCEWDGGR--ETH			Sequence 2, Appl1
QY	118	LATNLSLTKLRTVQODTCEYHNVGPHSCHIRDLALFTPEYIWEATRLGARSVD			Sequence 4, Appl1
DB	154	LETNFTLSEWATNHFADCKAKRDT--PTSCVTYSTVYFVNIEVWEAENALGKVS			Sequence 4, Appl1
QY	178	LTIDVLDVYTDPPDVYVRVGGLEDQLSVRWSPPLKDFLQAVQVIRYVEDSDV			Sequence 4, Appl1
DB	212	INFDVYVYKRNPNPNLSVITSEISLTKLKTWTN-PSIKSVII-LATINIQYRKDKASTW			Sequence 4, Appl1
QY	238	KVY--DDVSNQTSCLAGLPGTYFVQVRC			Sequence 6, Appl1

DB 270 SQIPEDTASTRSSFTVODLKPFTEYVFRIRC 301

RESULT 2

US-08-308-881-2

Sequence 2, Application US/08308881

Patent No. 5783672

GENERAL INFORMATION:

APPLICANT: Mosley, Bruce

APPLICANT: Cosman, David J.

TITLE OF INVENTION: Receptor for Oncostatin M

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Apple 7.1

SOFTWARE: Microsoft Word, Version 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/308,881

FILING DATE: 12-SEP-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/249,553

FILING DATE: 26-MAY-1994

ATTORNEY/AGENT INFORMATION:

NAME: Seese, Kathryn A.

REGISTRATION NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 2614-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

TELEX: 756822

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 708 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-308-881-2

Query Match

Best Local Similarity 19.3%; Score 290; DB 2; Length 708;

Matches 77; Conservative 47; Mismatches 136; Indels 12; Gaps 6;

DB 1 PTLIGSSLOATCSIHG---DTGATAGLTYWTLNGRRLPSELRLNTSLALALANLN 57
DB 36 PVOVLHNSFTAVCVLKEKCMDFHVNANNTYVWKTNHTIPKEQYTIINRTASSVTFTDIA 95
DB 58 GSRQSGDNLYCHARDGSIAGSCLVYGLPEPEKFNISCSWRNKKDLTCWTGAGHGETF 117
DB 96 SLNIQLTNCNLTITGQLEONYGIIISGLPEPEKPNKLSCLVNEGKKRCMDGR--ETH 153
DB 118 LHTNYSKLYKLWYGDONTCEHYTVGPHSCHIPKDLALFTPEIWEATNRLGSARSDV 177
DB 154 LETNFTLKSEWATHKFAADCKAKRDT--PTSCVDYSTVYFVNIEVWEAENALGKVTSDH 211
DB 178 LITDLVDVYTTDPPPPVHVSVRVGLLEQDLSVRVSPALKDLEQAKYQIRYVEDSDV 237
DB 212 INFDPYKVKPNPNNHLSVINSSELSILKLTWTN-PSISVYI-LKYNIQYRTKASTW 269
DB 238 KVV---DVSNOTSCRLAGLKGFTGVYVQVRC 266
DB 270 SQIPEDTASTRSSFTVODLKPFTEYVFRIRC 301

RESULT 3

PCT-US95-06530-2

Sequence 2, Application PC/TUS9506530

GENERAL INFORMATION:

APPLICANT: Mosley, Bruce

APPLICANT: Cosman, David J.

TITLE OF INVENTION: Receptor for Oncostatin M

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/06530

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/308,881

FILING DATE: 09-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: Anderson, Kathryn A.

REGISTRATION NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 2614-WO

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

TELEX: 756822

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 708 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-06530-2

Query Match

Best Local Similarity 19.3%; Score 290; DB 3; Length 708;

Matches 77; Conservative 47; Mismatches 136; Indels 12; Gaps 6;

DB 1 PTLIGSSLOATCSIHG---DTGATAGLTYWTLNGRRLPSELRLNTSLALALANLN 57
DB 36 PVOVLHNSFTAVCVLKEKCMDFHVNANNTYVWKTNHTIPKEQYTIINRTASSVTFTDIA 95
DB 58 GSRQSGDNLYCHARDGSIAGSCLVYGLPEPEKFNISCSWRNKKDLTCWTGAGHGETF 117
DB 96 SLNIQLTNCNLTITGQLEONYGIIISGLPEPEKPNKLSCLVNEGKKRCMDGR--ETH 153
DB 118 LHTNYSKLYKLWYGDONTCEHYTVGPHSCHIPKDLALFTPEIWEATNRLGSARSDV 177
DB 154 LETNFTLKSEWATHKFAADCKAKRDT--PTSCVDYSTVYFVNIEVWEAENALGKVTSDH 211
DB 178 LITDLVDVYTTDPPPPVHVSVRVGLLEQDLSVRVSPALKDLEQAKYQIRYVEDSDV 237
DB 212 INFDPYKVKPNPNNHLSVINSSELSILKLTWTN-PSISVYI-LKYNIQYRTKASTW 269
DB 238 KVV---DVSNOTSCRLAGLKGFTGVYVQVRC 266
DB 270 SQIPEDTASTRSSFTVODLKPFTEYVFRIRC 301

RESULT 4

US-07-923-976-4
; Sequence 4, Application US/07923976
; Patent No. 5574136
; GENERAL INFORMATION:
; APPLICANT: Nagata, Shigekazu
; APPLICANT: Fukunaga, Rikio
; TITLE OF INVENTION: DNA Encoding Granulocyte
; TITLE OF INVENTION: Colony-Stimulating Factor Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones, Tullar & Cooper, P.C.
; STREET: P.O. Box 2266 Eads Station
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/923,976
; FILING DATE: 19920922
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 74539/1990
; FILING DATE: 23-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 176629/1990
; FILING DATE: 03-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP91/00375
; FILING DATE: 22-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hellwege, James W.
; REGISTRATION NUMBER: 28,808
; REFERENCE/DOCKET NUMBER: 514853
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-415-1500
; TELEFAX: 703-415-1508
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 836 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-923-976-4

Query Match 14.88; Score 222; DB 1; Length 836;
Best Local Similarity 29.28; Pred. No. 1.5e-14;
Matches 84; Conservative 41; Mismatches 129; Indels 34; Gaps 14;
QY 1 PTLIGSSLOATCSHGTPGTAE-GLYTLNGRRRLPSELRLN--TSTLALANLN 57
DB 34 PIVHGDPTTASCILKQNCSHLDPQILMRGALPGRGQRSDGQESITLPHLN 93
QY 58 GSROOSGNLVCHADGS---ILAGSCLYVLPPKPPNISC-WSRNNKMDLTCRWTPGAH 113
DB 94 HTQA-----FLSCCLNMGNSLQILDVELRAGYPAIPNHTSLMLTSSILCQWEPGP- 149
QY 114 GETFLHTVYSIK-YLTRYGQ---DNCEEHYTVGPHSCHIP-KDLAFTPEYIWEATN 168
DB 149 -ETHLPSTFTLKSEKSRNCQOGDSILDCVPRKQSHCCIPRKHLLLYQNMGIWQAE 207
QY 169 RLGSARSDVLTLDVLY-----TDPDPDVHVSRYGGLLEDOLSVRWSPPALKDFL 220
DB 208 ALGISMSPQLCLDPRDLYVKLEPMLRTMDPSPEAAPQAGCQ---LCW--EFWQPGH 261
QY 221 FOAKQIYRYVE-DSVDMKVVDVSNQT-SCRLAGLKPQTYFYVQVRC 266
DB 262 INQKELHKKPRGSEASWALVGPLLEALQYELCGILPATATYTIQIRC 309

RESULT 5
US-07-923-976-6
; Sequence 6, Application US/07923976
; Patent No. 5574136
; GENERAL INFORMATION:
; APPLICANT: Nagata, Shigekazu
; APPLICANT: Fukunaga, Rikio
; TITLE OF INVENTION: DNA Encoding Granulocyte
; TITLE OF INVENTION: Colony-Stimulating Factor Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones, Tullar & Cooper, P.C.
; STREET: P.O. Box 2266 Eads Station
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/923,976
; FILING DATE: 19920922
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 74539/1990
; FILING DATE: 23-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 176629/1990
; FILING DATE: 03-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP91/00375
; FILING DATE: 22-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hellwege, James W.
; REGISTRATION NUMBER: 28,808
; REFERENCE/DOCKET NUMBER: 514853
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-415-1500
; TELEFAX: 703-415-1508
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-923-976-6

Query Match 14.88; Score 222; DB 1; Length 771;
Best Local Similarity 29.28; Pred. No. 1.4e-14;
Matches 84; Conservative 41; Mismatches 129; Indels 34; Gaps 14;
QY 1 PTLIGSSLOATCSHGTPGTAE-GLYTLNGRRRLPSELRLN--TSTLALANLN 57
DB 34 PIVHGDPTTASCILKQNCSHLDPQILMRGALPGRGQRSDGQESITLPHLN 93
QY 58 GSROOSGNLVCHADGS---ILAGSCLYVLPPKPPNISC-WSRNNKMDLTCRWTPGAH 113
DB 94 HTQA-----FLSCCLNMGNSLQILDVELRAGYPAIPNHTSLMLTSSILCQWEPGP- 149
QY 114 GETFLHTVYSIK-YLTRYGQ---DNCEEHYTVGPHSCHIP-KDLAFTPEYIWEATN 168
DB 149 -ETHLPSTFTLKSEKSRNCQOGDSILDCVPRKQSHCCIPRKHLLLYQNMGIWQAE 207
QY 169 RLGSARSDVLTLDVLY-----TDPDPDVHVSRYGGLLEDOLSVRWSPPALKDFL 220
DB 208 ALGISMSPQLCLDPRDLYVKLEPMLRTMDPSPEAAPQAGCQ---LCW--EFWQPGH 261
QY 221 FOAKQIYRYVE-DSVDMKVVDVSNQT-SCRLAGLKPQTYFYVQVRC 266

Db 262 INOKELRHKPORGESAWLVGPILEALQYELGGLPATATYTCIRC 309

RESULT 6

US-07-923-976-8
Sequence 8, Application US/07923976
Patent No. 5574136

GENERAL INFORMATION:

APPLICANT: Nagata, Shigekazu

APPLICANT: Fukunaga, Rikio

TITLE OF INVENTION: DNA Encoding Granulocyte

TITLE OF INVENTION: Colony-Stimulating Factor Receptor

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESS: Jones, Tullar & Cooper, P.C.

STREET: P.O. Box 2266 Eads Station

CITY: Arlington

STATE: Virginia

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/923,976

FILING DATE: 19920922

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 74539/1990

FILING DATE: 23-MAR-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 176629/1990

FILING DATE: 03-JUL-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP91/00375

FILING DATE: 22-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Hellwege, James W.

REGISTRATION NUMBER: 28,808

REFERENCE/DOCKET NUMBER: 514853

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-415-1508

TELEFAX: 703-415-1500

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 863 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-923-976-8

Query Match 14.8%; Score 222; DB 1; Length 863;

Best Local Similarity 29.2%; Pred. No. 1.6e-14;

Matches 84; Conservative 41; Mismatches 129; Indels 34; Gaps 14;

Db 1 PTLIGSSLOATCSHGDPGATAG-GLWTNGRRLPSELRL--NSTLALANL 57

Db 34 PIVHLDGDPYLAACITIKONCHLDPEQILRLAELOPGROQRSLDGTQESTITLPHN 93

Db 58 GSRQSGDNLYCHARDG--ILAGSLVYGLPERKFNISC-WSNMMDLTCRWTPGAH 113

Db 94 HTQA---FLSCGLMNGNSQLIDQYELRAGYPPALPHNLSCLMNTLSSLCQWEPGP- 149

Db 114 GEFFLNTNLSK-YKLRTYG--DNTCEYHNVGPHSCHIP-KDLALFTPYEIVWYATNL 168

Db 149 -EHLPTSFILKSFKSGKNCOTGDSILDCVPRDQSGHCCIPKRLHLLYONGMIVQAEH 207

Db 169 RLGSARSVDLTLDVLDVY-----TTDPDPVHVSRYGGLDQSLSVRYVSPALKDLF 220

Db 208 ALGTSMSPOLCLDPMVDVYKLEPPALRTMDSPEAAPQACLO---LCW--EPKOPGLH 261

QY 221 FOARTQIYRYE-DSVDMKVTVDVSNCT-SCRLAGKAGTYFFQVRC 266

RESULT 7

US-07-923-976-2
Sequence 2, Application US/07923976
Patent No. 5574136

GENERAL INFORMATION:

APPLICANT: Nagata, Shigekazu

APPLICANT: Fukunaga, Rikio

TITLE OF INVENTION: DNA Encoding Granulocyte

TITLE OF INVENTION: Colony-Stimulating Factor Receptor

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESS: Jones, Tullar & Cooper, P.C.

STREET: P.O. Box 2266 Eads Station

CITY: Arlington

STATE: Virginia

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/923,976

FILING DATE: 19920922

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 74539/1990

FILING DATE: 23-MAR-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 176629/1990

FILING DATE: 03-JUL-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP91/00375

FILING DATE: 22-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Hellwege, James W.

REGISTRATION NUMBER: 28,808

REFERENCE/DOCKET NUMBER: 514853

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-415-1508

TELEFAX: 703-415-1500

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 837 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-923-976-2

Query Match 14.7%; Score 221.5; DB 1; Length 837;

Best Local Similarity 28.9%; Pred. No. 1.7e-14;

Matches 83; Conservative 46; Mismatches 127; Indels 31; Gaps 14;

QY 1 PTLIGSSLOATCSHGDPGATAG-LYWTNGRRL-PSELRL--NSTLALANL 56

Db 34 PIVHLDGDPYLAACITISPNCSKIDQAKILMRQDDEPIQGDQNHLPDQTESLITLPHL 93

Db 57 NSRQSGDNLYCHARDG--ILAGSLVYGLPERKFNISCWSR-NMKDLTCRWTPGAH 115

Db 94 HT-QLPFLVPMEDSVOLLDQAEIHAGYPPASPSNLSCLMHLTNSLYCQWEPGP-E 150

QY 116 TELATNTNLSK-YKLRTY--WYGDNTCEYHNVGPHSCHIP-KDLALFTPYEIVWYATNL 170

Db 151 TELPTSFILKSFKSRADQYGGDTIPDCAKKRNNCSIPRNNLLLYOYMAIWOAEHNL 210

QY 171 GSARSVDLTLDVLDVYTTDPP-----PDVHVSRYGGLDQSLSVRYVSPALKDLF 221

Db 211 GSESEKCLDPMDVVKLEPPMLQALDIGPVVSHQPGCL-----WLSWKPKSEYM 263
 QY 222 OAKTOIRYRYE-DSVDMKVVDDY-SNOTSCRLAGLKPGTYFYQVRC 266
 Db 264 EOECELRYPOLKGNMTLVFHLPSKDOFELGGLHOAPYTLQMR 310

RESULT 8

US-08-419-652-6
 Sequence 6, Application US/08419652
 Patent No. 5831007

GENERAL INFORMATION:

APPLICANT: Chua, Anne O
 APPLICANT: Gubler, Ulrich A
 TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hoffmann-La Roche Inc.
 STREET: 340 Kingsland Street
 CITY: Nutley
 STATE: New Jersey
 COUNTRY: United States of America
 ZIP: 07110-1199

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: PC compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/419,652
 FILING DATE: 11-APR-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/248,532
 FILING DATE: 31-MAY-1994
 PRIOR APPLICATION NUMBER: US 08/094,713
 FILING DATE: 19-JUL-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Kass, Alan P
 REGISTRATION NUMBER: 32142
 REFERENCE/DOCKET NUMBER: CD 9174
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (201) 235-4205
 TELEFAX: (201) 235-3500
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 602 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Region
 LOCATION: 1..602
 OTHER INFORMATION: /note= "Represents residues 98 to
 OTHER INFORMATION: 731 of human granulocyte colony-stimulating
 factor-receptor."
 US-08-419-652-6

Query Match 13.2%; Score 199; DB 2; Length 602;
 Best Local Similarity 32.1%; Pred. No. 2.2e-12;
 Matches 63; Conservative 28; Mismatches 81; Indels 24; Gaps 10;

QY 87 PPEKPFNISC-SRNNKDLTCRWTPGAHGETFLHTNYSLK-YKLRVYGQ---DNTCEEYH 141
 Db 3 PPAIPRNLSCMLNLTSSILCOWEPGP--ETHLPSTFLKSFSSRNCQOGSDIIDCVF 60
 QY 142 TVGPHSCHLP-KDLALFTPEIWEATNRIGSARSVDLTLDVDTV-----TTDPPP 192
 Db 61 KGGOSHCCIPRKHLLLYQNNGIWVQAEMLGTSMSPOLCLDPADVVKLEPPMLRTMDPSP 120
 QY 193 DVHVSNGVGLLEQLSVRWVSPALKDPLFOAKTOIRYRYE-DSVDMKVVDDVSNQI-SCR 250

Db 121 EAAFPAGGLQ-----LCW--EPWQPLHINQKELNKRQGRGASNAVLGPLELQYRE 174
 QY 251 LAGLPGTYFYQVRC 266
 Db 175 LCGLLPATVATLQIRC 190

RESULT 9

US-08-419-652-5
 Sequence 5, Application US/08419652
 Patent No. 5831007

GENERAL INFORMATION:

APPLICANT: Chua, Anne O
 APPLICANT: Gubler, Ulrich A
 TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hoffmann-La Roche Inc.
 STREET: 340 Kingsland Street
 CITY: Nutley
 STATE: New Jersey
 COUNTRY: United States of America
 ZIP: 07110-1199

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: PC compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/419,652
 FILING DATE: 11-APR-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/248,532
 FILING DATE: 31-MAY-1994
 PRIOR APPLICATION NUMBER: US 08/094,713
 FILING DATE: 19-JUL-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Kass, Alan P
 REGISTRATION NUMBER: 32142
 REFERENCE/DOCKET NUMBER: CD 9174
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (201) 235-4205
 TELEFAX: (201) 235-3500
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 572 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Region
 LOCATION: 1..572
 OTHER INFORMATION: /note= "Represents residues 124 to
 OTHER INFORMATION: 742 of human gp130."
 US-08-419-652-5

Query Match 12.2%; Score 184; DB 2; Length 572;
 Best Local Similarity 27.2%; Pred. No. 7.3e-11;
 Matches 50; Conservative 21; Mismatches 59; Indels 54; Gaps 5;

QY 86 LPEKPFNISC-SRNNKDLTCRWTPGAHGETFLHTNYSLK-YKLRVYGQ---DNTCEEYH 145
 Db 1 LPEKPFNISC-SRNNKDLTCRWTPGAHGETFLHTNYSLK-YKLRVYGQ---DNTCEEYH 145
 QY 146 HSCHEPKDLALFTPEIWEATNRIGSARSVDLTLDVDTV-----TTDPPP 192
 Db 57 TSCOTVSYVYEVNIEVWEAENALGKVTSD-----HIN----- 91
 QY 206 LSVRWVSPALKDPLFOAKTOIRYRYE-DSVDMKVVDDVSNQI-SCR 250

```
Db      91 -----:| | |: | | :| | |  
        F0YRTKDAWSQIPEDASTSTSSFTVODLKFTEVF 12  
  
Qy      263 QVRC 266.:| |  
Db     130 RIRC 133
```

RESULT 10
 US-08-685-118-2
 Sequence 2, Application US/08685118
 Patent No. 5840530
 GENERAL INFORMATION:
 APPLICANT: Gubler, Ulrich A
 APPLICANT: Presky, David H
 TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hoffmann-La Roche Inc.
 STREET: 340 Kingsland street
 CITY: Nutley
 STATE: NJ
 COUNTRY: USA
 ZIP: 07110
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/685,118
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Silverman, Robert A.
 REGISTRATION NUMBER: 35,682
 REFERENCE/DOCKET NUMBER: CD 9195
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (201) 235-2363
 TELEFAX: (201) 235-2363
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 862 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-685-118-2

Query Match	11.8%	Score 178;	DB 2;	Length 862;
Best Local Similarity	24.8%	Pred.No. 5.5e-10;		
Matches 73; Conservative	43;	Mismatches 106;	Indels 72;	Gaps 12

```

Oy      3  LLIGSLIATCSIHDDTFGAATAEGLMYTL-----NORRLPESESR-L  44
Db      41  ILIGSTVITCSL-----KPRGCGFHRSRRKKLLYFEDRRINHHSHLSLNSQVTTGJPL  94
Oy      45  NTSTLALALANLNGSRQSGDNLYCHARDGSTILAGSCLLYGLPPEKRPENISCMWSHNK-D  103
Db      95  GTTLEFVCKLACINSDEIO-----ICGAEIFFYGAAPROPONCSIOKGEQGT  140
Oy     104  LTCRATPGAHGTEFLHTYVSLKY-----KLRWYGO--DNTCEERYHVVG-----PHSOHI  150
Db     141  VACTWERRG--DTHLYTEYITLQSGPKNLITWOKCKDLYC--DYLDGFGNLTLPESPESNFT  190
Oy     151  PKDLALFTPEYELWEATNRLGARSADVLTLDVATVYTDPEPDVHVSRYVGLEQDLSYRW  210
Db     198  AK-----YTAVNSIGSSSSSLPTFTFLDIYRPLRPMDIDIKFOKASVSRCITLYW  240
Oy     211  VSPPALKDFLFAKQVQIRRVEDSDVMKYVDDVSNQTSQRLAGLKPQGVYFYQV  264
Db     247  -----RDGGLVLLNRLRRPNSRLMNRYNVTAKGRHDLDLPLPEYEFQI  294

```

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RESULT 11
US-08-915-495-2
Sequence 2, Application US/08915495
Patent No. 5852176
GENERAL INFORMATION:
APPLICANT: GUDLEY, ULRICH A
APPLICANT: PRESKY, DAVID H
TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,495
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/665,118
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Robert A.
REGISTRATION NUMBER: 35,682
REFERENCE/DOCKET NUMBER: CD 9195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-2863
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 862 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-915-495-2

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Query Match	11.8%	Score 178	DB 2	Length 862
Best Local Similarity	24.8%	Pred. No. 5.5e-10		
Matches 73; Conservative	43;	Mismatches 106;	Indels 72;	Gaps 12;

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0Y 3 LLISSLOATGSHGDFGATGAEIYWTL-----NRRRLPSELSR-L 44
Db 41 ILLSIVATITSL-----KRGCGFIH SRKNKLLIKFDRINFHHSHLSNQVYTGPL 94
0Y 45 NTSLTALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLPPKRPNISCWSRNK-D 10
Db 95 GTTFVFCFKACINDEID-----IGAEIFVVAAPQONLSCIOKEGGT 144
0Y 104 LTCMTGPAHGEFLHNYSKY----KLRYGQ--DNTCEYHTVG-----PHSGHI 155
Db 141 VACIWERQ--DTHIYETITQLSGPKNLVQCKCKDLYC--DYLDGINTLPESPESFT 19
0Y 151 PKDIALFTPYEIMWEATNRIGASASDVLITLVDVYTTDPPDVVHVRGLEDOLSYRM 21
Db 198 AK-----TVAVSISSSSLSLSTETFFLDIVRLPMDIRIKFOKASVSRCLTYM 244
0Y 211 VSPALDGLFOAQYQYQRYREDSDVMKVVYDVSNOISCRLAGIKPGVYVYVQV 264
Db 247 -----RDEGLVTLNRLRIKRPSSNRIMNVAVYAKGCHHLLDKPFTETFEQI 294

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RESULT 12
US-07-865-878A-4
; Sequence 4, Application US/07865878A

Patent No. 5332672
GENERAL INFORMATION:
APPLICANT: Yancopoulos, George D. et al.
TITLE OF INVENTION: Cell Free Ciliary Neurotrophic
Factor/Receptor Complex
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/865,878A
FILING DATE: 19911202
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/801/562
FILING DATE: 02-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-082
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-07-865-878A-4

Query Match 11.5%; Score 172.5; DB 1; Length 372;
Best Local Similarity 26.8%; Pred. No. 6e-10;
Matches 73; Conservative 35; Mismatches 123; Indels 41; Gaps 14;
QY 5 IGSSLOATCSIHGDPGATAGELWTLNGRRLPSELSRLNTSTLALANNGSRQSG 64
DB 38 LGSVDTLPCGTANMDAAVT-----WRVNGTDLPD-----LHGELGHS 84
QY 65 DNLVCHARDGSLIAGS-CLYVGLPPEKPFNISCWGRNM-KDLTCRM-----TGANGE 115
DB 85 GLYACFHDSDWMLRQVLLHGLPPREP-VLSCRSNTYPKGYCSHMLPTPIYINTFN 143
QY 116 TELHTNYSIKYKLRMYGDNQCEEHYVGPCHSHPKDLALFT--PYELWEATNRLGSA 173
DB 144 TVLHSGSKIM-----VCEKDPAL-KNRCHI-RYVHLSTIKYKVISVSNALGH- 190
QY 174 RSDVLTLDLVDTDDPPDVHVSRYGLEDOLSVRWSPPLAKD-FLQAYQYQIRYVE 232
DB 190 NATATFDEFETIVKDPENNVARVPSPNRLLEVLTWQTPSWPDESPFLKFLIRRL 249
QY 233 DSDVWKVVDVSNQTSCLAGLPGTYFVOY 264
DB 250 ILDMQOHV-ELSDGTAHTITDAVAGREYIIQY 280

RESULT 13
US-07-676-647-2
Sequence 2, Application US/07676647
Patent No. 5426177
GENERAL INFORMATION:
APPLICANT: Davis, Samuel

APPLICANT: Squinto, Stephen P.
APPLICANT: Furch, Mark E.
APPLICANT: Yancopoulos, George D.
TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/676,647
FILING DATE: 19910328
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-676-647-2

Query Match 11.5%; Score 172.5; DB 1; Length 372;
Best Local Similarity 26.8%; Pred. No. 6e-10;
Matches 73; Conservative 35; Mismatches 123; Indels 41; Gaps 14;
QY 5 IGSSLOATCSIHGDPGATAGELWTLNGRRLPSELSRLNTSTLALANNGSRQSG 64
DB 38 LGSVDTLPCGTANMDAAVT-----WRVNGTDLPD-----LHGELGHS 84
QY 65 DNLVCHARDGSLIAGS-CLYVGLPPEKPFNISCWGRNM-KDLTCRM-----TGANGE 115
DB 85 GLYACFHDSDWMLRQVLLHGLPPREP-VLSCRSNTYPKGYCSHMLPTPIYINTFN 143
QY 116 TELHTNYSIKYKLRMYGDNQCEEHYVGPCHSHPKDLALFT--PYELWEATNRLGSA 173
DB 144 TVLHSGSKIM-----VCEKDPAL-KNRCHI-RYVHLSTIKYKVISVSNALGH- 190
QY 174 RSDVLTLDLVDTDDPPDVHVSRYGLEDOLSVRWSPPLAKD-FLQAYQYQIRYVE 232
DB 190 NATATFDEFETIVKDPENNVARVPSPNRLLEVLTWQTPSWPDESPFLKFLIRRL 249
QY 233 DSDVWKVVDVSNQTSCLAGLPGTYFVOY 264
DB 250 ILDMQOHV-ELSDGTAHTITDAVAGREYIIQY 280

RESULT 14
US-08-449-329-2
Sequence 2, Application US/08449329
Patent No. 5648334
GENERAL INFORMATION:
APPLICANT: Davis, Samuel
APPLICANT: Squinto, Stephen P.
APPLICANT: Furch, Mark E.
APPLICANT: Yancopoulos, George D.
TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,329
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/700,677
FILING DATE: 15-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-065
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-449-329-2

Query Match 11.5%; Score 172.5; DB 1; Length 372;
Best Local Similarity 26.8%; Pred. No. 6e-10;
Matches 73; Conservative 35; Mismatches 123; Indels 41; Gaps 14;

QY 5 IGSSLOATCSIHGDTPGATAGELWYTLNGRRPSELRLNTSLALANLNGSQSG 64
DB 38 LGSVDTLPCGTANMDAAVT-----WRVNGTDLAPD---LLNGSOLV-----LHGLELGS 84
QY 65 DNLVCHARDGSLIAGS-CLIVGLPPEKPFNISCWSRNM-KDITCRW-----TEGARGE 115
DB 85 GLYACFHRDSWHLRHQVLLHVLGPPREPV-LSCRSNTYPKGYCSMHLPTPTIINTENV 143
QY 116 TELHNTVSLKYLKRLMYGDNCEEHYVGPSCHIPKDLAFT--PYEIWEATNRLGSA 173
DB 144 TVLHGSKIM-----VCEKDPAL-KNRCHI-RYWHLPSTIKYKVISVSNALGH- 190
QY 174 RSDVTLFLVDLVYTTDPPPDVHVSRYVGLLEQLSVRWVSPPALKD-FLFOAKYQIRYRE 232
DB 190 NATATTFEFTIVKRPDENNVARVPSPNPRLEVTWQTPSWPDPESPFLKFLRYRPL 249
QY 233 DSVDMKVVDDVSNQTSCLAGLKPGTYFYVOY 264
DB 250 ILDGWOHV-ELSDGTATHTTDAVAGKEYTIQY 280

RESULT 15
US-08-445-073-2
Sequence 2, Application US/08445073
Patent No. 5849897
GENERAL INFORMATION:
APPLICANT: Davis, Samuel
APPLICANT: Squinto, Stephen P.
APPLICANT: Furtth, Mark E.
APPLICANT: Yancopoulos, George D.
TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,073
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,647
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-445-073-2

Query Match 11.5%; Score 172.5; DB 2; Length 372;
Best Local Similarity 26.8%; Pred. No. 6e-10;
Matches 73; Conservative 35; Mismatches 123; Indels 41; Gaps 14;

QY 5 IGSSLOATCSIHGDTPGATAGELWYTLNGRRPSELRLNTSLALANLNGSQSG 64
DB 38 LGSVDTLPCGTANMDAAVT-----WRVNGTDLAPD---LLNGSOLV-----LHGLELGS 84
QY 65 DNLVCHARDGSLIAGS-CLIVGLPPEKPFNISCWSRNM-KDITCRW-----TEGARGE 115
DB 85 GLYACFHRDSWHLRHQVLLHVLGPPREPV-LSCRSNTYPKGYCSMHLPTPTIINTENV 143
QY 116 TELHNTVSLKYLKRLMYGDNCEEHYVGPSCHIPKDLAFT--PYEIWEATNRLGSA 173
DB 144 TVLHGSKIM-----VCEKDPAL-KNRCHI-RYWHLPSTIKYKVISVSNALGH- 190
QY 174 RSDVTLFLVDLVYTTDPPPDVHVSRYVGLLEQLSVRWVSPPALKD-FLFOAKYQIRYRE 232
DB 190 NATATTFEFTIVKRPDENNVARVPSPNPRLEVTWQTPSWPDPESPFLKFLRYRPL 249
QY 233 DSVDMKVVDDVSNQTSCLAGLKPGTYFYVOY 264
DB 250 ILDGWOHV-ELSDGTATHTTDAVAGKEYTIQY 280

Search completed: September 16, 1999, 20:41:09
Job time: 5438 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:42:09 ; Search time 49.27 Seconds

(Without alignments)
226.065 Million cell updates/sec

Title: US-09-037-657-19

Perfect score: 1505
Sequence: 1 PTLIGSSLQATCSIHGDRP.....VFVOVRCNPFYIGSKKXG 278

Scoring table: BLOSUM62

Searched: 122810 seqs, 40065486 residues

Database:

PIR_60: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	308.5	20.5	622	2	A40144	prolactin receptor
2	302	20.1	206	2	A57018	prolactin receptor
3	292	19.4	830	2	I50455	prolactin receptor
4	291	19.3	303	2	I77524	prolactin receptor
5	291	19.3	292	2	I77525	prolactin receptor
6	291	19.3	608	2	I53269	prolactin receptor
7	290	19.3	918	2	A36337	membrane glycoprot
8	288.5	19.2	610	2	A34631	lactogen receptor
9	288.5	19.2	610	2	A36116	prolactin receptor
10	288.5	19.2	412	2	A41070	prolactin receptor
11	288.5	19.2	310	2	A29884	prolactin receptor
12	286	19.0	616	2	A30304	prolactin receptor
13	281.5	18.7	918	2	A44257	interleukin-6 sign
14	281	18.7	831	2	U01655	prolactin receptor
15	279	18.5	917	2	I49699	glycoprotein 130 -
16	276	18.3	581	2	I45971	prolactin receptor
17	233	15.5	630	2	I51086	prolactin receptor
18	222	14.8	783	2	JH0329	granulocyte colony
19	222	14.8	771	2	B38252	granulocyte colony
20	222	14.8	863	2	C38252	granulocyte colony
21	221.5	14.7	837	2	A44898	granulocyte colony
22	197.5	13.1	156	2	A32868	granulocyte colony
23	190	12.6	150	2	B34631	prolactin receptor
24	178.5	11.9	372	2	I58141	lactogen receptor
25	176.5	11.7	362	2	S60614	ciliary neurotroph
26	175	11.6	422	2	I57891	growth promoting a
27	172.5	11.5	372	1	UHHUCN	interleukin-11 rec
28	166	11.0	579	2	B45266	ciliary neurotroph
29	166	11.0	635	2	A45266	MPI-P protein prec
30	164	10.9	432	2	I48343	interleukin-11 rec
31	163.5	10.9	625	2	S35317	hematopoietic grow
32	161	10.7	894	2	UC4797	leptin receptor pr
33	161	10.7	1162	2	PC4184	leptin receptor, O
34	159.5	10.6	805	3	JC4897	leptin receptor, O
35	159.5	10.6	626	2	S37622	proto-oncogene - m
36	159	10.6	638	2	B28175	somatotropin recep
37	159	10.6	894	2	S68437	leptin receptor (V
38	159	10.6	900	2	S68440	leptin receptor (V
39	159	10.6	805	2	S68441	leptin receptor (V

40	158.5	10.5	468	1	A41242	interleukin-6 rece
41	156	10.4	895	2	S74225	leptin receptor, I
42	154.5	10.3	460	2	J10145	interleukin-6 rece
43	154.5	10.3	440	2	J10144	interleukin-6 rece
44	151	10.0	638	2	S12136	somatotropin recep
45	147.5	9.8	1097	2	S17308	leukemia inhibitor

ALIGNMENTS

RESULT 1

A40144

prolactin receptor long form precursor, hepatoma and breast cancer cells - human

C:Species: Homo sapiens (man)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Sep-1998

C:Accession: A40144

R:Boutin, J.M.; Ederly, M.; Shirota, M.; Jolicoeur, C.; Lesueur, L.; All, S.; Gould, M.L. Endocrinol. 3, 1455-1461, 1989

A:Title: Identification of a cDNA encoding a long form of prolactin receptor in hum

A:Reference number: A40144; MUID:90114212

A:Accession: A40144

A:Molecule type: mRNA

A:Residues: 1-622 <BOU>

A:Cross-references: GB:M31661; NID:9190361; PID:9190362

C:Genetics:

A:Gene: GDB:PRLR

A:Cross-references: GDB:120315; OMIM:176761

A:Map position: 5p13.3-5p13.1

C:Keywords: glycoprotein; transmembrane protein

F:1-24/Domains: signal sequence #status predicted <SIG>

F:25-622/Product: prolactin receptor, long form #status predicted <MUT>

F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 20.5%; Score 308.5; DB 2; Length 622;

Best Local Similarity 38.5%; Pred. No. 2.4e-20;

Matches 77; Conservative 27; Mismatches 85; Indels 11; Gaps 7;

DB 76 ILASGLIVG-LPEKPNISCSNMKDLTRMTPGAHEFTLNTSLKRLMYGOD 134

DB 15 LFLNCLLNGOLPGKPEFFKCRSPNKETFLWMRPGTDG--LPTNLSLYHREGETLM 72

OY 135 NTCEYHVVGPSCHIRPD-LALFPYELIWTATNRIGARSBDVLTDVLDVYTDPPD 193

DB 73 HECPTITGGPNSCHFGQYTSMTYITMVAATQKSSFSFDELYVDYTYVQDPPLE 132

OY 194 VVSNVGGLEDOLSVRWV--SPPALKDF---LEQAKYQIRYVEDSDVKVYDVSNOTS 248

DB 133 LAV-EVKPDEKRPYLMIKMSPTLIDLTGTGFTLLYEIRLKEPKAAWE-IHFGQOTE 190

OY 249 CRMLAGKPGYTVFOVRCNP 268

DB 191 FKILSLHPGKRYLVQVRCKP 210

RESULT 2

A57018 prolactin receptor - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-Jul-1996

C:Accession: A57018

R:Fuh, G.; Wells, J.A.

J. Biol. Chem. 270, 13133-13137, 1995

A:Title: Prolactin receptor antagonists that inhibit the growth of breast cancer cel

A:Reference number: A57018; MUID:95286597

A:Accession: A57018

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-206 <RES>

A:Cross-references: GB:S78505; NID:9999114; PID:9999115

Query Match 20.1%; Score 302; DB 2; Length 206;
 Best Local Similarity 39.2%; Pred. No. 2,2e-20;
 Matches 74; Conservative 25; Mismatches 80; Indels 10; Gaps 6;

86 LPEKPFNISCWNRNMDLTCRTPGAHGETFLHTNTSLKYLKMTYGODNTCEHYTGP 145
 2 LPPGKDEIFRCRSPNRETFCWMPKPGIDG--LPTNLSLYHREGFTLMECPDIYIGSP 59
 146 HSHRIPRD-LALFTPEIWEATNRIGSARSDVLTLDVDTVTTPDPDVHVSRYGLED 204
 60 NSHFRKQYTSMTKRTIIMVYVATNOMKSSFSDELVDYVTVIYVQDPPELAV-EVKQPED 118
 205 QLSVRYV--SPPLAKDF--LFOAKYQIRYVEDSVDMKVVDVSNQTSCLAGLKPGTV 259
 119 RKRYLWIKNSPPLILDLTQGMFTLLVEIRLKPKAEMWE-IHFRAGQOTEEKIISLHGOK 177
 260 YFVQVRCNP 268
 178 YLVQVRCRP 186

RESULT 3
 prolactin receptor - pigeon
 C:Species: Columba livia (domestic pigeon)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Sep-1996
 C:Accession: I50455
 R:Chen, X.; Horseman, N.D.
 Endocrinology 135, 269-276, 1994
 A:Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor.
 A:Reference number: I50455; MUID:94283267
 A:Accession: I50455
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-830 <CHE>
 A:Cross-references: EMBL:U07694; NID:g466381; PID:g466382

Query Match 19.4%; Score 292; DB 2; Length 830;
 Best Local Similarity 37.0%; Pred. No. 1,1e-18;
 Matches 70; Conservative 29; Mismatches 78; Indels 12; Gaps 7;

87 PEKPFNISCWNRNMDLTCRTPGAHGETFLH-TNYSKYLKMTYGODNTCEHYTGP 145
 231 PEKPTIILICRSPREKFTFCWMPKPGSDG--HPTNYTLLSKESGERVYECDFYTAGP 287
 146 HSGH-LPRLALFTPEIWEATNRIGSARSDVLTLDVDTVTTPDPDV--HVSRYGGL 202
 288 NSCYDDKHTSMITLYNIVKATNEIGSNVSDPLYVDYVTVIYVQDPVNVYTELKKTNR 347
 203 EDQLSVRYVSPPLAKDF--LFOAKYQIRYVEDSVDMKVVDVSNQTSCLAGLKPGTV 259
 348 KRYLVLTW-SPPLADVRSGLTLDLDELRLKPEAEEMETI-FVGQOTHYKMSLNPGRK 405
 260 YFVQVRCNP 268
 406 YLVQVRCRP 414

RESULT 4
 prolactin receptor precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 02-Aug-1996
 C:Accession: I77524
 R:Davis, J.A.; Linzer, D.I.H.
 Mol. Endocrinol. 3, 674-680, 1989
 A:Title: Expression of multiple forms of the prolactin receptor in mouse liver.
 A:Reference number: I57699; MUID:89261824
 A:Accession: I77524
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-303 <RES>

A:Cross-references: GB:M22958; NID:g200479; PID:g200480

Query Match 19.3%; Score 291; DB 2; Length 303;
 Best Local Similarity 33.6%; Pred. No. 3,7e-19;
 Matches 82; Conservative 37; Mismatches 85; Indels 40; Gaps 10;

40 LSRLLNTSTLALANLNGSRQSGDNLYCHARDGSIAGSCLYVGLPPEKPFNISCWNR 99
 1 MSSALAYMLLVLSISLNG--QS-----PPGKREIHKCRSP 34
 100 NMKDLTCRTPGAHGETFLHTNTSLKYLKMTYGODNT--CEEHYTGPSCHIPKD-LAL 156
 35 DKETFTCMWNPESDGG--LPTNLSLYSKE--GKNYTECPDKYISGPNSECFSSKQYTSI 90
 157 FPEIWEATNRIGSARSDVLTLDVDTVTTPDPDVHVSRYGLEDQLSVRYV--PP 214
 91 WKIYITVATNEMSGSDPLYVDYVTVIYVEPPRNLT-LVKQLKDKKTYLWYKMLPP 149
 215 ALKDF--LFOAKYQIRYVEDSVDMKVVDVSNQTSCLAGLKPGTVYFVQVRCNPGI 271
 150 TITDVTGWFTEYEIRLSEADWE-IHFGHOTQFVFDLYGOKYLVOTRCKPDHG 208
 272 YGSK 275
 209 YMSR 212

RESULT 5
 prolactin receptor precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 02-Aug-1996
 C:Accession: I77525
 R:Davis, J.A.; Linzer, D.I.H.
 Mol. Endocrinol. 3, 674-680, 1989
 A:Title: Expression of multiple forms of the prolactin receptor in mouse liver.
 A:Reference number: I57699; MUID:89261824
 A:Accession: I77525
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-292 <RES>
 A:Cross-references: GB:M22959; NID:g200481; PID:g200482

Query Match 19.3%; Score 291; DB 2; Length 292;
 Best Local Similarity 33.6%; Pred. No. 3,5e-19;
 Matches 82; Conservative 37; Mismatches 85; Indels 40; Gaps 10;

40 LSRLLNTSTLALANLNGSRQSGDNLYCHARDGSIAGSCLYVGLPPEKPFNISCWNR 99
 1 MSSALAYMLLVLSISLNG--QS-----PPGKREIHKCRSP 34
 100 NMKDLTCRTPGAHGETFLHTNTSLKYLKMTYGODNT--CEEHYTGPSCHIPKD-LAL 156
 35 DKETFTCMWNPESDGG--LPTNLSLYSKE--GKNYTECPDKYISGPNSECFSSKQYTSI 90
 157 FPEIWEATNRIGSARSDVLTLDVDTVTTPDPDVHVSRYGLEDQLSVRYV--PP 214
 91 WKIYITVATNEMSGSDPLYVDYVTVIYVEPPRNLT-LVKQLKDKKTYLWYKMLPP 149
 215 ALKDF--LFOAKYQIRYVEDSVDMKVVDVSNQTSCLAGLKPGTVYFVQVRCNPGI 271
 150 TITDVTGWFTEYEIRLSEADWE-IHFGHOTQFVFDLYGOKYLVOTRCKPDHG 208
 272 YGSK 275
 209 YMSR 212

RESULT 6
 prolactin receptor, long form - mouse

C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 29-Jan-1999
 C:Accession: I53269; J10671; S34356
 R:Clarke, D.L.; Linzer, D.I.H.
 Endocrinology 133, 224-232, 1993
 A:Title: Changes in prolactin receptor expression during pregnancy in the mouse ovary.
 A:Reference number: I53269; MUID:93307149
 A:Accession: I53269
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-608 <RES>
 A:Cross-references: GB:L14811; NID:9293769; PID:9293770
 R:Moore, R.C.; Oka, T.
 Gene 134, 263-265, 1993
 A:Title: Cloning and sequencing of the cDNA encoding the murine mammary gland long-form
 A:Reference number: J10671; MUID:94085788
 A:Accession: J10671
 A:Molecule type: mRNA
 A:Residues: 1-608 <MOO>
 A:Cross-references: GB:L13593; NID:9347398; PID:9347842
 R:Edery, M.; Pezet, A.; Nandi, S.; Kelly, P.A.
 submitted to the EMBL Data Library, June 1993
 A:Description: Isolation and nucleotide sequence of a mouse cDNA prolactin receptor.
 A:Reference number: S34356
 A:Accession: S34356
 A:Molecule type: mRNA
 A:Residues: 1-557, F, 559-608 <EDE>
 A:Cross-references: EMBL:X73372; NID:9312696; PID:9312697
 C:Comment: Prolactin receptor have long form and short form which are resulted from alternative splicing.
 C:Keywords: receptor; transmembrane protein
 F:230-253/Domain: transmembrane #status predicted <TMO>

Query Match 19.3%; Score 291; DB 2; Length 608;
 Best Local Similarity 33.6%; Pred. No. 9.3e-19;
 Matches 82; Conservative 37; Mismatches 85; Indels 40; Gaps 10;

40 LSRLNTSLALANLNGSRQSGDNLVCHARDGSLAGSCLYGLPPEKPNISCMNR 99
 1 MSSALAYMLVLISILNG--QS-----PQKPIHCRSP 34
 100 MKKDLTCKRTPGAGHGTFLHTNYSLKTKRMWGQDNT--CEEYHTVGPSPHCHPKD-LAL 156
 35 DKETFCWNNPSSDGG--LPTNYSLSYKE--GEKNTYCPDPTKTSGPSNCSFSSKQYTSI 90
 157 FFPYELWEATNRIGSARSDVLLDVLVYTTDPPDVHVSRYGSGLEDOLSTRWVS--PP 214
 91 WRTYITITVATNEMGSSSTSDPLVDYTYVEPEPRNLT-LVKKQLKDKRTYLMVWMLPP 149
 215 ALKDF--LFOAKYQIRYVEDSVDMKVVDVSNOTSCHLAGLPGTGYFYVQRCNPPGI 271
 150 TITDVKTGFTMEYELRLKSEFADENE-IHFTGHOTQFVFDLYPQOKYLVOTRCKPDHG 208
 272 YGSK 275
 209 YWSR 212

RESULT 7
 A36337
 membrane glycoprotein gp130 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-Sep-1998
 C:Accession: A36337
 R:Hihi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.
 Cell 63, 1149-1157, 1990
 A:Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
 A:Reference number: A36337; MUID:91084844
 A:Accession: A36337
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-918 <HIB>

A:Cross-references: GB:M57230; NID:9186353; PID:9186354
 C:Genetics:
 A:Gene: GDB:11657; GP130
 A:Cross-references: GDB:126725; OMIM:600694
 A:Map position: 5q11-5q11
 C:Keywords: glycoprotein; membrane protein

Query Match 19.3%; Score 290; DB 2; Length 918;
 Best Local Similarity 28.3%; Pred. No. 2e-18;
 Matches 77; Conservative 47; Mismatches 136; Indels 12; Gaps 6;

1 PTLIGSSIQATCSING--DTPGATAGIYTLNGRRLPSELRLNTSLALANLN 57
 36 PYVALSNFPAVCVLEKCKDYPHVANNTYKNTNFTPKEDYTIINNTASSVTDTDA 95
 58 GSRQSGDNLVCHARDGSLAGSCLYGLPPEKPNISCMNRMKDLTCRWTPGAGHGTFL 117
 96 SLNIQTLNLTFRGLEQNVYGTITISGLPPEKPNLSCLVNGSKMKRCMDGR--ETH 153
 118 LHTNYSLKTKRMYGQDNTCEEYHTVGPSPHCHPKDALFTPEYIWEATNRIGSARSDV 177
 154 LETNFTLKEEMATKRPADKAKRDT--PTSCYDYSTYVFNIEVWEAENALGKVTSDH 211
 178 LITDVLVDVYTTDPPDVHVSRYGSGLEDOLSVRWSPALKDFLQAKYQIRYVEDSVDM 237
 212 INDDPYKTKRPNPPLNLSYNSSELSSILKLTNTN-PSIKSVYI-LKYNIOYRTKDASTM 269
 238 KVV--DDVSNQTSCHLAGLKGTYFYVQVRC 266
 270 SQIPEDTASTSSFTVQDLKPTFEYVFRIC 301

RESULT 8
 A36331
 lactogen receptor 1 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 13-Jul-1990 #sequence_revision 09-Oct-1992 #text_change 10-Sep-1997
 C:Accession: A36331
 R:Zhang, R.; Buczko, E.; Tsai-Morris, C.H.; Hu, Z.Z.; Dufau, M.L.
 Biochem. Biophys. Res. Commun. 168, 415-422, 1990
 A:Title: Isolation and characterization of two novel rat ovarian lactogen receptor cD
 A:Reference number: A34631; MUID:902441201
 A:Accession: A34631
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-610 <ZHA>
 A:Cross-references: GB:M34083; NID:9205122; PID:9205123
 A:Note: the authors translated the codon GAG for residue 533 as Gly

Query Match 19.2%; Score 288.5; DB 2; Length 610;
 Best Local Similarity 36.4%; Pred. No. 1.6e-18;
 Matches 76; Conservative 34; Mismatches 80; Indels 19; Gaps 9;

75 SILAGSCLYGLPPEKPNISCMNRMKDLTCRWTPGAGHGTFLHTNYSLKTKRMYGQD 134
 15 SLKNGQS--PQKPIHCRSPDKETFCWNNPGRDGG--LPTNYSLSYKE--GEK 65
 135 NT--CEEYHTVGPSPHCHPKD-LALFTPEYIWEATNRIGSARSDVLLDVLVYTTDPP 191
 66 TTYECPDYKTSGPSNCSFSSKQYTSIMKTIITVNTNMGSSSDPLVDYTYVEPEPP 125
 192 PDVHVSRYGSGLEDOLSVRW--SPALNDF--LFOAKYQIRYVEDSVDMKVVDVSNQ 246
 126 RNLTL-EVKQLKDKRTYLMVWMSPTIIDVKTGWTMEYELRLKSEFADENE-IHFTGHQ 183
 247 TSCRAGLKPCTGVYVQVRCNPPGIYGSK 275
 184 TQKFVFDLYPQOKYLVQTRCKRDPDHGYSR 212

RESULT 9

A:Residues: 41-58, 'X', 60-66; 90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108-150-164, 'XX', 167
 A>Note: the amino end of the mature protein was blocked
 C:Keywords: blocked amino end; glycoprotein; transmembrane protein
 F:1-24/Domains: signal sequence #status predicted <SIG>
 F:25-616/Product: prolactin receptor 2 #status predicted <MAT>
 F:235-258/Domains: transmembrane #status predicted <TM>
 F:59,104,132,347,369,411/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.0%; Score 286; DB 2; Length 616;
 Best Local Similarity 37.8%; Pred. No. 2, 7e-18;
 Matches 71; Conservative 26; Mismatches 81; Indels 10; Gaps 6;

QY 87 PPEKPNISCSWNRKMDLTCRWTPGAGHETFLHNTSLKYKLRMYGDNCEHTVGP 146
 DB 27 PPKGPFIFKCRSPKERTFCWNRPGADG--LPNTLYLHNGEITHECPDKYKGN 84
 QY 147 SCHI-PKDALFPEIWEATNRGASASDVLTDVYVTTDPPDVHVSRGLEQ 205
 DB 85 SCYFSKHTSWTITITVYVATNOMSSVSDRYVDVITVDPDVNLT-EVXHEDR 143
 QY 206 LSVRWVS--PPALKDF---LFOAKYQIRYVEDSDMKVYDVDSNOTSCLAGLPGTV 260
 DB 144 KYLWVKNLPFLVYDRSGWLTQYELRLKPEKALWE-THRAGQOTPKILSLPGQRY 202
 QY 261 FYQVRCNP 268
 DB 203 LVQVRCNP 210

RESULT 13
 A44257
 Interleukin-6 signal transducing molecule gp130 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
 R:Accession: A44257
 R:Wang, Y.; Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M.
 Genomics 14, 666-672, 1992
 A:Title: Molecular cloning and characterization of the rat liver IL-6 signal transducing
 A:Reference number: A44257; MUID:99052397
 A:Accession: A44257
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-918 <MAN>
 A:Experimental source: liver
 A>Note: sequence extracted from NCBI backbone (NCBIP:118488)
 C:Keywords: transmembrane protein

Query Match 18.7%; Score 281.5; DB 2; Length 918;
 Best Local Similarity 29.0%; Pred. No. 1, 2e-17;
 Matches 79; Conservative 46; Mismatches 132; Indels 15; Gaps 7;

QY 1 PTLIGSLQATCSIHG--DTPGATAGLYTLNGRRLPSLSLTLSTALALANLN 57
 DB 36 PVOVGRSMTATCYLKEKCLQVSVNATYIWKTNHVAPEQVTVINRTASSVTFIDV 95
 QY 58 GSROSGDNVCHARDGSLIAGSLYGLPPEKPNISCSWNRKMDLTCRWTPGAGHET 117
 DB 96 FQNVOLCNILSFQIEQVNYGIIILSGYPPDIPNLSCIYNEKNNMLCOLDPER-ET 153
 QY 118 LHTNYSKLYKLRMYGOD-NTCEYHTVGRSCHIPKDALFPEIWEATNRGASASD 176
 DB 154 LETVYTLKSE--WATEKFPDCRTH--GTSCAMGYPIYVNTVEWAEANLGNVSE 209
 QY 177 VLLIDVLDVTTDPPDVHVSRGLEQDLSVWVSPALDFTFOAKYQIRYVEDSDV 236
 DB 210 PINFDPVDKVPSPHNLVSNSELSIILKLVANSL--DSLRLKSLDGYTKDAST 267
 QY 237 WKVY--DDVSNQTSCLAGLPGTVFYQVR 265
 DB 268 WQVPLEDVTSPRTSFTVQDLKPEYVFRIR 299

RESULT 14
 J01655
 Prolactin receptor precursor - chicken

C:Species: Gallus gallus (chicken)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 10-Sep-1997
 C:Accession: J01655
 R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
 Biochem. Biophys. Res. Commun. 188, 450-456, 1992
 A:Title: Double antenna structure of chicken prolactin receptor deduced from the cD
 A:Reference number: J01655; MUID:93075121
 A:Accession: J01655
 A:Molecule type: mRNA
 A:Residues: 1-831 <MAN>

A:Cross-references: DDBJ:D13154; NID:g222848; PID:d1002939; PID:g222849
 A:Experimental source: kidney
 C:Keywords: glycoprotein; transmembrane protein
 F:1-23/Domains: signal sequence #status predicted <SIG>
 F:24-831/Product: prolactin receptor #status predicted <MAT>
 F:439-462/Domains: transmembrane #status predicted <TM>
 F:59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (c

Query Match 18.7%; Score 281; DB 2; Length 831;
 Best Local Similarity 36.0%; Pred. No. 1, 1e-17;
 Matches 68; Conservative 27; Mismatches 82; Indels 12; Gaps 7;

QY 87 PPEKPNISCSWNRKMDLTCRWTPGAGHETFLHNTSLKYKLRMYGDNCEHTVGP 145
 DB 230 PPEKPTIICKRSPKERTFCWNRPGADG---HPNTILLSKEEEDVYECPPDRTAGP 286
 QY 146 HSCHT-PKDALFPEIWEATNRGASASDVLTDVYVTTDPPDV--HVSRGVL 202
 DB 287 NSCYFDKHTSFMTITVYVATNMGSSNDPXYVDVITVQDPVNTLKKPINR 346
 QY 203 EDOLSVRWVSPALKDF---LFOAKYQIRYVEDSDMKVYDVDSNOTSCLAGLPGTV 259
 DB 347 KYLWLTN-SPPLADVRSGWLTLEYELRLKPEGEWEIT-FVGOQOTYKMFSLPGKK 404
 QY 260 FYQVRCNP 268
 DB 405 YIIQIHCKP 413

RESULT 15
 I49699
 glycoprotein 130 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 07-Feb-1997
 R:Salto, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.
 J. Immunol. 148, 4066-4071, 1992
 A:Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, g
 A:Reference number: I49699; MUID:92291532
 A:Accession: I49699
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-917 <RES>
 A:Cross-references: GB:M83336; NID:g193591; PID:g193592
 A:Accession: I49370
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-917 <RES>
 A:Cross-references: EMBL:X62646; NID:g840816; PID:g840817
 C:Genes: gp130
 C:Keywords: glycoprotein

Query Match 18.5%; Score 279; DB 2; Length 917;
 Best Local Similarity 28.7%; Pred. No. 2e-17;
 Matches 78; Conservative 46; Mismatches 132; Indels 16; Gaps 7;

QY 1 PTLIGSSLOATCSING--DTPGATAGLWTLNGRRLPSELSRLNTSTIALALANLN 57
 Db 36 PVOGRGSNFTACIKLKEACLOHYVNASIYWKTNHAAVREQVTYINRTSSVTFDVS 95
 QY 58 GSRQSGDNLYCHARDGSIILAGSCLYGLPPEKPFNISCHSRNKKDLTCRWTPGANGETF 117
 Db 96 LPSVOLTCNLTSEGOIEQNYGVMTLSEFPDPKPTNLTICVNEGKNMLCOMDPER--ETY 153
 QY 118 LHTNYSILKYKLRWYGOD-NTCEEHVTVGPHSCHIPKDLALFTPEIIVEATNRLGSARSD 176
 Db 154 LETNYTLKSE--WATEKFPCCQSKHGT---SCHWSYMPITYYVNIWVEAENALGKYSSE 208
 QY 177 VLTLDVLDVVTTPDPDVHVSRYVGLEDQLSVWVSEPALKDFQAKYQIRYVEDSDV 236
 Db 209 SINEPDVDKVPYPPYNLSTVNSEELSSILKLSWSSGL--GGLDLKSDIOYRTKDAST 266
 QY 237 WKYV---DVSNOTSCRLAGLAKPGIYFVOVR 265
 Db 267 WQVPLEDTMSPRTSFTVODLKPFTEYFRIR 298

Search completed: September 16, 1999, 20:42:10
 Job time: 3403 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 17, 1999, 03:10:13 ; Search time 35.09 Seconds

(without alignments)
223.955 Million cell updates/sec

Title: US-09-037-657-19

Sequence: 1 PTLIGSSLIQACSIHGDP.....VFVQVRCNPFYGSKKG 278

Scoring table: BLOSUM62

Searched: 77977 seqs, 28268293 residues

Database: SwissProt_37.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	308.5	20.5	622	1	PRLR_HUMAN	P16471 homo sapien
2	292	19.4	830	1	PRLR_COLLI	O90374 columba liv
3	291	19.3	608	1	PRLR_MOUSE	O08501 mus musculu
4	290	19.3	918	1	IL6B_HUMAN	P40189 homo sapien
5	288.5	19.2	610	1	PRLR_HUMAN	P05710 oryctolagus
6	286	19.0	616	1	PRLR_RABIT	P14787 oryctolagus
7	281	18.7	918	1	IL6B_RAT	P40190 rattus norv
8	281	18.7	831	1	PRLR_CHICK	O04594 gallus gall
9	280	18.6	917	1	PRLR_MELGA	O91094 melagris g
10	279	18.5	917	1	IL6B_MOUSE	O00560 mus musculu
11	276.5	18.4	581	1	PRLR_CEREL	O28233 cervus elap
12	276	18.3	581	1	PRLR_BOVIN	O28172 bos taurus
13	233	15.5	630	1	PRLR_ORENT	O91513 oreochromis
14	222	14.8	836	1	GCSR_HUMAN	O09062 homo sapien
15	221.5	14.7	837	1	GCSR_MOUSE	P40223 mus musculu
16	178.5	11.9	372	1	CNTR_HUMAN	O08406 rattus norv
17	176.5	11.7	362	1	CNTR_RAT	P51641 gallus gall
18	172.5	11.5	372	1	CNTR_CHICK	P26992 homo sapien
19	166	11.0	635	1	TPOR_HUMAN	O08351 mus musculu
20	159	10.9	625	1	TPOR_MOUSE	P19941 oryctolagus
21	159	10.6	638	1	GHR_RABIT	P48356 mus musculu
22	159	10.6	1165	1	IL6A_MOUSE	P08887 homo sapien
23	158.5	10.5	468	1	IL6A_HUMAN	P22272 mus musculu
24	154.5	10.3	460	1	IL6A_MOUSE	P23273 rattus norv
25	154.5	10.3	462	1	IL6A_RAT	P19756 sus scrofa
26	151	10.0	638	1	GHR_PIG	P47702 homo sapien
27	147.5	9.8	1097	1	LEPR_HUMAN	P48357 homo sapien
28	146	9.7	1165	1	LEPR_HUMAN	P10912 homo sapien
29	145	9.6	638	1	ANOL_HUMAN	P22063 rattus norv
30	143.5	9.5	1040	1	ANOL_RAT	O28575 oris aries
31	142.5	9.5	634	1	GHR_SHEEP	P16310 rattus norv
32	142	9.4	638	1	GHR_MOUSE	P16882 mus musculu
33	140.5	9.3	650	1	GHR_MOUSE	P16590 mus musculu
34	140.5	9.3	297	1	GHR_MOUSE	O02092 gallus gall
35	136	9.0	608	1	GHR_CHICK	P79194 macaca mla
36	136	9.0	638	1	GHR_MOUSE	O00993 mus musculu
37	135.5	9.0	888	1	UFO_MOUSE	P75108 bos taurus
38	134	8.9	634	1	GHR_BOVIN	P42703 mus musculu
39	133.5	8.9	1092	1	LIFR_MOUSE	P28828 mus musculu
40	133.5	8.9	1452	1	PRPM_MOUSE	O90375 columba liv
41	131.5	8.7	611	1	GHR_COLLI	P28827 homo sapien
42	130.5	8.7	1452	1	PRPM_HUMAN	O07303 rattus norv
43	129.5	8.6	507	1	EPOR_RAT	

ALIGNMENTS

RESULT	1	PRLR_HUMAN	STANDARD	PRT	622 AA.
AC	P16471				
DT	01-AUG-1990 (REL. 15, CREATED)				
DT	01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)				
DT	15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)				
DE	PROLACTIN RECEPTOR PRECURSOR (PRL-R).				
GN	PRLR.				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;				
OC	PRIMATES; CATARRHINI; HOMINIDAE; HOMO.				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 95075462.				
RA	SOMERS W., ULTSCH M., DE VOS A.M., KOSSIAKOFF A.A.;				
RT	"The X-ray structure of a growth hormone-prolactin receptor complex."				
RL	NATURE 372:478-481(1994).				
CC	-1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.				
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.				
CC	-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.				
CC	-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.				
CC	-1- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib.ch).				
CC	EMBL: M3161; G190362; -				
DR	PIR: A40144; A40144.				
DR	PDB: 1BP3; 23-SEP-98.				
DR	MM: 176761; -				
DR	PROSITE: PS00241; RECEPTOR CYTOKINES 1; 1.				
DR	PROSITE: PS00340; RECEPTOR CYTOKINES 2; 1.				
DR	PFAM: PF00041; fn3; 2.				
DR	RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT; 3D-STRUCTURE.				
FT	SIGNAL	1	24		
FT	CHAIN	25	622		
FT	DOMAIN	25	234		
FT	DOMAIN	25	258		
FT	TRANSMEM	259	622		
FT	DOMAIN	25	122		
FT	DOMAIN	123	227		
FT	DISULFID	36	46		
FT	DISULFID	75	86		
FT	CARBOHYD	59	59		
FT	CARBOHYD	104	104		
FT	CARBOHYD	233	233		
FT	SEQUENCE	622 AA;	69505 MW;	6924E155 CRC32;	

Query Match 20.58; Score 308.5; DB 1; Length 622;
Best Local Similarity 38.53; Pred. No. 3.5e-20;
Matches 77; Conservative 27; Mismatches 85; Indels 11; Gaps 7;

```

QY 76 ILASCLVYG-LPEKPFNISCWNRNMDLRCWTPGAHGETFLHTNYSIKYLRMGOD 134
DB 15 LFLNTCLNQLPPGKKEIRKCRSPNKEFTTCWMPGTIDG--LPTNYSILYHREGTLM 72
QY 135 NTCSEYHTVGHSCHEPRD-LALFTPYEIWEATNRLGASADVLTLDVDTTPDP 133
DB 73 HECDDPYITGGNSCHFGKQTSMTWTYIMAVNATNGSSSDLYDYVYIYQDPDPLE 132
QY 194 VHSRVGGLDQLSVRWV--SPPLAKDF---LFOAKYQIRYVEDSVDMKYVDVSNQTS 248
DB 133 LAV-EVQPEDRKRYLTKNSPFTLIDKLGWFTLVEIRLKPKEAEWE- IHPAGQOTE 190
QY 249 CRLAGLKPRTYFYQVQCNP 268
DB 191 FKILSLHPGQRYLVQVCKP 210

RESULT 2
PRLR_COLL1 STANDARD; PRT; 830 AA.
AC Q90374;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS COLUMBA LIVIA (DOMESTIC PIGEON).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
OC NEOGNATHAE; COLUMBIFORMES; COLUMBIDAE; COLUMBA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CORPASC;
RX MEDLINE; 94283267.
RA CHEN X., HORSEMAN N.D.;
RT "Cloning, expression, and mutational analysis of the pigeon prolactin receptor.";
RT ENDOCRINOLOGY 135:269-276(1994).
RL -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC -----
DR EMBL; U07694; G466382;
DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 2.
DR PRAM; PS00340; RECEPTOR_CYTOKINES_2; 2.
DR PRAM; PF00041; fn3; 4.
DR HSP; P16471; IBP3.
KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
FT SIGNAL 1 23
FT CHAIN 24 830
FT DOMAIN 24 439
FT TRANSMEM 440 460
FT DOMAIN 461 830
FT DOMAIN 123 122
FT DOMAIN 123 226
FT DOMAIN 229 326
FT DOMAIN 327 429
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 91 91
FT CARBOHYD 100 100
FT CARBOHYD 112 112

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FT CARBOHYD 132 132 POTENTIAL.
FT CARBOHYD 263 263 POTENTIAL.
FT CARBOHYD 304 304 POTENTIAL.
FT CARBOHYD 316 316 POTENTIAL.
FT CARBOHYD 336 336 POTENTIAL.
SQ SEQUENCE 830 AA; 94507 MW; 5EFAED51 CRC32;

Query Match 19.4%; Score 292; DB 1; Length 830;
Best Local Similarity 37.0%; Pred. No. 1,5e-18;
Matches 70; Conservative 29; Mismatches 78; Indels 12; Gaps 7;

QY 87 PPEKPFNISCWNRNMDLRCWTPGAHGETFLH-TNYSIKYLRMGODNTECEYHTVGP 145
DB 231 PPEKPFNISCWNRNMDLRCWTPGAHGETFLH-TNYSIKYLRMGODNTECEYHTVGP 287
QY 146 HSCHEI-PKDLALFTPYEIWEATNRLGASADVLTLDVDTTPDPDV--VHSRVGL 202
DB 288 NSCYFDPKHTSEFTYINITYKATNELGSNVSDDLVDYVYIYQDTPVAVTLELKTIVNR 347
QY 203 EDQLSVRWVSPPLAKDF---LFOAKYQIRYVEDSVDMKYVDVSNQTSCLAGLKPRTY 259
DB 348 KPYLVLTW--SPPLADVRSGLTLDYELRLKPEAEWEETI-FVGOQTHYKMFSLNPGKK 405
QY 260 YFYQVQCNP 268
DB 406 YFYQVQCNP 414

RESULT 3
PRLR_MOUSE STANDARD; PRT; 608 AA.
AC Q08501; Q62099; P15213; P15212;
DT 01-APR-1990 (REL. 14, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A. (FORM PRL-R3).
RC STRAIN=C3H; TISSUE=MAMMARY GLAND;
RX MEDLINE; 94085788.
RA MOORE R.C., OKA T.;
RT "Cloning and sequencing of the cDNA encoding the murine mammary gland long-form prolactin receptor.";
RT GENE 134:263-265(1993).
RL [2]
RN SEQUENCE FROM N.A. (FORM PRL-R3).
RC STRAIN=SWISS WEBSTER; TISSUE=LIVER;
RX MEDLINE; 93307149.
RA CLARKE D.L., LINZER D.I.H.;
RT "Changes in prolactin receptor expression during pregnancy in the mouse ovary.";
RL ENDOCRINOLOGY 133:224-232(1993).
RN [3]
RP SEQUENCE FROM N.A. (FORM PRL-R3).
RA SASAKI M.;
RN SUBMITTED (JUL-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [4]
RP SEQUENCE FROM N.A. (FORM PRL-R3).
RC STRAIN=BALB/C; TISSUE=MAMMARY GLAND;
RA EDER M., PEZER A., NANDI S., KELLY P.A.;
RN SUBMITTED (JUN-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [5]
RP SEQUENCE FROM N.A. (FORMS PRL-R2 AND PRL-R1).
RC STRAIN=SWISS WEBSTER; TISSUE=LIVER;
RX MEDLINE; 89261824.
RA DAVIS J.A., LINZER D.I.H.;
RT "Expression of multiple forms of the prolactin receptor in mouse liver."

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FT DOMAIN 223 324 FIBRONECTIN TYPE-III.
 FT DOMAIN 325 423 FIBRONECTIN TYPE-III.
 FT DOMAIN 424 517 FIBRONECTIN TYPE-III.
 FT DOMAIN 518 613 FIBRONECTIN TYPE-III.
 FT DOMAIN 725 755 SER-RICH.
 FT DISULFID 134 144
 FT DISULFID 172 182
 FT CARBOHYD 43 43 POTENTIAL.
 FT CARBOHYD 83 83 POTENTIAL.
 FT CARBOHYD 131 131 POTENTIAL.
 FT CARBOHYD 157 157 POTENTIAL.
 FT CARBOHYD 227 227 POTENTIAL.
 FT CARBOHYD 379 379 POTENTIAL.
 FT CARBOHYD 383 383 POTENTIAL.
 FT CARBOHYD 390 390 POTENTIAL.
 FT CARBOHYD 553 553 POTENTIAL.
 FT CARBOHYD 564 564 POTENTIAL.
 SQ SEQUENCE 918 AA, 103522 MW, 7C0C0605 CRC32;

Query Match 19.3%; Score 290; DB 1; Length 918;
 Best Local Similarity 28.3%; Pred. No. 2.6e-18;
 Matches 77; Conservative 47; Mismatches 136; Indels 12; Gaps 6;

QY 1 PILLISSIAQATCSHG---DPGATAEELVTLNGLRRLPSELRLNTSTALANIN 57
 DB 36 PVVQLHSNFTAVCVLKEKCMDFHVNANIYMTNHTLPKQYTLINFTASSYPTDIA 95
 QY 58 GSRQSGDNLVCHARGCSLGLASCLVGPPEPFHISCSRMMDLTGRTPGAGET 117
 DB 96 SLNTQLTCHILTFGLEQNVYGTITISGPEPKNLSCIVNEGKKRMWGGGR--ETH 153
 QY 118 LHTNLSLKYKLWYGGDNTCEHYHVPSCHIPKDLAFTPEIWEATNRLGSARSDV 177
 DB 154 LENTFLKEMATNKRADOKARDT--PSCIVDYSTVYFVNIWEVLEMLKGYTSDH 211
 QY 178 LILDVLDVTTDPDPVHVSRVGLDQSVRWSPALKDPLFOAKYQIRRVEDSVDM 237
 DB 212 INEDPYKVPNPNNLSYINSEELSSILKLTWNTN-PSIKSYII-LKYNIGYRTDASW 269
 QY 238 KVV---DVSNOTSCLAGKPGTYFVQVC 266
 DB 270 SQIPEDNSTRSSFTVQDLKPEYEVFRIC 301

RESULT 5

PRLR_RAT STANDARD: PRT: 610 AA.
 ID P05710; Q63451; Q63723; Q62832; Q64274; Q63479;
 AC 01-NOV-1988 (REL. 09, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (LACTOGEN RECEPTOR).
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIURONATHI; MURIDAE; MURINAE; RATTUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 91155946.
 RA SHIROTA M., BANVILLE D., ALI S., JOLICOEUR C., BOUTIN J.M.,
 EDERY M., DJIANE J., KELLY P.A.;
 RT "Expression of two forms of prolactin receptor in rat ovary and
 liver."
 RL MOL. ENDOCRINOL. 4:1136-1143(1990).
 RP SEQUENCE FROM N.A. (LONG FORM AND SHORT FORM).
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY;
 RX MEDLINE: 90241201.
 RA ZHANG R., BUCZKO E., TSAI-MORRIS C.H., HU Z.Z., DUBAU M.L.;
 RT "Isolation and characterization of two novel rat ovarian lactogen
 receptor cDNA species."
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 168:415-422(1990).

RN [3]
 RP SEQUENCE OF 281-610 FROM N.A.
 RA BANVILLE D., STOCO R., MURPHY K.K., BOYE Y., KELLY P.A.;
 RN SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDJ DATA BANKS.
 RL [4]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (MEDIUM FORM).
 RC TISSUE-LIVER;
 RX MEDLINE: 88165059.
 RA BOUTIN J.-M., JOLICOEUR C., OKAMURA H., GAGNON J., EDERY M.,
 SHIROTA M., BANVILLE D., DUSANTER-FOUR I., DJIANE J., KELLY P.A.;
 RT "Cloning and expression of the rat prolactin receptor, a member of
 the growth hormone/prolactin receptor gene family."
 RL CELL 53:69-77(1988).
 RP [5]
 RP SEQUENCE FROM N.A. (FORM NB2).
 RC TISSUE-LYMPHOMA;
 RX MEDLINE: 92041834.
 RA ALI S., PELLIGRINI I., KELLY P.A.;
 RT "A prolactin-dependent immune cell line (NB2) expresses a mutant form
 of prolactin receptor."
 RL J. BIOL. CHEM. 266:20110-20117(1991).
 RN [6]
 RP SEQUENCE FROM N.A. (FORM NB2).
 RX MEDLINE: 95014432.
 RA O'NEAL K.D., YU-LEE L.Y.;
 RT "Differential signal transduction of the short, NB2, and long
 prolactin receptors. Activation of interferon regulatory factor-1 and
 cell proliferation."
 RL J. BIOL. CHEM. 269:26076-26082(1994).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
 CC -1- ALTERNATIVE PRODUCTS: DIFFERENT FORMS ARE PRODUCED BY ALTERNATIVE
 SPLICING OF THE PRLR GENE.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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 CC -----
 DR EMBL: M57668; G206367; -;
 DR EMBL: M34083; G205123; -;
 DR EMBL: L48060; G1019651; -;
 DR EMBL: U34730; G1223859; -;
 DR EMBL: M19304; G206365; -;
 DR EMBL: M74152; G206380; -;
 DR EMBL: U07567; G641964; -;
 DR PIR: A29884; A29884.
 DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1;
 DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR PFM: PF00041; fn3; 2.
 DR HSP: P16471; 18P3.
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT;
 KW ALTERNATIVE SPLICING.
 FT SIGNAL 1 19
 FT CHAIN 20 610
 FT DOMAIN 20 229
 FT TRANSSEM 230 253
 FT DOMAIN 254 254
 FT DOMAIN 254 253
 FT DOMAIN 254 253
 FT DISULFID 119 119
 FT DISULFID 31 41
 FT DISULFID 70 81
 FT CARBOHYD 54 54
 FT CARBOHYD 54 54
 FT CARBOHYD 99 99
 FT CARBOHYD 127 127
 FT VARSPLIC 131 150
 FT -----
 FT POTENTIAL.
 FT EXTRACELLULAR (BY SIMILARITY).
 FT BY SIMILARITY.
 FT CYTOPLASMIC (BY SIMILARITY).
 FT FIBRONECTIN TYPE-III.
 FT FIBRONECTIN TYPE-III.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT POTENTIAL.
 FT EVOLKDRKTYLWKNKSPPT -> DYRWVSCHEALPKSA
 KLN (IN SHORT FORM).

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FT  VARSPLIC 151 610 MISSING (IN SHORT FORM).
FT  VARSPLIC 281 310 KGRSEELSLAGCODEPTDCEDLIVEFL ->
FT  VARSPLIC 311 610 TGSPPKRYVDLYALPGCFKLDNAGLDY (IN
FT  VARSPLIC 342 539 MEDIUM FORM).
FT  VARSPLIC 342 539 MISSING (IN MEDIUM FORM).
FT  CONFLICT 236 236 V -> A (IN REF. 2).
FT  CONFLICT 236 236 G -> V (IN REF. 2).
FT  CONFLICT 345 345 E -> K (IN REF. 1).
FT  CONFLICT 465 465 Q -> E (IN REF. 2).
FT  CONFLICT 466 466 A -> G (IN REF. 2).
FT  CONFLICT 469 469 T -> M (IN REF. 1).
FT  CONFLICT 541 541 Q -> K (IN REF. 2).
FT  CONFLICT 555 555
SQ  SEQUENCE 610 AA: 68599 MW: C579BC43 CRC32:

Query Match 19.2%; Score 288.5; DB 1; Length 610;
Best Local Similarity 36.4%; Pred. No. 2.1e-18;
Matches 76; Conservative 34; Mismatches 80; Indels 19; Gaps 9;

OY 75 SLIAGSCLYVGLPPEKPFNISCWSRNKMDLTCRTPGANGETFLHNTYSIKYKLRMTGOD 134
DB 15 SLKSGS-----PGKPELHKCSPPKETFCTWMPGTGG--LPNTYSLTYSKE--GEK 65
OY 135 NT--CEEHTVGPCHIPKD-LALFTPEIWEATNRLGSARSVDLTLDVDTTDP 191
DB 66 TTECPDXYTSGSPNSCFESKOYTSIKKIYITVYNNATNOMGSSSDLYVDYIVYEPEPP 125
OY 192 PDVHVSRYGGLEDQSVRV--SPRLKDF--LFOAKQIIRYVEDSVDMRVVDVSNQ 246
DB 126 RNLTJ-EVKOLDKTKTYLWVKWSPPTITVKTGMFEYERILKPEAEAEWE-IHTGHO 183
OY 247 TSCRLAGLKPGTYEVQVRCNPFYIGSK 275
DB 184 TQFKVEDLYPGOKYLVORCKRDPDRGWSR 212

RESULT 6
PRLR-RABIT STANDARD: PRT: 616 AA.
AC P14787:
DT 01-APR-1990 (REL. 14, CREATED)
DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS ORCTOLAGUS CUNICULUS (RABBIT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC LAGOMORPHA; LEPORIDAE; ORCTOLAGUS.
RN [1]
RN RP
RN RC TISSUE-MAMMARY GLAND;
RN RX MEDLINE: 89184578.
RA EDEBT W., JOLICOEUR C., LEVI-MEYRUEIS C., DUSANTER-FOUR I.,
RA PETRIDOU B., BOUIN J.M., LESIEUR L., KELLY P.A., DJANE J.;
RT Identification and sequence analysis of a second form of prolactin
RT receptor by molecular cloning of complementary DNA from rabbit
RT mammary gland.
RL PROC. NATL. ACAD. SCI. U.S.A. 86:2112-2116(1989).
RN [2]
RN RP
RN RC 3D-STRUCTURE MODELLING OF 30-228.
RN RX MEDLINE: 97248733.
RA HALABY D., THOREAU E., DJANE J., MORNON J.P.;
RT Homology modeling of rabbit prolactin hormone complexed with its
RT receptor.
RL PROTEINS 27:459-468(1997).
RN [3]
RN RP
RN RC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
RN CC PROLACTIN.
RN CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
RN CC -1- SIMILARITY: BELONGS TO THE CITRORINE FAMILY OF RECEPTORS.
RN CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
RN CC
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CC
DR EMBL: J04510; G165670; -
DR PIR: A30304; A30304.
DR PDB: 1AN3; 03-DEC-97.
DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
DR PRAM: PF00041; fn3; 2.
KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT; 3D-STRUCTURE.
FT SIGNAL 1 24
FT CHAIN 25 616 PROLACTIN RECEPTOR.
FT DOMAIN 25 234 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 235 258 POTENTIAL.
FT DOMAIN 259 616 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 122 FIBRONECTIN TYPE-III.
FT DOMAIN 124 227 FIBRONECTIN TYPE-III.
FT DISULFID 36 46 BY SIMILARITY.
FT DISULFID 75 86 BY SIMILARITY.
FT CARBOHYD 59 59 POTENTIAL.
FT CARBOHYD 104 104 POTENTIAL.
FT CARBOHYD 132 132 POTENTIAL.
SQ SEQUENCE 616 AA: 68840 MW: FB6170B1 CRC32:

Query Match 19.0%; Score 286; DB 1; Length 616;
Best Local Similarity 37.8%; Pred. No. 3.6e-18;
Matches 71; Conservative 26; Mismatches 81; Indels 10; Gaps 6;

OY 87 PREKPNISCWSRNKMDLTCRTPGANGETFLHNTYSIKYKLRMTGODNTCEEHTVGP 146
DB 27 PGKPELHKCSPPKETFCTWMPGTGG--LPNTYSLTYSKE--GEK 65
OY 147 SCHI-PKDIATFTPEIWEATNRLGSARSVDLTLDVDTTDPDPVHVSRYGGLEDQ 205
DB 85 SCYFSKHTSIWITIIITVYNNATNOMGSSSDLYVDYIVYEPEPPVLTJ-EVHNPDR 143
OY 206 LSVRVVS--PPRLKDF--LFOAKQIIRYVEDSVDMRVVDVSNQTSCLAGLKPGTY 260
DB 144 KEYLWVKMLPPTLVDRSGWLTLYEIRLKEPEAEAEWE-THPAGQTOFKLSLPGSKY 202
OY 261 FYOVRGNP 268
DB 203 LVQVCKRP 210

RESULT 7
IL6B-RAT STANDARD: PRT: 918 AA.
ID IL6B-RAT
AC P40190:
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).
GN IL6ST.
OS RATUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIURGNATHI; MORIDAE; MORINAE; RATUS.
RN [1]
RN RP
RN RC TISSUE-LIVER;
RN RX MEDLINE: 93052397.
RA WANG Y., NESBITT J.E., FOENTES N.L., FULLER G.M.;
RT Molecular cloning and characterization of the rat liver IL-6 signal
RT transducing molecule gp130.
RL GENOMICS 14:666-672(1992).
RN [2]
RN RP
RN CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
RN CC IL-6, ILF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING

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CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
 CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
 CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
 CC EMBRYONIC DEVELOPMENT (BY SIMILARITY).
 CC -1- SUBUNIT: HETERODIMER OF TYPE I ALPHA AND A BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS
 CC AND ENDOTHELIAL CELLS.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -----
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 CC -----
 DR EMBL: M92340; -; NOT_ANNOTATED_CDS.
 DR PIR: A44257; A44257.
 DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR PFM: PFO0041; fn3; 3.
 DR HSP: P40189; 1B0U.
 DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
 KM REPEAT.
 FT SIGNAL 1 22
 FT CHAIN 23 918
 FT DOMAIN 23 618 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
 FT TRANSMEM 619 640 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 641 918 POTENTIAL.
 FT DOMAIN 26 120 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 124 221 IG-LIKE C2-TYPE DOMAIN.
 FT DOMAIN 221 221 FIBRONECTIN TYPE-III.
 FT DOMAIN 322 333 FIBRONECTIN TYPE-III.
 FT DOMAIN 334 422 FIBRONECTIN TYPE-III.
 FT DOMAIN 423 516 FIBRONECTIN TYPE-III.
 FT DOMAIN 517 612 FIBRONECTIN TYPE-III.
 FT DOMAIN 724 754 SER-RICH.
 FT DISULFID 134 144 BY SIMILARITY.
 FT DISULFID 172 181 BY SIMILARITY.
 FT CARBOHYD 43 43 POTENTIAL.
 FT CARBOHYD 61 61 POTENTIAL.
 FT CARBOHYD 83 83 POTENTIAL.
 FT CARBOHYD 131 131 POTENTIAL.
 FT CARBOHYD 157 157 POTENTIAL.
 FT CARBOHYD 205 205 POTENTIAL.
 FT CARBOHYD 226 226 POTENTIAL.
 FT CARBOHYD 382 382 POTENTIAL.
 FT CARBOHYD 389 389 POTENTIAL.
 FT CARBOHYD 477 477 POTENTIAL.
 FT CARBOHYD 552 552 POTENTIAL.
 SQ SEQUENCE 918 AA; 102450 MW; E6EFCDD0 CRC32;

Query Match 18.7%; Score 281.5; DB 1; Length 918;
 Best Local Similarity 29.0%; Pred. No. 1.5e-17;
 Matches 79; Conservative 46; Mismatches 132; Indels 15; Gaps 7;

QY 1 PTLIGSSLOATCSIHG---DFPGATAGLYWLNIGRRLPSELRLNTSTLALANLN 57
 DB 36 PVOGRSNFATLVKCKLOYVSVNATYIVKTNHVAVKEQVYINIRASSVFTD 95
 QY 58 GSRQSGSDNLYCARQDSILAGSCLVGLPPEPFNISCSRNKADITCMTFGANGET 117
 DB 96 FQNVOLCNLTISGQLEQNYGTLISGYPPDIPFNTNISCIVNKGKMLCOLDFGR--ET 153
 QY 118 LHNYSKLYKLWYAGD-NTCEHTWGRSHCHPDLAFTYEIVETATNRLSGAR 176
 DB 154 LENTYILKSE--WATEFPPCKRTKH--GTSSCMAGTPIYFVNIWEVLENALGVNS 209
 QY 177 VLLIDVLDVVTDPDPDVHVSRYVGGLEDQLSVRWSPALKDLFQAKYQIRRVEDSV 236

DB 210 PINEDPVAKVPSPHNLSYNSELSILKAWNSGL--DSLRLKSDIQRTKAST 267
 QY 237 MKV---DDVSNQTSCLAGLPGIVYFQVR 265
 DB 268 WIOVLEDVTSRPSFTVODLKPFTEYFRLR 299

RESULT 8
 ID PRLR_CHICK STANDARD; PRT; 831 AA.
 AC 004594;
 DT 01-JUN-1994 (REL. 29, CREATED)
 DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
 DT 15-JUN-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (CRLT).
 GN PRLR.
 OS GALLUS GALLUS (CHICKEN).
 CC EURAROTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
 CC NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WHITE, LEIGHORN; TISSUE-KIDNEY;
 RX MEDLINE; 93075121.
 RA TANAKA M., MAEDA K., OKUBO T., NAKASHIMA K.;
 RT "Double antenna structure of chicken prolactin receptor deduced from
 the cDNA sequence".
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 188:490-496(1992).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -----
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 CC -----
 DR EMBL: D13154; G222849; -
 DR PIR: J01655; J01655.
 DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 2.
 DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 2.
 DR PFM: PFO0041; fn3; 4.
 DR HSP: P16471; 1BP3.
 DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
 FT SIGNAL 1 23
 FT CHAIN 24 831
 FT DOMAIN 24 438 PROLACTIN RECEPTOR.
 FT TRANSMEM 439 459 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 460 831 POTENTIAL.
 FT DOMAIN 25 122 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 123 225 FIBRONECTIN TYPE-III.
 FT DOMAIN 328 325 FIBRONECTIN TYPE-III.
 FT DOMAIN 428 428 FIBRONECTIN TYPE-III.
 FT DISULFID 36 46 BY SIMILARITY.
 FT DISULFID 75 86 BY SIMILARITY.
 FT CARBOHYD 59 59 POTENTIAL.
 FT CARBOHYD 91 91 POTENTIAL.
 FT CARBOHYD 100 100 POTENTIAL.
 FT CARBOHYD 112 112 POTENTIAL.
 FT CARBOHYD 132 132 POTENTIAL.
 FT CARBOHYD 262 262 POTENTIAL.
 FT CARBOHYD 303 303 POTENTIAL.
 FT CARBOHYD 315 315 POTENTIAL.
 FT CARBOHYD 335 335 POTENTIAL.
 SQ SEQUENCE 831 AA; 94102 MW; B977BE07 CRC32;

Query Match 18.7%; Score 281; DB 1; Length 831;

4 DOMAIN 326 428 FIBRONECTIN TYPE-III.

SYNOPSIS: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE IG-LIKE DOMAIN.

CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 CC
 DR EMBL: X62646; G840817; -
 DR EMBL: M83336; G193592; -
 DR MGI: 96560; IL6ST.
 DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR PFAM: PF00041; fn3; 3.
 DR HSSP: P40189; 180U.
 DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
 KM REPEAT.
 FT SIGNAL 1 22
 FT CHAIN 23 917
 FT DOMAIN 23 617
 FT TRANSMEM 618 639
 FT DOMAIN 640 917
 FT DOMAIN 26 120
 FT DOMAIN 124 220
 FT DOMAIN 221 322
 FT DOMAIN 323 420
 FT DOMAIN 422 515
 FT DOMAIN 516 611
 FT DOMAIN 723 741
 FT DISULFID 134 144
 FT DISULFID 172 180
 FT CARBOHYD 43 43
 FT CARBOHYD 61 61
 FT CARBOHYD 83 83
 FT CARBOHYD 131 131
 FT CARBOHYD 157 157
 FT CARBOHYD 225 225
 FT CARBOHYD 388 388
 FT CARBOHYD 476 476
 FT CARBOHYD 551 551
 SQ SEQUENCE 917 AA; 102452 MW; A5DCD259 CRC32;
 Query Match 18.5%; Score 279; DB 1; Length 917;
 Best Local Similarity 28.7%; Pred. No. 2.5e-17;
 Matches 78; Conservative 46; Mismatches 132; Indels 16; Gaps 7;
 QY 1 PTLIGSSLOATGSIHG---DTPGATAGLWTLNGLRLPSELRLNTSTLALANLN 57
 Db 36 PVOGRSGFTAIYVKEKACLOHYVNAASYIWKINHAAPREOVTVIKRTISSVTFIDV 95
 QY 58 GSROOSGDNLYCHARDGSIILAGSCLYVGLPPEKPNISCSNRNMDLTCRTPGAHGETE 117
 Db 96 LPSVQLGRTNIIISFGQIEGNVGYVIMLSGFPDPKPTNLFCYNEGNMLCQMDPGR--ETV 153
 QY 118 LHTNLSKLYKLKRWGQD--NTCEETHVTPHSCHIKDALTPPEIIVTEANRRGASARD 176
 Db 154 LETNYTLKSE--WATERPPDCOSKHGT--SCMVSAMPYVYVNIWVEAENALGKYSSE 208
 QY 177 VLLIDLVAVTDPDPDVHVSNGVLEQGLSVRWSPALMDLEQAQYQIRYREDEVD 236
 Db 209 SINFPVAVKVPPTPPNIVSNVSELSLTKISWSSGL--GGLDLKSDIOYRKDKNST 266
 QY 237 WQVYV---DDVSNQTSCLAGLKGTVYEQVR 265
 Db 267 WIOVPLEDTMSPRTSFTYQDCLKPEIYFRIR 298
 RESULT 11
 PRIR_CEREL STANDARD; PRT; 581 AA.
 ID PRIR_CEREL

AC Q28235;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
 GN PRLR.
 OS CERUUS ELAPHUS (RED DEER).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC ARTIODACTYLIA; RUMINANTIA; PECORA; CERVOIDEA; CERVIDAE; CERVINAE;
 OC CERUUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE: 96030711.
 RA CLARE L.A., EDERY M., LOUDON A.S., RANDALL V.A., POSTEL-VINAY M.C.,
 RA KELLY P.A., JABBOUR H.N.;
 RT "Expression of the prolactin receptor gene during the breeding and
 RT non-breeding seasons in red deer (Cervus elaphus): evidence for the
 RT expression of two forms in the testis.";
 RL J. ENDOCRINOL. 146:313-321(1995).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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 CC
 DR EMBL: X94953; E218406; -
 DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
 DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR PFAM: PF00041; fn3; 2.
 DR HSSP: P14787; 1AN3.
 DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
 KM REPEAT.
 FT SIGNAL 1 24
 FT CHAIN 25 581
 FT DOMAIN 25 234
 FT TRANSMEM 235 258
 FT DOMAIN 259 581
 FT DOMAIN 25 122
 FT DOMAIN 123 227
 FT DOMAIN 36 46
 FT DISULFID 75 86
 FT DISULFID 59 59
 FT CARBOHYD 132 132
 FT CARBOHYD 233 233
 SQ SEQUENCE 581 AA; 65159 MW; 721F0366 CRC32;
 Query Match 18.4%; Score 276.5; DB 1; Length 581;
 Best Local Similarity 34.0%; Pred. No. 2.4e-17;
 Matches 71; Conservative 35; Mismatches 88; Indels 15; Gaps 7;
 QY 73 DGSILAGSCLYVGLPPEKPNISCSNRNMDLTCRTPGAHGETLHTNSLAKRLMYG 132
 Db 18 NASLLNGS-----PPKPKRIIKRSPGKEFTGMBPGSDG--LPTNYTLTYHKEGET 70
 QY 133 QDNTECEHYHVPSCSI--PRDLALFPPEIIVTEANRRGASARDVLLIDLVAVTDP 191
 Db 71 LIHCPCPYKGGPTCFESKRTHSIMKIYITVAINOMGVSSDPLVDTYIVPEPP 130
 QY 192 PDVAVSRVGLLEDOLSVRWVS--PPALKDF---LEQAKYQIRYREDESDVAKVVDVSNQ 246
 Db 131 ANLVL-ELKHEDKRPILMIKMPPLILDVYSGWFMIOYELRLKPEIAADNE-IHFAKQ 188
 QY 247 TSCRLAGLKGTVYEQVRCPFGIYGSK 275

Db 189 TOLKIFSLYPGOKLYVQVRCCKPDHGYMSE 217

RESULT 12

PRLR_BOVIN STANDARD; PRT: 581 AA.

AC 028172;

DT 01-NOV-1997 (REL. 35, CREATED)

DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

DE 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

GN PRLR.

OS BOS TAURUS (BOVINE)

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVIDEA; BOVINA; BOVINAE; BOS.

RP SEQUENCE FROM N.A.

RA TISSUE-ENDOMETRIUM;

MEIDLINE; 93246019.

SCOTT P., KESSLER M.A., SCHULER L.A.;

"Molecular cloning of the bovine prolactin receptor and distribution of prolactin and growth hormone receptor transcripts in fetal and utero-placental tissues."

RL MOL. CELL. ENDOCRINOL. 89:47-58(1992).

CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

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CC EMBL: L02549; G163618; PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1. DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1. DR PFAM: PF00041; fn3; 2. DR HSSP: P14787; fn3; 2. KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT. FT SIGNAL 1 24 POTENTIAL. FT CHAIN 25 581 PROLACTIN RECEPTOR. FT DOMAIN 25 234 EXTRACELLULAR (POTENTIAL). FT TRANSMEM 235 258 POTENTIAL. FT DOMAIN 259 581 CYTOPLASMIC (POTENTIAL). FT DOMAIN 259 581 FIBRONECTIN TYPE-III. FT DOMAIN 259 581 FIBRONECTIN TYPE-III. FT DISULFID 123 227 FIBRONECTIN TYPE-III. FT DISULFID 36 46 BY SIMILARITY. FT DISULFID 75 86 BY SIMILARITY. FT CARBOHYD 59 59 POTENTIAL. FT CARBOHYD 132 132 POTENTIAL. SQ SEQUENCE 581 AA; 65153 MW; COECA0A2 CRC32;

Query Match 18.3%; Score 276; DB 1; Length 581; Best Local Similarity 32.18; Pred. No. 2.6e-17; Matches 78; Conservative 37; Mismatches 88; Indels 40; Gaps 9;

Db 41 SRLMTSTALALANINGSHQSGDNLVCHARGSLAGSCLVGLPPEPFNISCMSRN 100

Db 7 SRVFLFLFLSLVSLNG--QS-----PPEPKLYVKCRSPG 40

Db 101 MDLJCRMTPGAHEFTLNTSLKYLKMYGODNTCEHYTVGPHSCRI--PDLLFTP 159

Db 41 KEFTCWMPEGADG--LPTNVLTLTHKKESETLIHCPOKKTGPNKSCYKSKHTSIWKA 98

Db 160 YELWENATNRLGASRSDVLTLDVLTVDTPPDVHVSRYVGLDOLSVRW--SPALK 217

Db 99 YITVAINAIOMGISSDPLVHTVYIIVEPEPPANLTL-ELKHEDRKRPLYMIKMSPTMT 157

Query 218 D-----FLQAKYQIYRVEDSYDAKTVDDVSNQTSCLAGLKPCTVYFVQVRCNPFgiY 272

Db 158 DVKSGWFIIO--YEIRLKEKATDWE--THFTLKQOLKIFNLYPGOKLYVQVRCAPDgiY 214

Query 273 GSK 275

Db 215 MSE 217

RESULT 13

PRLR_ORENI STANDARD; PRT: 630 AA.

AC 091513;

DT 01-NOV-1997 (REL. 35, CREATED)

DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

DE 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

GN PRLR.

OS OROCHOMIS NILOTICUS (NILE TILAPIA) (TILAPIA NILOTICA).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;

OC TELEOSTEI; EUTELEOSTEI; ACANTHOPTERYGII; PERCOMORPHA; PERCIFORMES;

OC LABROIDEI; CICHLIDAE; TILAPIA.

RP SEQUENCE FROM N.A.

RA TISSUE-KIDNEY;

MEIDLINE; 95320210.

SANDRA O., SOHM F., DE LUZE A., PRUNET P., EDERY M., KELLY P.A.;

"Expression cloning of a cDNA encoding a fish prolactin receptor."

PROC. NATL. ACAD. SCI U S A. 92:6037-6041(1995).

CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

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CC EMBL: L34783; G903847; PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1. DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1. DR PFAM: PF00041; fn3; 2. DR HSSP: P16471; fn3; 2. KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT. FT SIGNAL 1 23 POTENTIAL. FT CHAIN 24 630 PROLACTIN RECEPTOR. FT DOMAIN 24 234 EXTRACELLULAR (POTENTIAL). FT TRANSMEM 235 258 POTENTIAL. FT DOMAIN 259 630 CYTOPLASMIC (POTENTIAL). FT DOMAIN 259 630 FIBRONECTIN TYPE-III. FT DOMAIN 259 630 FIBRONECTIN TYPE-III. FT DISULFID 124 228 FIBRONECTIN TYPE-III. FT DISULFID 37 47 BY SIMILARITY. FT DISULFID 76 87 BY SIMILARITY. FT CARBOHYD 92 92 POTENTIAL. FT CARBOHYD 101 101 POTENTIAL. SQ SEQUENCE 630 AA; 70810 MW; E9A4E53 CRC32;

Query Match 15.5%; Score 233; DB 1; Length 630; Best Local Similarity 33.78; Pred. No. 2.1e-13; Matches 64; Conservative 25; Mismatches 85; Indels 16; Gaps 8;

Db 88 PERPNTSCSMRMDLJCRMTPGAHEFTLNTSLKYLKMYGODNTCEHYTVGPHS 147

Db 29 PKPFTIKRSPEKEFTCWMPGSDG--LPTTALYLRKSGSDVVEHCPDYHTAGRNS 86

Query 148 CHIPDALL-FTPEIWEATNRLGASRSDVLTLDVLTVDTPPDVHVSRYVGLDGO 206

DB 87 CEFNNKNTLWVSYNITVATNALGCTSDPDQIDVYVYIOPHPPEKLEVT---YAKDOG 143
 QY 206 ---LSRWVSPALKDF---LQAKQIQRVED-SVWKVYDDVSNQTSCLAGKPGT 258
 DB 144 WPLRLVSM-EPPKADIRSGWITLILYELKLEDESEME-NMAQCKMFTFSIRSGG 201
 QY 259 VYFVQVRCNP 268
 DB 202 TYLIQVRCNP 211

RESULT 14
 GCSR_HUMAN
 ID GCSR_HUMAN STANDARD: PRT: 836 AA.
 AC 099062;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE GRANULOCYTE COLONY STIMULATING FACTOR RECEPTOR PRECURSOR (G-CSF-R)
 DE (CD114 ANTIGEN).
 GN CSF3R OR GCSR.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RC MEDLINE: 91011257.
 RA LARSEN A., DAVIS T., CURTIS B.M., GIMPEL S., SIMS J.E., COSMAN D.,
 RA PARK L., SORENSEN E., MARCH C.J., SMITH C.A.;
 RT "A cDNA clone expressed in natural killer and T cells that likely
 RT encodes a secreted protein.";
 RL J. EXP. MED. 172:1559-1570(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RC MEDLINE: 91062348.
 RA FUKUNAGA R., SETO Y., MIZUSHIMA S., NAGATA S.;
 RT "Three different mRNAs encoding human granulocyte colony-stimulating
 RT factor receptor.";
 RL PROC. NATL. ACADE. SCI. U.S.A. 87:8702-8706(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC MEDLINE: 92091782.
 RA SETO Y., FUKUNAGA R., NAGATA S.;
 RT "Chromosomal gene organization of the human granulocyte colony-
 RT stimulating factor receptor.";
 RL J. IMMUNOL. 148:259-266(1992).
 RN [4]
 RP DOMAINS STRUCTURE.
 RC MEDLINE: 92007729.
 RA FUKUNAGA R., ISHIZAKA-IKEDA E., PAN C.-X., SETO Y., NAGATA S.;
 RT "Functional domains of the granulocyte colony-stimulating factor
 RT receptor.";
 RL EMBO J. 10:2855-2865(1991).
 RN [5]
 RP STRUCTURE BY NMR OF 227-334.
 RC MEDLINE: 97331327.
 RA YAMASAKI K., NAITO S., ANAGUCHI H., OKUBO T., OTA Y.;
 RT "Solution structure of an extracellular domain containing the WSXWS
 RT motif of the granulocyte colony-stimulating factor receptor and its
 RT interaction with ligand.";
 RL NAT. STRUCT. BIOL. 4:498-503(1997).
 RN [6]
 RP 3D-STRUCTURE MODELING OF 125-331.
 RC MEDLINE: 98037802.
 RA LAYTON J.E., IARIA J., SMITH D.K., TREUTLEIN H.R.;
 RT "Identification of a ligand-binding site on the granulocyte colony-
 RT stimulating factor receptor by molecular modeling and mutagenesis.";
 RL J. BIOL. CHEM. 273:29735-29741(1997).
 CC -1- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR (G-
 CC CSF). IN ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION

CC -1- EVENTS AT THE CELL SURFACE.
 CC -1- SUBUNIT: DIMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE GCSR-2 FORM,
 CC WHICH LACKS THE TRANSMEMBRANE DOMAIN, MAY REPRESENT A SOLUBLE FORM
 CC OF THE RECEPTOR.
 CC -1- TISSUE SPECIFICITY: ONE OR SEVERAL FORMS HAVE BEEN FOUND IN
 CC MYELOGENOUS LEUKEMIA CELL LINE KG-1, LEUKEMIA U937 CELL LINE, IN
 CC BONE MARROW CELLS, PLACENTA, AND PERIPHERAL BLOOD GRANULOCYTES.
 CC THE GCSR-2 FORM HAS BEEN FOUND ONLY IN LEUKEMIA U937 CELLS. THE
 CC GCSR-3 FORM IS HIGHLY EXPRESSED IN PLACENTA.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST FOUR FORMS, GCSR-1 (SHOWN UNDER),
 CC GCSR-2, GCSR-3 AND GCSR-4/D7, ARE PROBABLY PRODUCED BY
 CC ALTERNATIVE SPLICING OF THE SAME GENE. THEY DIFFER IN THEIR C-
 CC TERMINAL PORTION.
 CC -1- DISEASE: DEFECTS IN CSF3R ARE A CAUSE OF KOSTMANN SYNDROME;
 CC ALSO KNOWN AS SEVERE CONGENITAL NEUTROPENIA (SCN).
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- DATABASE: NAME-PROV, NOTE-CD guide CD114 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd114.htm".
 CC
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 CC
 CC EMBL: X55721; G31697; -;
 CC EMBL: X55720; G31699; -;
 CC EMBL: S71484; G240884; -;
 CC EMBL: M59818; G183047; -;
 CC EMBL: M59819; G485364; -;
 CC EMBL: M59820; G183049; -;
 CC PIR: JH0329; JH0329;
 CC PIR: JH0330; JH0330;
 CC PIR: A38252; A38252;
 CC PDB: 1A27; 28-JAN-98.
 CC DR MIM: 138971; -;
 CC DR MIM: 202700; -;
 CC DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1;
 CC DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1;
 CC DR PFM: PF00041; I13; 3;
 CC KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
 CC REPEAT: ALTERNATIVE SPLICING; 3D-STRUCTURE.
 CC FT SIGNAL 1 24
 CC FT CHAIN 25 836
 CC FT
 CC FT DOMAIN 25 627
 CC FT TRANSMEM 628 650
 CC FT DOMAIN 651 836
 CC FT DOMAIN 25 117
 CC FT DOMAIN 121 227
 CC FT DOMAIN 228 332
 CC FT DOMAIN 333 428
 CC FT DOMAIN 429 525
 CC FT DOMAIN 526 621
 CC FT DISULFID 131 142
 CC FT DISULFID 248 295
 CC FT DISULFID 266 309
 CC FT CARBOHYD 51 51
 CC FT CARBOHYD 93 93
 CC FT CARBOHYD 128 134
 CC FT CARBOHYD 134 134
 CC FT CARBOHYD 389 389
 CC FT CARBOHYD 474 474
 CC FT CARBOHYD 579 579
 CC FT CARBOHYD 610 610
 CC FT VARSPLIC 750 783
 CC FT
 CC FT GRANULOCYTE COLONY STIMULATING FACTOR
 CC RECEPTOR.
 CC EXTRACELLULAR (POTENTIAL).
 CC POTENTIAL.
 CC CYTOPLASMIC (POTENTIAL).
 CC IG-LIKE C2-TYPE DOMAIN.
 CC FIBRONECTIN TYPE-III.
 CC FIBRONECTIN TYPE-III.
 CC FIBRONECTIN TYPE-III.
 CC FIBRONECTIN TYPE-III.
 CC FIBRONECTIN TYPE-III.
 CC FIBRONECTIN TYPE-III.
 CC BY SIMILARITY.
 CC POTENTIAL.
 CC POTENTIAL.
 CC POTENTIAL.
 CC POTENTIAL.
 CC POTENTIAL.
 CC POTENTIAL.
 CC VLYGGLSPSPGSHYLRCDSTOPLAGLTPS ->
 CC AGPPRSAYFKQMLHAPRGLGLCPITPSVL

FT VARSPLIC 784 836 (IN GCSF-4/D7)
 FT VARSPLIC 680 680 MISSING (IN GCSF-4/D7).
 FT VARSPLIC 622 836 E -> ELPGPBGWLGOTSEMSRALTPEPCVO
 (IN GCSF-3).
 FT VARSPLIC 622 836 EGSEHLLIGLGLLLTLTCLGTCAMLCGSPRRKMPSPV
 PDPAHSHSNSEETIMEDADQPLGCTPITKLVLEDE
 KKPVPESHNSSETGEPVLVQTVYLOQDPRAVVSQPOS
 GTSQVLYGOLGSPSPGPHYLACDSTOPLAFLTPSPK
 SYENLMFQASPLGLVTPAPSOEDCVGPIINPLGIGIR
 VHGMALGSE -> APGRIPSGGVSOICOTRAAARPCPOS
 WRRMSSCPALARPSPSSQCCMRKRCRCGSPITACRPV
 ASPHSPMRCRGTORPSPSPNSLAIALISFMGSCWAP
 OAGQGTISAVTLPSPSPWRASPPAPSPMTSGSRAPMGPN
 (IN GCSF-2).
 FT SEQUENCE 836 AA; 92156 MM; 9CC075DD CRC32;

Query Match 14.8%; Score 222; DB 1; Length 836;
 Best Local Similarity 29.2%; Pred. No. 2.9e-12;
 Matches 84; Conservative 41; Mismatches 129; Indels 34; Gaps 14;

QY 1 PTLIGSSLOATCSIHGDPGATAE-GLYTLNGRRRLPSELSRLN--TSTIALALANL 57
 DB 34 PIVHLDGPITASCILKQNCSHLDEPQILMLRLAGLPGKQOQLSDGTOSITLPLN 93
 QY 58 GSROOSDNLVCHARDG--ILAGSCLYVGLPPEKPNISC-MSRNNKDLTCRWTPAH 113
 DB 94 HTQD---FLSCCLMNGNSLIQILDVLRAGYPPAIPNLCLMNLITSSILCOEPGP- 149
 QY 114 GEPFLHNTYSK-KLMLWYGO---DNICEEHTYVPHSCHIP-KDLALFTYEIWEATN 168
 DB 149 -ETHLPSTFLKSKSGNCGTQGSILDCVPKDGQSHCCIPRHLHLLYQNMGIWQAN 207
 QY 169 RLGSARSDVLTLDVLYV-----TTDPPDVHVSNGLEQQLSIRWSPALNDEL 220
 DB 208 ALGTSMSPOLCLDPMDVYKLEPMLRTMDSPPEAPPAQAGLO---LCW--EPWQGLH 261
 QY 221 FQAKYQIRIYVE-DSYDVKVYDVVSNQ-TSCRLAGLPGYVYVQVNC 266
 DB 262 INKCELRHPRGEGASMAVGLPLPALOYELGCLLPATVITQING 309

RESULT 15
 ID GCSF_MOUSE STANDARD; PRT; 837 AA.
 AC P40223;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE GRANULOCYTE COLONY STIMULATING FACTOR RECEPTOR PRECURSOR (G-CSF-R).
 CSF3R OR CSFGR.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIROGNATHI; MORIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 90235283.
 RA FUKUNAGA R., ISHIZAKA-IKEDA E., SENO Y., NAGATA S.;
 RT "Expression cloning of a receptor for murine granulocyte colony-
 stimulating factor.";
 RL CELL 61:341-350(1990).
 RN [2]
 RP STRUCTURE BY NMR OF 225-333.
 RX MEDLINE; 97331327.
 RA YAMASAKI K., NAITO S., ANAGUCHI H., OKUBO T., OTA Y.;
 RT "Solution structure of an extracellular domain containing the WSWMS
 motif of the granulocyte colony-stimulating factor receptor and its
 interaction with ligand.";
 RL NAT. STRUCT. BIOL. 4:498-504(1997).
 CC -1- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR. IN
 CC ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION EVENTS AT
 CC THE CELL SURFACE.
 CC -1- SUBUNIT: DIMER (PROBABLE).

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: FOUND IN BONE MARROW.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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DR EMBL; M58288; G193455;
 DR PIR; A34898; A34898;
 DR PDB; 1GCF; 22-OCT-97.
 DR PDB; 1CTO; 22-OCT-97.
 DR MGI; 86533; CSFGR.
 DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
 DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR PFM; PFO0041; fn3; 3.
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
 KW REPEAT: 3D-STRUCTURE.
 FT SIGNAL 1 25
 FT CHAIN 26 837
 FT DOMAIN 26 626
 FT TRANSMEM 627 650
 FT DOMAIN 651 837
 FT DOMAIN 26 118
 FT DOMAIN 122 228
 FT DOMAIN 229 333
 FT DOMAIN 334 431
 FT DOMAIN 432 528
 FT DOMAIN 529 624
 FT DISULFID 132 143
 FT DISULFID 249 296
 FT DISULFID 267 310
 FT CARBOHYD 51 51
 FT CARBOHYD 94 94
 FT CARBOHYD 129 129
 FT CARBOHYD 186 186
 FT CARBOHYD 279 279
 FT CARBOHYD 392 392
 FT CARBOHYD 408 408
 FT CARBOHYD 474 474
 FT CARBOHYD 487 487
 FT CARBOHYD 582 582
 FT CARBOHYD 613 613
 SO SEQUENCE 837 AA; 93406 MM; D55F84D4 CRC32;

Query Match 14.7%; Score 221.5; DB 1; Length 837;
 Best Local Similarity 28.9%; Pred. No. 3.2e-12;
 Matches 83; Conservative 46; Mismatches 127; Indels 31; Gaps 14;

QY 1 PTLIGSSLOATCSIHGDPGATAE-GLYTLNGRRRLPSELSRLN--TSTIALALANL 56
 DB 34 PIVHLDGPVASCISIPNSKSLDQAKILMLRLADEPIQGDROHNLDPDGTOSLITLPLH 93
 QY 57 NGSROOSDNLVCHARDG--ILAGSCLYVGLPPEKPNISCMSR-NKKDLTCRWTPAHGE 115
 DB 94 N7T-QAFLFCIVPMWESYVGLLOAEHLHAGYPPASPNLSCLMHLTNSLYCOMEPGP--E 150
 QY 116 TPLATYISK-YKLR---WYGDNICEEHTYVPHSCHIP-KDLALFTYEIWEATNRL 170
 DB 151 THLPSTFLKSKSGNCGTQGSILDCVPKDGQSHCCIPRHLHLLYQNMGIWQANL 210
 QY 171 GSARSDVLTLDVLYV-----PDVHVSNGLEQQLSIRWVS-PPALKDLFL 221
 DB 211 GSSESPKCLDPMVDVYKLEPMLRLAGLPGKQOQLSDGTOSITLPLN 263

OY 222 OAKYORAVE-DYDMKVYDDV-SNOTSCRLAGKPGYVYVQRC 266
Db 264 EOCELRIOPOUKGANWILVHLPSSKDOFEICGLHOAPVYTLQMRG 310

Search completed: September 17, 1999, 03:10:14
Job time: 294 sec

QY	1	PTLLIGSSILATCSHGTGPATMEGLVITNGRRLPELSRLNTSLTALALANLNGSR	60
Db	48	PTLLIGSSILATCSVHGPBPATMEGLVITNGRRLPELSRLNTSLTALALANLNGSR	107
QY	61	QOSGDNLYCHARDGSIILAGSCLVYGLPEPEKFNISCSWRNKDITJCMTPGAHGETFLHT	120
Db	108	QOSGDNLYCHARDGSIILAGSCLVYGLPEPEKFNISCSWRNKDITJCMTPGAHGETFLHT	167
QY	121	NYSLKYKLFMTGQONTCEEHVTVGPHSCHIPKDIALTTPYEIWEANRNLGASRSDVLT	186
Db	168	NYSLKYKLFMTGQONTCEEHVTVGPHSCHIPKDIALTTPYEIWEANRNLGASRSDVLT	227
QY	181	DVLDVYTTDPPDVHVSRRVSGLEDQLSVRWVSPALNDYFOAKYQIRYRVSDVDKVV	246
Db	228	DVLDVYTTDPPDVHVSRRVSGLEDQLSVRWVSPALNDYFOAKYQIRYRVSDVDKVV	287
QY	241	DDVSNQNSCRLAGLPGTYFFVQYRCNCPBISYSSKKAAG	278
Db	288	DDVSNQNSCRLAGLPGTYFFVQYRCNCPBISYSSKKAAG	325

Query Match	20.18;	Score 302;	DB 4;	Length 206;
Best Local Similarity	39.28;	Pred. No. 4.9e-22;		

[illegible]

RESULT 5
ID 018880 PRELIMINARY: PRT: 296 AA.
AC 018880:
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE PROLACTIN RECEPTOR SHORT FORM.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97375450.
RA SCHUEER L.A., NAGEL R.J., GAO J., HORSEMAN N.D., KESSLER M.A.;
RT "Prolactin receptor heterogeneity in bovine fetal and maternal
tissues.";
RW Endocrinology 138:3187-3194(1997).
OR EMBL: AF027403; AAB83999.1; -
OR PFAM: PF00041; fn3; 2.
OR SEQUENCE 296 AA; 33854 MW; 8B40CCD8 CRC32;

Query Match
Best Local Similarity 18.3%; Score 276; DB 6; Length 296;
Matches 78; Conservative 37; Mismatches 88; Indels 40; Gaps 9;
41 SLALTSTLALALANLNGSRQSGDNLVCHARDGSLAGSLCYGLPPEKPNISGWSRN 100
7 SRVVFILFLFSLNG-----QS-----PPEKPLVRCRSPG 40
101 MKDLCTPTGAGHGTFTHTNSLTKYKLMWGYODNTCEHYHTVPHSCH-PRDALFTF 159
41 KETFCWEPGADG--LPTNYTLHYHKEGELIHECPYKKGPNCSFKSKHNSRM 98
160 YEIWEATNRGASRDVLTLDVYVTTDPPDVHVSRLGLEDQSYRVY--SPALK 217
99 YVIVNAINONGISSDPLVHYVYVEPEPPANTL-ELKHEDRKRYLWKNSPPVMT 157
218 D-----ELFOAKYQIRYVEDSVPMKYVDVSNQSCSLAGLKPCTVTFVQVRCNPFQ 272
158 DVKSGMFLIO--YEIRLKPKEATDWE-THFTLKQTQKIFMLYPOKYLQVIRCPDHG 214
273 GSK 275
215 WSE 217

SUPT 6
ID 093404 PRELIMINARY: PRT: 346 AA.
AC 093404:
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-MAY-1999 (TREMblrel. 10, Last annotation update)
DE PROLACTIN RECEPTOR (FRAGMENT).
OS Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorphia;
OC Perciformes; Labroidae; Cichlidae; Tilapia.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-GILL;
RA SHIRAIISHI K., MATSUDA M., MORI T., TETSUYA H.;
RT "Expression of prolactin and cortisol receptor gene in early-life
stages of tilapia (Oreochromis mossambicus).";
RW Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
OR EMBL: AF080247; AAC31825.1; -
OR PFAM: PF00041; fn3; 2.
OR NOR_TER 346 346
OR SEQUENCE 346 AA; 39203 MW; 1E8A63B9 CRC32;

Query Match
Best Local Similarity 15.9%; Score 240; DB 13; Length 346;
Matches 64; Conservative 27; Mismatches 83; Indels 16; Gaps 8;
QY 88 PEKPNISGWSRNMDLCTPTGAGHGTFTHTNSLTKYKLMWGYODNTCEHYHTVPHSCH 147
DB 29 PGKPEITCRSPKEKETFQWPKPSDGG--LPTNYTLHYHKEGELIHECPYKKGPNCSFKSKHNSRM 86
QY 148 CHIRK-DLALTPEIWEATNRGASRDVLTLDVYVTTDPPDVHVSRLGLEDQ- 205
DB 87 CFENKNDTLIWSYINITYVATNALGKTSYDVIDVYIYKPHPEKLEVT--VMKDOG 143
QY 206 ---LSVRVSPALKDF---LFOAKYQIRYVED-SYDMKYVDVSNQSCSLAGLKPCT 258
DB 144 WPELRVSW-EPPHADRSGMWTILYELRVKLEDESEWE-NHAAGQKKNFNLFSRSG 201
QY 259 YVIVQVRCNP 268
DB 202 TYLIQVRCNP 211

RESULT 7
ID 018985 PRELIMINARY: PRT: 198 AA.
AC 018985:
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE SOLUBLE PROLACTIN RECEPTOR.
OS Cervus elaphus nelsoni (American elk).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae; Cervidae;
RN [1]
RP SEQUENCE FROM N.A.
RX JABBOUR H.N.;
RA Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
OR EMBL: Y14753; CAJ75048.1; -
OR PFAM: PF00041; fn3; 1.
OR SEQUENCE 198 AA; 22652 MW; COABAB0 CRC32;

Query Match
Best Local Similarity 15.3%; Score 230.5; DB 6; Length 198;
Matches 62; Conservative 31; Mismatches 76; Indels 15; Gaps 7;
QY 73 DGSILAGSCLYGLPPEKPNISGWSRNMDLCTPTGAGHGTFTHTNSLTKYKLMWY 132
DB 18 NASLNGS-----PEKPKIIRCRSPGKETFTCWEPGSDG--LPTNYTLHYHKEGEL 70
QY 133 QDNTCEHYHTVPHSCH-PRDALFTPEIWEATNRGASRDVLTLDVYVTTDPP 191
DB 71 LIHECPDYKSGNCTCYFSKHSIKRIYIVYVATNALNGVSSDPLVYIYVPEPP 130
QY 192 PDVHVSRLGLEDQSYRVY--PPALKDF---LFOAKYQIRYVEDSVDMKYVDVSNQ 246
DB 131 ANLTL-ELKHEDRKRYLWKNSPPVMTLTVKSGMFLIOYEIRLKPKEATDWE-HDDLHP 188
QY 247 TSCR 250
DB 189 TSSR 192

RESULT 8
ID 046386 PRELIMINARY: PRT: 217 AA.
AC 046386:
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-MAY-1999 (TREMblrel. 10, Last annotation update)
DE PROLACTIN RECEPTOR (FRAGMENT).
RN PRLR.

OS Mustela vison (American mink).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-TESTIS;
 RA DOUGLAS D.A., SONG J.-H., HOUDE A., MURPHY B.D.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF029294; AAB8899.1;
 FR PFM; PF00041; fn3; 1;
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 217 AA; 24850 MW; F77A3B9D CRC32;

Query Match 13.8%; Score 208; DB 6; Length 217;
 Best Local Similarity 32.7%; Pred. No. 8.4e-13;
 Matches 54; Conservative 29; Mismatches 72; Indels 10; Gaps 6;

OY 110 PGHGFTHNTYSLKRYKRWGDNTECEYHTVGPSCHI-PKDLALFTEIWEATN 168
 DB 2 PEDGG--PRTYTLTHHEGETTTECPDYITSGPNSCTFKNKTSITMTITINATN 59
 OY 169 RIGSARSDVLTLDVYTTDPDPVHVRVSGLEDQLSVRWVS--PPALKEF--LFOA 223
 DB 60 EMGSSSDRYVTLTYIVEDPPVNSTL-ELKQPEDKTYIMTKWPTPLVDVRSGLML 118
 OY 224 KVOIRVEDSDVKYVDVSNQTSCLAGLKGTYFYOVRCNP 268
 DB 119 OYIRLKEKATDME-THFAGLOTOKILSYGOKYLVORCKP 162

RESULT 9
 ID P79203 PRELIMINARY; PRT; 335 AA.
 AC P79203;
 DT 01-MAY-1997 (Tremblrel. 03, Created)
 DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE PROLACTIN RECEPTOR (FRAGMENT).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 OC Caprinae; Ovis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-M22/80; TISSUE-ANTERIOR PITUITARY;
 RA FORTONESE D.T., BROOKS J., INGLETON P., MCNEILLY A.S.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y10578; CAA71597.1;
 FR PFM; PF00041; fn3; 1;
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 335 AA; 38326 MW; 88A05AB1 CRC32;

Query Match 13.5%; Score 203; DB 6; Length 335;
 Best Local Similarity 31.5%; Pred. No. 4.6e-12;
 Matches 53; Conservative 28; Mismatches 63; Indels 24; Gaps 6;

OY 114 GETPLHTYSLKRYKRWGDNTECEYHTVGPSCHI-PKDLALFTEIWEATNRLGS 172
 DB 8 GETLH-----ECPDYITGSPNSCTFKNKTSITMTITINATN 51
 OY 173 ARSDVLTLDVYTTDPDPVHVRVSGLEDQLSVRWVS--PPALKEF--LFOA 227
 DB 52 SSDDPLVDVYTYIVEDPPVNSTL-ELKQPEDKTYIMTKWPTPLVDVRSGLML 110
 OY 228 RYVEDSDVKYVDVSNQTSCLAGLKGTYFYOVRCNPFGITGSK 275
 DB 111 RLKPEKATDME-THFAPKLTOKILSYGOKYLVORCKPDPHGWSE 157

RESULT 10
 ID 099665 PRELIMINARY; PRT; 862 AA.
 AC 099665;
 DT 01-MAY-1997 (Tremblrel. 03, Created)
 DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE IL-12 RECEPTOR BETA2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA PRESKY D.H., YANG H., MINETTI L.J., CHUA A.O., MDAVI N., WOU C.Y.,
 RA GATELY M.K., GUBLER U.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U64198; AAB36675.1;
 FR PFM; PF00041; fn3; 37134 MW; 5FE4FBD5 CRC32;
 SQ SEQUENCE 862 AA; 97134 MW; 5FE4FBD5 CRC32;

Query Match 11.8%; Score 178; DB 4; Length 862;
 Best Local Similarity 24.8%; Pred. No. 4.6e-09;
 Matches 73; Conservative 43; Mismatches 106; Indels 72; Gaps 12;

OY 3 LLIGSLATCSIHDTPOATAGLWTL-----NGRRPSELRL-L 44
 DB 41 ILGSTVNTCSL-----KPRQGFHYSRNKLILYKFRDRINRHHGSLNSQVGLPL 94
 OY 45 NSTALALANNGSGNDLVNCHARGSTILASCLVYG-PPEKPFISGSRMK-D 103
 DB 95 GTTLFVCKLACINSDEIQ-----ICGAEITVGAPEOPONLSCTQKQEOGT 140
 OY 104 LCRMTPGAHGETLHTNLSKY---KLRYGQ--DNTCEHYTVG-----PHSCH 150
 DB 141 VACTWGRG--DTHLYTETTLQSGPKNTWKQCKDLYC-DYLDGINLPSPESNFT 197
 OY 151 PKDLALFTEIWEATNRLGSARSDVLTLDVYTTDPDPVHVRVSGLEDQLSVRW 210
 DB 198 AK-----VTAVNSIGSSSSLPSTFTEFDIVRPMPWIRIKFORASVRCGLVW 246
 OY 211 VSPALKEFLFOAKYIRRVEDSDVKYVDVSNQTSCLAGLKGTYFYOV 264
 DB 247 -----RDEGLVLLNRLRYRPSNSRLMNVNVTKANGRHDLCKPTEYEFQI 294

RESULT 11
 ID 016542 PRELIMINARY; PRT; 422 AA.
 AC 016542; 014626;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE INTERLEUKIN-11 RECEPTOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-MUSCLE;
 RC MEDLINE; 95399754.
 RA CHEREL M., SOREL M., LEBEAU B., DUBOIS S., MOREAU J.F., BATAILLE R.,
 RA MINVILLE S., JACOUES Y.;
 RT "Molecular cloning of two isoforms of a receptor for the human
 hematopoietic cytokine interleukin-11.";
 RL Blood 86:2534-2540(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA VAN LEUVEN F., STAS L., HILLIKER C., MIYAKE Y., GOSSLER A.;
 RA Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 3-390 FROM N.A.
 RC TISSUE-PLACENTA;

RA CHEREL M., SOREL M., DUBOIS S., LEBEAU B., MOREAU J., JACQUES Y.,
 RA MINVILLE S.,
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U32324; AAB36492.1;
 DR EMBL: 238102; CAAB6224.1;
 DR EMBL: U32323; AAB36491.1;
 DR EMBL: 246595; CAAB6570.1;
 DR PFAM: PF00041; fn3; 2;
 DR PFAM: PF00047; fn3; 1;
 SO SEQUENCE 422 AA; 45222 MW; 29011292 CRC32;

Query Match 11.6%; Score 175; DB 4; Length 422;
 Best Local Similarity 24.3%; Pred. No. 3.5e-09;
 Matches 70; Conservative 46; Mismatches 118; Indels 54; Gaps 13;

OY 6 GSSLOATGSHHDTGATN-EGLYTLNG--RLDSELSRLNTSLALANLNGSRQO 62
 DB 41 GRVYKLC- - - - -GVTAGDPSWFRDEPKLQGPDSGLGHELVLAQADSTDEGT- - - - - 92
 OY 63 SGDNLVCHARDGSIAGSGLYVGLPREKPFNISCWSRNKDLCTKTPAHGETFLHNY 122
 DB 92 - - - - -YICOTLGBALGCTVTLQIGYPPAPV-VSCQADYENFSCWSPSQ--ISGLPTRY 144
 OY 123 SLKKYKLVYGDNTCEHYVPHSCHIPK- - - - -LALFPEIWEATNRLG 171
 DB 145 LTVYRKKTIVLGDSDRSRSPSTGPPWC--PDPLGAARCVHAERWSQIRIVTEVNPGL 202
 OY 172 SARSDVLTLDVLTVDVTPDPDVHVSRYGLEDQSVRWSP--PALKDFQAKYQIR 228
 DB 203 -ASTRLDVSLOSILRPDPQGLRVEVPGYPRRLRASMTYVPSMPCQPHFL--KFRQ 259
 OY 229 YRVDSYDMKVVDDVSNQTSCLAGL- - - - -PGTYFFVOYRNP 269
 DB 260 YRPAQHAFMSTVEP- - - - -AGLEEVITDAVAGLPHAVRVSARDF 298

RESULT 12
 ID 088507 PRELIMINARY; PRT: 372 AA.
 AC 088507;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
 DE CILIARY NEUROTROPHIC FACTOR RECEPTOR ALPHA PRECURSOR.
 GN CNTRF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 (1)

SEQUENCE FROM N.A.
 RC TISSUE-BRAIN, SKELETAL MUSCLE;
 RA MAEDA M., YAGUCHI N., HANYU C., NAKATA Y., ONODA N., TULIN E.E.,
 RA KOJIMA T., HASEGAWA M., KIKUCHI Y., NOKURA H.;
 RT "Mouse homolog of human ciliary neurotrophic factor receptor."
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF066615; AAC25711.1;
 DR PFAM: PF00041; fn3; 1;
 DR PFAM: PF00047; fn3; 1;
 KW Signal.

FT SIGNAL 21 20 POTENTIAL.
 FT CHAIN 21 336 CILIARY NEUROTROPHIC FACTOR RECEPTOR
 FT FT
 SO SEQUENCE 372 AA; 40831 MW; 9A40FE12 CRC32;

Query Match 11.5%; Score 172.5; DB 11; Length 372;
 Best Local Similarity 28.1%; Pred. No. 5.2e-09;
 Matches 73; Conservative 34; Mismatches 114; Indels 39; Gaps 14;

OY 20 PGATAE- - - - -GLYTLNGRLPSELRLNTSLALANLNGSRQSGDVLVCHARGSI 76
 DB 45 PCGTASDAVAIVRVNGTDLAPD- - - - -LLNQSILRLSELGHSGLYA- - - - -CFHRDSWH 96

OY 77 LAGS-CLYVGLPREKPFNISCWSRNK-DLTCRW- - - - -TPGAHGETFLHNTSLKTK 127
 DB 97 LRHQVLHVLGGLPREPV-LSGRSNTYKGFYCSMHPRTTYLPNTFNVTYLGSKIM- - - - - 153
 OY 128 LRRYGDNTCEHYVPHSCHIPDLALFT--PYEIWEATNRLGARSVDLTLDV 185
 DB 153 - - - - -VCEKDPAL-KNRCHI-RYMLFSTIKKYSISVSNALGH-NTTAITDEFTI 201
 OY 186 YTTDPDVHVSRYGLEDQSVRWSPALKD-FLFQAKYQIRRVDSYDMKVVDSV 244
 DB 202 VKPDPPENVAPVPSNPRRLVETWQTPSTMPDPSFPLKFLRYRPLLDQMOHV-ELS 260
 OY 245 NOTSCLAGLKPQTYFFVOY 264
 DB 261 DGTAMITDAVAGKEIIV 280

RESULT 13
 ID P97378 PRELIMINARY; PRT: 874 AA.
 AC P97378;
 DT 01-MAY-1997 (Tremblrel. 03, Created)
 DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE INTERLEUKIN 12 RECEPTOR, BETA 2 (IL-12 RECEPTOR BETA2).
 GN IL12RB2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 (1)
 RC SEQUENCE FROM N.A.
 RA PRESKY D.H., YANG H., MINETTI L.J., CHUA A.O., NABAYI N., WOU C.Y.,
 RA GATELY M.K., GUBLER U.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U64199; AAB36676.1;
 DR MGI: 1270861; IL12RB2.
 DR PFAM: PF00041; fn3; 4;
 SO SEQUENCE 874 AA; 98196 MW; 9B90EB47 CRC32;

Query Match 11.4%; Score 171; DB 11; Length 874;
 Best Local Similarity 24.8%; Pred. No. 2.3e-08;
 Matches 73; Conservative 54; Mismatches 115; Indels 52; Gaps 14;

OY 1 PTLIGSSLATGSH- - - - -GDTPGATA- - - - -EGLYTLNGRL- - - - -PSLSR 42
 DB 39 PVYPLGSANISCSLNRKQCSHRPSSNELILKLVNDVLYENLHGKVDHGHSTFQ 98
 OY 43 LLNTST-LALANLNGSRQSGDNL-VCHARDGSIAGSCLYVGLPREKPFNISCWSRN 100
 DB 99 VTNLSLQMTLFCVCKLNSNOKKPPVVC- - - - -GVEISGVAPBPONISVQOEG 149
 OY 101 MK-DLTCRWTPGAHGETFLHNTSLKTKLRMGODN-TCE-EYHTVGPHSC- - - - -HI 150
 DB 150 ENGVASWNSGR-VTYLKTNTYQLS- - - - -GPNILTCQKQCFSDNRQNCRLDGINTL 203
 OY 151 PDLALFTPEIWEATNRLGARSVDLTLDVLTVDVTPDPDVHVSRYGLEDQSVRW 210
 DB 204 SPDLA-ESREIVVTAINDGNSSLPHEFTFDIVLPLPMDIRLNFNLASSRGTLCM 262
 OY 211 VSPPALKDFLQAKYQIRRVDSYDMKVVDSVNOTSCLAGLAKGTYFFVOY 264
 DB 263 - - - - -EDSGVYVNLQRLRQPLNTSMNVNATNAGKYDLRLRPFTEFEFOI 310

RESULT 14
 ID P70225 PRELIMINARY; PRT: 432 AA.
 AC P70225; 009074;
 DT 01-FEB-1997 (Tremblrel. 02, Created)
 DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)

DE INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 2 PRECURSOR (IL11RA2)
 DE (IL-11RBETA) (INTERLEUKIN-11 RECEPTOR BETA CHAIN).
 GN IL11RA2 OR IL-11RBETA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CD1; TISSUE-TESTIS;
 RX MEDLINE: 97129000.
 RA BILINSKI P., HALL M.A., NEUHAUS H., GISSEL C., HEATH J.K.,
 RA GOSSLER A.;
 RT "Two differentially expressed interleukin-11 receptor genes in the
 RT mouse genome.";
 RL Biochem. J. 320:359-363(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CD1; TISSUE-TESTIS;
 RX MEDLINE: 96278810.
 RA ROBB L., HILTON D.J., WILSON T.A., BEGLEY C.G.;
 RT Structural analysis of the gene encoding the murine interleukin-11
 RT receptor alpha-chain and a related locus.";
 RL J. Biol. Chem. 271:13754-13761(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CD1; TISSUE-TESTIS;
 RX MEDLINE: 97230451.
 RA ROBB L., HILTON D.J., BROOK-CARTER P.T., BEGLEY C.G.;
 RT Identification of a second murine interleukin-11 receptor
 RT alpha-chain gene (IL11RA2) with a restricted pattern of expression.";
 RL Genomics 40:387-394(1997).
 CC [1]- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11.
 CC [1]- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC [1]- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC [1]- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC [1]- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC [1]- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 DR EMBL: X94157; CA63872.1; JOINED.
 DR EMBL: X94158; CA63872.1; JOINED.
 DR EMBL: X94159; CA63872.1; JOINED.
 DR EMBL: X94160; CA63872.1; JOINED.
 DR EMBL: X94161; CA63872.1; JOINED.
 DR EMBL: X98519; CA67144.1; JOINED.
 DR EMBL: U69491; AAC53114.1; JOINED.
 DR MGD: MGI:109123; IL11RA2.
 DR PFAM: PF00041; fn3; 2.
 DR PFAM: PF00047; fn3; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin fold; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 432 INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 2.
 FT DOMAIN 24 367 EXTRACELLULAR (POTENTIAL).
 FT TRAMSEM 368 393 POTENTIAL.
 FT DOMAIN 394 432 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 41 102 IG-LIKE C2-TYPE DOMAIN.
 FT CAROHD 127 127 POTENTIAL.
 FT CAROHD 127 127 POTENTIAL.
 FT CAROHD 194 194 S -> P (IN CA63872).
 FT CONFLICT 200 200 S -> L (IN CA63872).
 FT CONFLICT 384 384 V -> L (IN CA63872).
 SO SEQUENCE 432 AA; 46721 MW; C4FD7DEC CRC32;

Query Match 11.0%; Score 165; DB 11; Length 432;
 Best Local Similarity 25.9%; Pred. No. 3.4e-08;
 Matches 63; Conservative 39; Mismatches 105; Indels 36; Gaps 12.

DB 100 VSGWVTLKLGFPNAP- EVSCADVNFSCWSPGO--VGLPTRTITSTYKRTLPGA 156

OY 135 NCEEHYVGPSCHPKD-----LALFPEIWEATNRLGARSVDVLTLDV 183
 DB 157 EGRSPSTGPPMC--PQPLEASRCVVGAEWSEYRINVEVNSLG-ASTCLDVRQ 213
 OY 184 DVVTDPPDVHVSRYGLEDLVYRWSPALK---DLFOAKYOIRYVEDSDYMKV 240
 DB 214 SLRPDPGLRVESVPGYPRRLHSMWTYPASWRQPHFL--KPRLOYRPAQHPAMSTV 271
 OY 241 DDV 243
 DB 272 EPI 274

RESULT 15
 ID 064385 PRELIMINARY; PRT; 432 AA.
 AC 064385;
 DT 01-JAN-1998 (TRENBLREL. 05, Created)
 DT 01-JAN-1998 (TRENBLREL. 05, Last sequence update)
 DT 01-NOV-1998 (TRENBLREL. 08, Last annotation update)
 DE INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 1 PRECURSOR (NR1) (ETL2)
 DE (IL-11RA1) (IL11RA1).
 GN IL11RA1 OR IL11RA OR ETL2 OR ETL2/IL11 REC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6 X CBA; TISSUE-LIVER;
 RX MEDLINE: 95045367.
 RA HILTON D.J., HILTON A.A., RAJCEVIC A., RAKAR S., HARRISON-SMITH M.,
 RA GOUCH N.M., BEGLEY C.G., METCALF D., NICOLA N.A., WILSON T.A.;
 RT Cloning of a murine IL-11 receptor alpha-chain; requirement for
 RT gp130 for high affinity binding and signal transduction.";
 RL EMBO J. 13:4765-4775(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C AND C57BL/6; TISSUE-EMBRYO;
 RA NEUHAUS H., BETENHAUSEN B., BILINSKI P., SIMON-CHARZOTTES D.,
 RA GOSLER J.L., GOSSLER A.;
 RL Dev. Biol. 166:521-542(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C AND C57BL/6;
 RA GOSLER A., AND C57BL/6;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC MEDLINE: 97129000.
 RA BILINSKI P., HALL M.A., NEUHAUS H., GISSEL C., HEATH J.K.,
 RA GOSSLER A.;
 RT "Two differentially expressed interleukin-11 receptor genes in the
 RT mouse genome.";
 RL Biochem. J. 320:359-363(1996).
 CC [1]- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11.
 CC [1]- BINDS TO IL-11 WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A
 CC SIGNAL.
 CC [1]- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC [1]- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC [1]- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC [1]- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC [1]- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 DR EMBL: X74953; CA532908.1; JOINED.
 DR EMBL: U14412; AA53248.1; JOINED.
 DR EMBL: X94162; CA63873.1; JOINED.
 DR EMBL: X94163; CA63873.1; JOINED.
 DR MGD: MGI:107426; IL11RA1.
 DR PFAM: PF00041; fn3; 2.
 DR PFAM: PF00047; fn3; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin fold; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 432 INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 2.
 FT DOMAIN 24 367 EXTRACELLULAR (POTENTIAL).
 FT TRAMSEM 368 393 POTENTIAL.
 FT DOMAIN 394 432 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 41 102 IG-LIKE C2-TYPE DOMAIN.
 FT CAROHD 127 127 POTENTIAL.
 FT CAROHD 127 127 POTENTIAL.
 FT CAROHD 194 194 S -> P (IN CA63872).
 FT CONFLICT 200 200 S -> L (IN CA63872).
 FT CONFLICT 384 384 V -> L (IN CA63872).
 SO SEQUENCE 432 AA; 46721 MW; C4FD7DEC CRC32;

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: September 17, 1999, 03:08:15 ; Search time 64.1 Seconds

(without alignments)
129.331 Million cell updates/sec

Title: US-09-037-657-25

Perfect score: 1919

Sequence: 1 TLNGRRLPPELSRVLNASTL.....TRGSCPRADGAREVLPDKL 350

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database: A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1919	100.0	350	W55015	Amino acid sequence
2	1919	100.0	392	W70840	Human zcyto5 vari
3	1919	100.0	389	W70844	Human zcyto5 vari
4	1919	100.0	425	W70861	Allelic variant of
5	1918	99.9	389	W70850	Human zcyto5 vari
6	1918	99.9	389	W70851	Human zcyto5 vari
7	1917	99.9	389	W70852	Human zcyto5 vari
8	1916	99.8	389	W70846	Human zcyto5 vari
9	1916	99.8	389	W70847	Human zcyto5 vari
10	1915	99.8	389	W70849	Human zcyto5 vari
11	1915	99.8	389	W70848	Human zcyto5 vari
12	1914	99.7	389	W70853	Human zcyto5 vari
13	1800	93.6	408	W59805	Amino acid sequence
14	1796	93.6	422	W70860	Human zcyto5 vari
15	1789	93.2	385	W70839	Human zcyto5 vari
16	1789	93.2	385	W70842	Human zcyto5 vari
17	1772	92.3	413	W55011	Novel haemopoietin
18	1768	92.1	425	W55012	Novel haemopoietin
19	1768	92.1	425	W59804	Nucleotide sequence
20	1768	92.1	385	W70841	Human zcyto5 vari
21	1768	92.1	425	W70862	Rat zcyto5 vari
22	1436	74.8	303	W70845	Human zcyto5 vari
23	1432	74.6	303	W70843	Human zcyto5 vari
24	1330	68.8	278	W55014	Protein sequence
25	631.5	32.9	155	W55013	Novel haemopoietin
26	506	26.4	186	W55016	Amino acid sequence
27	332	17.3	622	R10795	Human prolactin re
28	331.5	17.3	211	R10795	Human prolactin re
29	323.5	17.0	211	R10795	Human prolactin re
30	299	15.6	917	R26334	Human gp130-C-gam
31	292.5	15.2	332	R10799	Human gp130-C-gam
32	290.5	15.1	918	R10545	Human gp130-C-gam
33	290.5	15.1	918	R10545	Human gp130-C-gam
34	290.5	15.1	918	R10545	Human gp130-C-gam
35	290.5	15.1	918	R10545	Human gp130-C-gam
36	290.5	15.1	918	R10545	Human gp130-C-gam
37	290.5	15.1	918	R10545	Human gp130-C-gam
38	290.5	15.1	918	R10545	Human gp130-C-gam
39	289	15.1	329	R10545	Human gp130-C-gam
40	277.5	14.5	708	R37859	Rheumatoid arthrit
41	263.5	13.7	630	R37804	Human gp130 N-term
42	263.5	13.7	630	R37804	Human gp130 N-term
43	250.5	13.1	180	W00404	Interleukin-6 anta

ALIGNMENTS

RESULT 1

44 236 12.3 837 1 R14254
45 233.5 12.2 334 1 R99140

W55015 standard; Protein; 350 AA.
W55015
AC W55015;
DT 29-SEP-1998 (first entry)
DE Amino acid sequence of clone Hfx-66 encoding human NR6.
KW Hemopoietin receptor; cell proliferation; cell differentiation; cancer;
KW cell survival; therapeutic; neuronal proliferation; drug screening;
KW human.
OS Homo sapiens.
PN MO9811225-A2.
PD 19-MAR-1998.
PF 11-SEP-1997; G02479.
PR 11-SEP-1996; AU-002246.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PI (DZIE/) DIEGLEWSKA H E.
PI Alexander W, Fabrl L, Farley A, Hilton DJ, Kikuchi Y,
PI Kojima T, Maeda M, Nash A, Nicola NA, Raker S, Willison T,
PI Zhang J,
DR WPI; 98-260970/23.
DR N-PSDB; V27144.
PT New isolated haemopoietin receptor - used for developing products
PT for modulating proliferation, differentiation and survival of cells,
PS e.g. neuronal cells
PS Claim 18; Page 102-104; 182pp; English.
CC The NR6 protein is a novel Haemopoietin receptor (HR). Interaction
CC between the novel HR and a ligand facilitates proliferation,
CC differentiation and survival of a wide variety of cells. The HR and its
CC derivatives can be used for modulating the activity of the receptors e.g.
CC to regulate development, maintenance or regeneration in an array of
CC different cells and tissues in vitro and in vivo. They can be present in
CC therapeutics used for modulating neuronal proliferation, differentiation
CC and survival. The products can also be used for detection and diagnosis,
CC e.g. for cancers or predisposition to cancers, or for drug screening.
SO Sequence 350 AA;

Query Match. 100.0%; Score 1919; DB 1; Length 350;
Best local similarity 100.0%; Pred. No. 2.6e-173;

Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLNGRRLPPELSRVLNASTLALANLNGSRSGDNLYCHARDGSIILAGSCLYVGLPPE 60
DB 1 TLNGRRLPPELSRVLNASTLALANLNGSRSGDNLYCHARDGSIILAGSCLYVGLPPE 60
QY 61 KPNVNCWSKMKMDLCRTWPGAHGTFILNTSLKYLKRWYQDNTCEHYTVGPHSCH 120
DB 61 KPNVNCWSKMKMDLCRTWPGAHGTFILNTSLKYLKRWYQDNTCEHYTVGPHSCH 120
QY 121 IPDNLALFPPELVEATNRLGARSVDVLTLDVVTATDPPDVHVRGLEDLSVR 180
DB 121 IPDNLALFPPELVEATNRLGARSVDVLTLDVVTATDPPDVHVRGLEDLSVR 180
QY 181 WSPPLAKDFLFOAKQIQRVEDSVDMRVVDVSNQTSCLAGLKPQTVYEVQVRCNPF 240
DB 181 WSPPLAKDFLFOAKQIQRVEDSVDMRVVDVSNQTSCLAGLKPQTVYEVQVRCNPF 240
QY 241 GIGSKKAGIWSHPTAASPRSRPPGGGACPRGCESSGVRRELKQFLGLMK 300
DB 241 GIGSKKAGIWSHPTAASPRSRPPGGGACPRGCESSGVRRELKQFLGLMK 300
QY 301 HAYCSNLSFRLYDQWRAWQKSHKTRNQRTRGSCPRADGAREVLPDKL 350
DB 301 HAYCSNLSFRLYDQWRAWQKSHKTRNQRTRGSCPRADGAREVLPDKL 350

RESULT 2
 ID W70840 standard; Protein: 392 AA.
 AC W70840:
 DT 17-MAR-1999 (first entry)
 DE Human zcyto5 variant.
 KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KW cardiac pathology; heart enlargement; zcyto5 ligand; variant.
 OS Homo sapiens.
 PN MO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelnberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1; Page 81-82; 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcyto5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SQ Sequence 392 AA;

Query Match 100.0%; Score 1919; DB 1; Length 392;
 Best Local Similarity 100.0%; Pred. No. 3e-173;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLNGRRRLPELSESRVNLASTLALANLNGSRQSGDNLVCHARDGSIAGSLYGLPE 60
 DB 43 TLNGRRRLPELSESRVNLASTLALANLNGSRQSGDNLVCHARDGSIAGSLYGLPE 102
 QY 61 KPVNISCSKMKKDLTCMTGAGETFLHTNYSIKYLRMYGQDNCEHYHTVGPSSCH 120
 DB 103 KPVNISCSKMKKDLTCMTGAGETFLHTNYSIKYLRMYGQDNCEHYHTVGPSSCH 162
 QY 121 IPKDLALFTPEIWEATNRLGARSVDLTLDIDVYTTDPPDVHVRVGLDQLSVR 180
 DB 163 IPKDLALFTPEIWEATNRLGARSVDLTLDIDVYTTDPPDVHVRVGLDQLSVR 222
 QY 181 WSPSPALKDLEFOAKYQIRYVEDSVDMKVVDDVSNQTSCLAGLKPCTYVFVQRCNPF 240
 DB 223 WSPSPALKDLEFOAKYQIRYVEDSVDMKVVDDVSNQTSCLAGLKPCTYVFVQRCNPF 282
 QY 241 GYGSKKAIGSEMSHPAASPTPSERPGGACPEPSSGPPVRELKQFLGMLKK 300
 DB 283 GYGSKKAIGSEMSHPAASPTPSERPGGACPEPSSGPPVRELKQFLGMLKK 342
 QY 301 HAYCSNLSFRILYDQWRAMOKSHKTRNOHRTGSCPRADGARREVLDPKL 350
 DB 343 HAYCSNLSFRILYDQWRAMOKSHKTRNOHRTGSCPRADGARREVLDPKL 392

DE Human zcyto5 variant.
 KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KW cardiac pathology; heart enlargement; zcyto5 ligand; variant.
 OS Homo sapiens.
 PN MO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelnberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for, e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1; Page 87-88; 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcyto5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and
 CC therapeutically to modify zcyto5 ligand effects.
 SQ Sequence 389 AA;

Query Match 100.0%; Score 1919; DB 1; Length 389;
 Best Local Similarity 100.0%; Pred. No. 3e-173;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLNGRRRLPELSESRVNLASTLALANLNGSRQSGDNLVCHARDGSIAGSLYGLPE 60
 DB 40 TLNGRRRLPELSESRVNLASTLALANLNGSRQSGDNLVCHARDGSIAGSLYGLPE 99
 QY 61 KPVNISCSKMKKDLTCMTGAGETFLHTNYSIKYLRMYGQDNCEHYHTVGPSSCH 120
 DB 100 KPVNISCSKMKKDLTCMTGAGETFLHTNYSIKYLRMYGQDNCEHYHTVGPSSCH 159
 QY 121 IPKDLALFTPEIWEATNRLGARSVDLTLDIDVYTTDPPDVHVRVGLDQLSVR 180
 DB 160 IPKDLALFTPEIWEATNRLGARSVDLTLDIDVYTTDPPDVHVRVGLDQLSVR 219
 QY 181 WSPSPALKDLEFOAKYQIRYVEDSVDMKVVDDVSNQTSCLAGLKPCTYVFVQRCNPF 240
 DB 220 WSPSPALKDLEFOAKYQIRYVEDSVDMKVVDDVSNQTSCLAGLKPCTYVFVQRCNPF 279
 QY 241 GYGSKKAIGSEMSHPAASPTPSERPGGACPEPSSGPPVRELKQFLGMLKK 300
 DB 280 GYGSKKAIGSEMSHPAASPTPSERPGGACPEPSSGPPVRELKQFLGMLKK 339
 QY 301 HAYCSNLSFRILYDQWRAMOKSHKTRNOHRTGSCPRADGARREVLDPKL 350
 DB 340 HAYCSNLSFRILYDQWRAMOKSHKTRNOHRTGSCPRADGARREVLDPKL 389

RESULT 4
 ID W70861 standard; Protein: 425 AA.
 AC W70861:
 DT 17-MAR-1999 (first entry)
 DE Allelic variant of human zcyto5.
 KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KW cardiac pathology; heart enlargement; zcyto5 ligand; allelic variant.
 OS Homo sapiens.

PN W09849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 DR N-PSDB: V70895.
 PT New mammalian cytokinin-like receptor Zcytors - useful for, e.g.
 PT down-regulating Zcytors natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1: Page 71-72; 55pp; English.
 CC The present sequence represents an allelic variant of protein designated
 CC Zcytors, which is a cytokinin-like receptor. Soluble Zcytors may be
 CC administered to down-regulate the effects of a growth and/or maintenance
 CC factor in thyroid, heart, and skeletal muscle for example to lessen the
 CC effect of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytors could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible Zcytors ligands. A probe
 CC comprising Zcytors DNA or RNA can be used to determine the presence
 CC and integrity of the Zcytors gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcytors and
 CC therapeutically to modify Zcytors ligand effects.
 SQ Sequence 425 AA;

Query Match 100.0%; Score 1919; DB 1; Length 425;
 Best Local Similarity 100.0%; Pred. No. 3,4e-173;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLNGRLPELPSVYLAATLALANLNGSRSGDNLVCHARDGSLAGSCLYGLPPE 60
 DB 76 TLNGRLPELPSVYLAATLALANLNGSRSGDNLVCHARDGSLAGSCLYGLPPE 135
 QY 61 KPVNISCWKNMKDLCRTPGAHGETFLHTNYSKYLKRWYGDNTCEHYHVGHSCH 120
 DB 136 KPVNISCWKNMKDLCRTPGAHGETFLHTNYSKYLKRWYGDNTCEHYHVGHSCH 195
 QY 121 IPKDLALFPEIWEATNRLGARSADVLTLDLVYTTDPPDVHVSRYGLEDOLSVR 180
 DB 196 IPKDLALFPEIWEATNRLGARSADVLTLDLVYTTDPPDVHVSRYGLEDOLSVR 255
 QY 181 WSPPLAKDFLFQAKQIQRVEDSVDMKRVYDVNSQTSCLAGLPGTYVEVQVRCNPF 240
 DB 256 WSPPLAKDFLFQAKQIQRVEDSVDMKRVYDVNSQTSCLAGLPGTYVEVQVRCNPF 315
 QY 241 GIYGSKKAIGWEMSHPTASTPRSERPPGGACPRGGEPSGVRRELKQFLGWLKK 300
 DB 316 GIYGSKKAIGWEMSHPTASTPRSERPPGGACPRGGEPSGVRRELKQFLGWLKK 375
 QY 301 HAYCSNLSFRLYDQWRAMWQKSHKTRNGHRTGSCPRADGARREVL.PDKL 350
 DB 376 HAYCSNLSFRLYDQWRAMWQKSHKTRNGHRTGSCPRADGARREVL.PDKL 425
 RESULT 5
 W70850
 ID W70850 standard; Protein; 389 AA.
 AC W70850:
 DT 17-MAR-1999 (first entry)
 DE Human Zcytors variant.
 KW Zcytors; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KW cardiac pathology; heart enlargement; Zcytors ligand; variant.
 OS Homo sapiens.
 PN W09849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 01-MAY-1997; US-074721.
 PR 13-FEB-1998; US-045287.
 PR 13-FEB-1998; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 DR N-PSDB: V70895.
 PT New mammalian cytokinin-like receptor Zcytors - useful for, e.g.
 PT down-regulating Zcytors natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1: Page 71-72; 55pp; English.
 CC The present sequence represents an allelic variant of protein designated
 CC Zcytors, which is a cytokinin-like receptor. Soluble Zcytors may be
 CC administered to down-regulate the effects of a growth and/or maintenance
 CC factor in thyroid, heart, and skeletal muscle for example to lessen the
 CC effect of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytors could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible Zcytors ligands. A probe
 CC comprising Zcytors DNA or RNA can be used to determine the presence
 CC and integrity of the Zcytors gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcytors and
 CC therapeutically to modify Zcytors ligand effects.
 SQ Sequence 425 AA;

PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 DR N-PSDB: V70895.
 PT New mammalian cytokinin-like receptor Zcytors - useful for, e.g.
 PT down-regulating Zcytors natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1: Page 95-96; 55pp; English.
 CC The present sequence represents a Zcytors variant protein. Zcytors
 CC is a cytokinin-like receptor. Soluble Zcytors may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytors could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible Zcytors ligands. A probe
 CC comprising Zcytors DNA or RNA can be used to determine the presence
 CC and integrity of the Zcytors gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcytors and
 CC therapeutically to modify Zcytors ligand effects.
 SQ Sequence 389 AA;

Query Match 99.9%; Score 1918; DB 1; Length 389;
 Best Local Similarity 99.7%; Pred. No. 3,7e-173;
 Matches 349; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLNGRLPELPSVYLAATLALANLNGSRSGDNLVCHARDGSLAGSCLYGLPPE 60
 DB 40 TLNGRLPELPSVYLAATLALANLNGSRSGDNLVCHARDGSLAGSCLYGLPPE 99
 QY 61 KPVNISCWKNMKDLCRTPGAHGETFLHTNYSKYLKRWYGDNTCEHYHVGHSCH 120
 DB 100 KPVNISCWKNMKDLCRTPGAHGETFLHTNYSKYLKRWYGDNTCEHYHVGHSCH 159
 QY 121 IPKDLALFPEIWEATNRLGARSADVLTLDLVYTTDPPDVHVSRYGLEDOLSVR 180
 DB 160 IPKDLALFPEIWEATNRLGARSADVLTLDLVYTTDPPDVHVSRYGLEDOLSVR 219
 QY 181 WSPPLAKDFLFQAKQIQRVEDSVDMKRVYDVNSQTSCLAGLPGTYVEVQVRCNPF 240
 DB 220 WSPPLAKDFLFQAKQIQRVEDSVDMKRVYDVNSQTSCLAGLPGTYVEVQVRCNPF 279
 QY 241 GIYGSKKAIGWEMSHPTASTPRSERPPGGACPRGGEPSGVRRELKQFLGWLKK 300
 DB 280 GIYGSKKAIGWEMSHPTASTPRSERPPGGACPRGGEPSGVRRELKQFLGWLKK 339
 QY 301 HAYCSNLSFRLYDQWRAMWQKSHKTRNGHRTGSCPRADGARREVL.PDKL 350
 DB 340 HAYCSNLSFRLYDQWRAMWQKSHKTRNGHRTGSCPRADGARREVL.PDKL 389
 RESULT 6
 W70851
 ID W70851 standard; Protein; 389 AA.
 AC W70851:
 DT 17-MAR-1999 (first entry)
 DE Human Zcytors variant.
 KW Zcytors; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KW cardiac pathology; heart enlargement; Zcytors ligand; variant.
 OS Homo sapiens.
 PN W09849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 DR N-PSDB: V70895.
 PT New mammalian cytokinin-like receptor Zcytors - useful for, e.g.
 PT down-regulating Zcytors natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1: Page 95-96; 55pp; English.
 CC The present sequence represents a Zcytors variant protein. Zcytors
 CC is a cytokinin-like receptor. Soluble Zcytors may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytors could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible Zcytors ligands. A probe
 CC comprising Zcytors DNA or RNA can be used to determine the presence
 CC and integrity of the Zcytors gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify Zcytors and
 CC therapeutically to modify Zcytors ligand effects.
 SQ Sequence 389 AA;

PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcytors - useful for, e.g.
 PT down-regulating zcytors natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1; Page 96-97; 55pp; English.
 CC The present sequence represents a zcytors variant protein. Zcytors
 CC is a cytokinin-like receptor. Soluble zcytors may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytors could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible zcytors ligands. A probe
 CC comprising zcytors DNA or RNA can be used to determine the presence
 CC and integrity of the zcytors gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcytors and
 CC therapeutically to modify zcytors ligand effects.
 SO Sequence 389 AA;

Query Match 99.9%; Score 1918; DB 1; Length 389;
 Best Local Similarity 99.7%; Pred. No. 3.7e-173;
 Matches 349; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLNGRRRLPELSRVLNASTLALANLNGSRGSDNLYCHARDGSIAGSCLYGLPPE 60
 DB 40 TLNGRRRLPELSRVLNASTLALANLNGSRGSDNLYCHARDGSIAGSCLYGLPPE 99
 QY 61 KPVNISCSKMKDLTCRWTPGAGETFLHTNYSIKYKLRYGQDNCEEHYHTVPSCH 120
 DB 100 KPVNISCSKMKDLTCRWTPGAGETFLHTNYSIKYKLRYGQDNCEEHYHTVPSCH 159
 QY 121 IPKDALTPEIWEATNRLGARSADVLTLIDVYTTDPPDVHVRVSGLEQSLSVR 180
 DB 160 IPKDALTPEIWEATNRLGARSADVLTLIDVYTTDPPDVHVRVSGLEQSLSVR 219
 QY 181 WSPSPALKDFLFOAKYQIRYVEDSVDMKYVDVSNQTSCLAGIKPGTYVYVQRCNPF 240
 DB 220 WSPSPALKDFLFOAKYQIRYVEDSVDMKYVDVSNQTSCLAGIKPGTYVYVQRCNPF 279
 QY 241 GIYSKKGAGIEMSHPTAASPRESRPGGACGEPGSSGPVARELKOFLGWLKK 300
 DB 280 GIYSKKGAGIEMSHPTAASPRESRPGGACGEPGSSGPVARELKOFLGWLKK 339
 QY 301 HAYCSNLSFRLYDQWRAMQMSHKTNRNHRGSCPRADGARREVLDPKLT 350
 DB 340 HAYCSNLSFRLYDQWRAMQMSHKTNRNHRGSCPRADGARREVLDPKLT 389

RESULT 7
 W70852
 ID W70852 standard; Protein: 389 AA.
 AC W70852;
 DT 17-MAR-1999 (first entry)
 DE Human zcytors variant.
 KW zcytors; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KW cardiac pathology; heart enlargement; zcytors ligand; variant.
 OS Homo sapiens.
 PN WO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; 008865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 PT New mammalian cytokinin-like receptor zcytors - useful for, e.g.
 PT down-regulating zcytors natural ligands or detecting cardiotrophin-1
 PT in blood

PS Claim 1; Page 98-99; 55pp; English.
 CC The present sequence represents a zcytors variant protein. Zcytors
 CC is a cytokinin-like receptor. Soluble zcytors may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytors could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible zcytors ligands. A probe
 CC comprising zcytors DNA or RNA can be used to determine the presence
 CC and integrity of the zcytors gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcytors and
 CC therapeutically to modify zcytors ligand effects.
 SO Sequence 389 AA;

Query Match 99.9%; Score 1917; DB 1; Length 389;
 Best Local Similarity 99.7%; Pred. No. 4.6e-173;
 Matches 349; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLNGRRRLPELSRVLNASTLALANLNGSRGSDNLYCHARDGSIAGSCLYGLPPE 60
 DB 40 TLNGRRRLPELSRVLNASTLALANLNGSRGSDNLYCHARDGSIAGSCLYGLPPE 99
 QY 61 KPVNISCSKMKDLTCRWTPGAGETFLHTNYSIKYKLRYGQDNCEEHYHTVPSCH 120
 DB 100 KPVNISCSKMKDLTCRWTPGAGETFLHTNYSIKYKLRYGQDNCEEHYHTVPSCH 159
 QY 121 IPKDALTPEIWEATNRLGARSADVLTLIDVYTTDPPDVHVRVSGLEQSLSVR 180
 DB 160 IPKDALTPEIWEATNRLGARSADVLTLIDVYTTDPPDVHVRVSGLEQSLSVR 219
 QY 181 WSPSPALKDFLFOAKYQIRYVEDSVDMKYVDVSNQTSCLAGIKPGTYVYVQRCNPF 240
 DB 220 WSPSPALKDFLFOAKYQIRYVEDSVDMKYVDVSNQTSCLAGIKPGTYVYVQRCNPF 279
 QY 241 GIYSKKGAGIEMSHPTAASPRESRPGGACGEPGSSGPVARELKOFLGWLKK 300
 DB 280 GIYSKKGAGIEMSHPTAASPRESRPGGACGEPGSSGPVARELKOFLGWLKK 339
 QY 301 HAYCSNLSFRLYDQWRAMQMSHKTNRNHRGSCPRADGARREVLDPKLT 350
 DB 340 HAYCSNLSFRLYDQWRAMQMSHKTNRNHRGSCPRADGARREVLDPKLT 389

RESULT 8
 W70846
 ID W70846 standard; Protein: 389 AA.
 AC W70846;
 DT 17-MAR-1999 (first entry)
 DE Human zcytors variant.
 KW zcytors; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
 KW cardiac pathology; heart enlargement; zcytors ligand; variant.
 OS Homo sapiens.
 PN WO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; 008865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 PT New mammalian cytokinin-like receptor zcytors - useful for, e.g.
 PT down-regulating zcytors natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1; Page 89-90; 55pp; English.
 CC The present sequence represents a zcytors variant protein. Zcytors
 CC is a cytokinin-like receptor. Soluble zcytors may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect

CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytors could be used to detect cardiotoxin-1 in the
 CC blood, and to discover other possible zcytors ligands. A probe
 CC comprising zcytors DNA or RNA can be used to determine the presence
 CC and integrity of the zcytors gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcytors and
 CC therapeutically to modify zcytors ligand effects.
 SQ Sequence 389 AA;

Query Match 99.88; Score 1916; DB 1; Length 389;
 Best Local Similarity 99.78; Pred. No. 5,7e-173;
 Matches 349; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 TLNRRRLPELSESLVNLSTALALANLNGSRSGDNLVCHARGSLIAGSCLVGLPPE 60
 40 TLNRRRLPELSESLVNLSTALALANLNGSRSGDNLVCHARGSLIAGSCLVGLPPE 99
 61 KPVNISCSNMKMDLTCRWTPGAGETFLHTNYSLKRYKLMYGDNTCEHYHVPSCSCH 120
 100 KPVNISCSNMKMDLTCRWTPGAGETFLHTNYSLKRYKLMYGDNTCEHYHVPSCSCH 159
 121 IPPDLALFTPEIWEATNRLGARSVDLTLDLIDVYTTDPDPVHVSRYVGLDQLSVR 180
 160 IPPDLALFTPEIWEATNRLGARSVDLTLDLIDVYTTDPDPVHVSRYVGLDQLSVR 219
 181 WSPSPALKDLFOAKYQIRRVEDSVDMKYVDVSNOTSCRLAGLKGTYFVQVRCNPF 240
 220 WSPSPALKDLFOAKYQIRRVEDSVDMKYVDVSNOTSCRLAGLKGTYFVQVRCNPF 279
 241 GYGSKKAGIMSEWSHPTASTPRSERPGGACPERGSGPVRRLKQFLGLTKK 300
 280 GYGSKKAGIMSEWSHPTASTPRSERPGGACPERGSGPVRRLKQFLGLTKK 339
 301 HAYCSNLSFLYDQWRAMQKSHKTRNQHTRGSCPRADGAREVLPDKL 350
 340 HAYCSNLSFLYDQWRAMQKSHKTRNQHTRGSCPRADGAREVLPDKL 389

RESULT 9

ID W70847 standard; Protein; 389 AA.
 AC W70847;
 DT 17-MAR-1999 (first entry)
 DE Human zcytors variant.
 KW zcytors; cytochrome-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
 KW cardiac pathology; heart enlargement; zcytors ligand; variant.
 OS Homo sapiens.
 PN MO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; 008865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM.
 PT Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytochrome-like receptor zcytors - useful for, e.g.
 PT down-regulating zcytors natural ligands or detecting cardiotoxin-1
 PT in blood
 PS Claim 1: Page 91-92; 55pp; English.
 CC The present sequence represents a zcytors variant protein. Zcytors
 CC is a cytochrome-like receptor. Soluble zcytors may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytors could be used to detect cardiotoxin-1 in the
 CC blood, and to discover other possible zcytors ligands. A probe
 CC comprising zcytors DNA or RNA can be used to determine the presence
 CC and integrity of the zcytors gene on chromosome 19. Antibodies and the

CC anti-idiotypic antibody could be used to purify zcytors and
 CC therapeutically to modify zcytors ligand effects.
 SQ Sequence 389 AA;

Query Match 99.88; Score 1916; DB 1; Length 389;
 Best Local Similarity 99.78; Pred. No. 5,7e-173;
 Matches 349; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 TLNRRRLPELSESLVNLSTALALANLNGSRSGDNLVCHARGSLIAGSCLVGLPPE 60
 40 TLNRRRLPELSESLVNLSTALALANLNGSRSGDNLVCHARGSLIAGSCLVGLPPE 99
 61 KPVNISCSNMKMDLTCRWTPGAGETFLHTNYSLKRYKLMYGDNTCEHYHVPSCSCH 120
 100 KPVNISCSNMKMDLTCRWTPGAGETFLHTNYSLKRYKLMYGDNTCEHYHVPSCSCH 159
 121 IPPDLALFTPEIWEATNRLGARSVDLTLDLIDVYTTDPDPVHVSRYVGLDQLSVR 180
 160 IPPDLALFTPEIWEATNRLGARSVDLTLDLIDVYTTDPDPVHVSRYVGLDQLSVR 219
 181 WSPSPALKDLFOAKYQIRRVEDSVDMKYVDVSNOTSCRLAGLKGTYFVQVRCNPF 240
 220 WSPSPALKDLFOAKYQIRRVEDSVDMKYVDVSNOTSCRLAGLKGTYFVQVRCNPF 279
 241 GYGSKKAGIMSEWSHPTASTPRSERPGGACPERGSGPVRRLKQFLGLTKK 300
 280 GYGSKKAGIMSEWSHPTASTPRSERPGGACPERGSGPVRRLKQFLGLTKK 339
 301 HAYCSNLSFLYDQWRAMQKSHKTRNQHTRGSCPRADGAREVLPDKL 350
 340 HAYCSNLSFLYDQWRAMQKSHKTRNQHTRGSCPRADGAREVLPDKL 389

RESULT 10

ID W70849 standard; Protein; 389 AA.
 AC W70849;
 DT 17-MAR-1999 (first entry)
 DE Human zcytors variant.
 KW zcytors; cytochrome-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
 KW cardiac pathology; heart enlargement; zcytors ligand; variant.
 OS Homo sapiens.
 PN MO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; 008865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM.
 PT Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytochrome-like receptor zcytors - useful for, e.g.
 PT down-regulating zcytors natural ligands or detecting cardiotoxin-1
 PT in blood
 PS Claim 1: Page 94-95; 55pp; English.
 CC The present sequence represents a zcytors variant protein. Zcytors
 CC is a cytochrome-like receptor. Soluble zcytors may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytors could be used to detect cardiotoxin-1 in the
 CC blood, and to discover other possible zcytors ligands. A probe
 CC comprising zcytors DNA or RNA can be used to determine the presence
 CC and integrity of the zcytors gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcytors and
 CC therapeutically to modify zcytors ligand effects.
 SQ Sequence 389 AA;

Query Match 99.8%; Score 1916; DB 1; Length 389;
 Best Local Similarity 99.7%; Pred. No. 5.7e-173;
 Matches 349; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLNGRRLLPELSRVLNASTLALANLNGSRSGDNLYCHARDGSIILAGSCLYVGLPPE 60
 DB 40 TLNGRRLLPELSRVLNASTLALANLNGSRSGDNLYCHARDGSIILAGSCLYVGLPPE 99

QY 61 KPNVISCWKNMKDLTCRMTPGAAGETFLHTNYSKTKLRWYGQDNTCEHYHTVGHSCH 120
 DB 100 KPNVISCWKNMKDLTCRMTPGAAGETFLHTNYSKTKLRWYGQDNTCEHYHTVGHSCH 159

QY 121 IPKDLALFTPEIWEATNRLGARSADVLTLDLVVTTDPPDVHVSRYGLEDQLSVR 180
 DB 160 IPKDLALFTPEIWEATNRLGARSADVLTLDLVVTTDPPDVHVSRYGLEDQLSVR 219

QY 181 WSPPALKDFLFOAKYQIRYVEDSVDMKVVYDVSNQTSCLAGLPGTYVYVQVRCNPF 240
 DB 220 WSPPALKDFLFOAKYQIRYVEDSVDMKVVYDVSNQTSCLAGLPGTYVYVQVRCNPF 279

QY 241 GYGSKKAGINSEMSHPTASTPRSEPRGGACPRGEGSSGVRRELKQFLGWLK 300
 DB 280 GYGSKKAGINSEMSHPTASTPRSEPRGGACPRGEGSSGVRRELKQFLGWLK 339

QY 301 HAYCSNLSFRLYDQWRAMQSKHTRNOHRTGSCPRADGARREVLDPDL 350
 DB 340 HAYCSNLSFRLYDQWRAMQSKHTRNOHRTGSCPRADGARREVLDPDL 389

RESULT 11
 W70848
 ID W70848 standard; Protein; 389 AA.
 AC W70848:
 DT 17-MAR-1999 (first entry)
 DE Human zcytor5 variant.
 KW zcytor5; cytokinin-like receptor; down-regulation; growth factor;
 KM maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
 OS Homo sapiens.
 PN WO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI; 99-034662/03.
 PT New mammalian cytokinin-like receptor zcytor5 - useful for, e.g.
 PT down-regulating zcytor5 natural ligands or detecting cardiotoxin-1
 PT in blood
 PS Claim 1; Page 92-93; 55pp; English.
 CC The present sequence represents a zcytor5 variant protein. zcytor5
 CC is a cytokinin-like receptor. Soluble zcytor5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcytor5 could be used to detect cardiotoxin-1 in the
 CC blood, and to discover other possible zcytor5 ligands. A probe
 CC comprising zcytor5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcytor5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcytor5 and
 CC therapeutically to modify zcytor5 ligand effects.
 SO Sequence 389 AA;

Query Match 99.8%; Score 1915; DB 1; Length 389;
 Best Local Similarity 99.7%; Pred. No. 7.1e-173;
 Matches 349; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLNGRRLLPELSRVLNASTLALANLNGSRSGDNLYCHARDGSIILAGSCLYVGLPPE 60

DB 40 TLNGRRLLPELSRVLNASTLALANLNGSRSGDNLYCHARDGSIILAGSCLYVGLPPE 99

QY 61 KPNVISCWKNMKDLTCRMTPGAAGETFLHTNYSKTKLRWYGQDNTCEHYHTVGHSCH 120
 DB 100 KPNVISCWKNMKDLTCRMTPGAAGETFLHTNYSKTKLRWYGQDNTCEHYHTVGHSCH 159

QY 121 IPKDLALFTPEIWEATNRLGARSADVLTLDLVVTTDPPDVHVSRYGLEDQLSVR 180
 DB 160 IPKDLALFTPEIWEATNRLGARSADVLTLDLVVTTDPPDVHVSRYGLEDQLSVR 219

QY 181 WSPPALKDFLFOAKYQIRYVEDSVDMKVVYDVSNQTSCLAGLPGTYVYVQVRCNPF 240
 DB 220 WSPPALKDFLFOAKYQIRYVEDSVDMKVVYDVSNQTSCLAGLPGTYVYVQVRCNPF 279

QY 241 GYGSKKAGINSEMSHPTASTPRSEPRGGACPRGEGSSGVRRELKQFLGWLK 300
 DB 280 GYGSKKAGINSEMSHPTASTPRSEPRGGACPRGEGSSGVRRELKQFLGWLK 339

QY 301 HAYCSNLSFRLYDQWRAMQSKHTRNOHRTGSCPRADGARREVLDPDL 350
 DB 340 HAYCSNLSFRLYDQWRAMQSKHTRNOHRTGSCPRADGARREVLDPDL 389

RESULT 12
 W70853
 ID W70853 standard; Protein; 389 AA.
 AC W70853:
 DT 17-MAR-1999 (first entry)
 DE Human zcytor5 variant.
 KW zcytor5; cytokinin-like receptor; down-regulation; growth factor;
 KM maintenance factor; thyroid; heart; skeletal muscle; cardiotoxin-1;
 OS Homo sapiens.
 PN WO9849307-A1.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI; 99-034662/03.
 PT New mammalian cytokinin-like receptor zcytor5 - useful for, e.g.
 PT down-regulating zcytor5 natural ligands or detecting cardiotoxin-1
 PT in blood
 PS Claim 1; Page 99-100; 55pp; English.
 CC The present sequence represents a zcytor5 variant protein. zcytor5
 CC is a cytokinin-like receptor. Soluble zcytor5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotoxin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcytor5 could be used to detect cardiotoxin-1 in the
 CC blood, and to discover other possible zcytor5 ligands. A probe
 CC comprising zcytor5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcytor5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcytor5 and
 CC therapeutically to modify zcytor5 ligand effects.
 SO Sequence 389 AA;

Query Match 99.7%; Score 1914; DB 1; Length 389;
 Best Local Similarity 99.7%; Pred. No. 8.8e-173;
 Matches 349; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TLNGRRLLPELSRVLNASTLALANLNGSRSGDNLYCHARDGSIILAGSCLYVGLPPE 60
 DB 40 TLNGRRLLPELSRVLNASTLALANLNGSRSGDNLYCHARDGSIILAGSCLYVGLPPE 99

QY 61 KPNVISCWKNMKDLTCRMTPGAAGETFLHTNYSKTKLRWYGQDNTCEHYHTVGHSCH 120

Db 100 KPVNISCSKNNKDLTCRWTPGAGETFLHTNYSLKTKYKRWYGODNCEHYTVGPHSCH 159
 QY 121 IPKDLAFTPEIWEATNRLGARSADVLTLDIDVYTTTPPPVHVSRRVGGLEDQLSVR 180
 Db 160 IPKDLAFTPEIWEATNRLGARSADVLTLDIDVYTTTPPPVHVSRRVGGLEDQLSVR 219
 QY 181 WSPPALKDFLFQAKYQIRRYVEDSVDMKYVDVSNQTSCLAGLKPGTYFYVQVRNPF 240
 Db 220 WSPPALKDFLFQAKYQIRRYVEDSVDMKYVDVSNQTSCLAGLKPGTYFYVQVRNPF 279
 QY 241 GIGSKKAGIWMSEMSHPTAATPRSERPGGACERGPSSGYPVRELKQFLGWLKK 300
 Db 280 GIGSKKAGIWMSEMSHPTAATPRSERPGGACERGPSSGYPVRELKQFLGWLKK 339
 QY 301 HAYCSNLSFRLTYDQWRAWMOKSHKTRNQHTRSSCPADARREYLPDKL 350
 Db 340 HAYCSNLSFRLTYDQWRAWMOKSHKTRNQHTRSSCPADARREYLPDKL 389

RESULT 13

W59805
 ID W59805 standard; Protein: 408 AA.
 AC W59805;
 DE 26-OCT-1998 (first entry)
 DE Amino acid sequence of the human U4 protein.
 KW Human; U4 protein; haematopoietic receptor superfamily;
 KW cell proliferation; immune response; antibody; cell differentiation;
 KW autoimmune disease; cancer; allergy.
 OS Homo sapiens.
 PN W09831811-A1.
 PD 23-JUL-1998.
 PR 15-JAN-1998; U00334.
 PR 16-JAN-1997; US-784863.
 PA (GENE) GENETICS INST INC.
 PI Collins M, Donaldson DD, Neben T, Walters M;
 DR MPI: 98-414109/35.
 DR N-PSDB: V41689.
 PT New nucleic acid encoding U4 haematopoietic receptor superfamily
 chain - potentially useful, e.g. for modulating cell proliferation
 or immune response, for treating cancer and auto-immune disease
 CS Claim 9; Pages 29-30; 38pp; English.
 PS This is the amino acid sequence of the human U4 protein from the
 haematopoietic receptor superfamily, used in the method of the
 invention for the modulation of cell proliferation, or the immune
 response. Transformed mammalian cells are used to produce recombinant
 U4 protein. The U4 protein is used to screen for specific binding
 agents, raise antibodies. It is also used as reagents for assays and
 as tissue markers for isolation of cognate ligands and receptors, and
 in pharmaceutical compositions which may modulate cell proliferation,
 cell differentiation, and the immune system (e.g. for treating immune
 deficiency, inherited or the result of infection, autoimmune diseases,
 cancer, and allergy).
 CC Sequence 408 AA;

Query Match 93.8%; Score 1800; DB 1; Length 408;
 Best Local Similarity 100.0%; Pred. No. 5.5e-162;
 Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLNGRRLLPELSRVNASTLALALANLNGSRORSNDNLVCHARDSIAGSCLTYGLPPE 60
 Db 63 TLNGRRLLPELSRVNASTLALALANLNGSRORSNDNLVCHARDSIAGSCLTYGLPPE 122
 QY 61 KPVNISCSKNNKDLTCRWTPGAGETFLHTNYSLKTKYKRWYGODNCEHYTVGPHSCH 120
 Db 123 KPVNISCSKNNKDLTCRWTPGAGETFLHTNYSLKTKYKRWYGODNCEHYTVGPHSCH 182
 QY 121 IPKDLAFTPEIWEATNRLGARSADVLTLDIDVYTTTPPPVHVSRRVGGLEDQLSVR 180
 Db 183 IPKDLAFTPEIWEATNRLGARSADVLTLDIDVYTTTPPPVHVSRRVGGLEDQLSVR 242
 QY 181 WSPPALKDFLFQAKYQIRRYVEDSVDMKYVDVSNQTSCLAGLKPGTYFYVQVRNPF 240

Db 243 WSPPALKDFLFQAKYQIRRYVEDSVDMKYVDVSNQTSCLAGLKPGTYFYVQVRNPF 302
 QY 241 GIGSKKAGIWMSEMSHPTAATPRSERPGGACERGPSSGYPVRELKQFLGWLKK 300
 Db 303 GIGSKKAGIWMSEMSHPTAATPRSERPGGACERGPSSGYPVRELKQFLGWLKK 362
 QY 301 HAYCSNLSFRLTYDQWRAWMOKSHKTRNQ 328
 Db 363 HAYCSNLSFRLTYDQWRAWMOKSHKTRNQ 390

RESULT 14

W70860
 ID W70860 standard; Protein: 422 AA.
 AC W70860;
 DE 17-MAR-1999 (first entry)
 DE Human zcyto5 protein sequence.
 KW zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 KW cardiac pathology; heart enlargement; zcyto5 ligand.
 OS Homo sapiens.
 PN W09849307-A1.
 PD 05-NOV-1998.
 PR 01-MAR-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Jelmberg AC, Lehner JW,
 PI Lox S, Plesneil SR, Whitmore TE;
 DR MPI: 99-034662/03.
 DR N-PSDB: V70894.
 PT New mammalian cytokinin-like receptor. Zcyto5 - useful for, e.g.
 down-regulating zcyto5 natural ligands or detecting cardiostrophin-1
 in blood.
 PS Claim 1; Page 66-67; 55pp; English.
 CS The present sequence represents a protein designated zcyto5, which is
 a cytokinin-like receptor. Soluble zcyto5 may be administered to
 down-regulate the effects of a growth and/or maintenance factor in
 thyroid, heart, and skeletal muscle for example to lessen the effect
 of cardiostrophin-1 on cardiac pathologies, so preventing heart
 enlargement. Zcyto5 could be used to detect cardiostrophin-1 in the
 blood, and to discover other possible zcyto5 ligands. A probe
 comprising zcyto5 DNA or RNA can be used to determine the presence
 and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 anti-idiotypic antibody could be used to purify zcyto5 and
 therapeutically to modify zcyto5 ligand effects.
 CC Sequence 422 AA;

Query Match 93.6%; Score 1796; DB 1; Length 422;
 Best Local Similarity 99.7%; Pred. No. 1.4e-161;
 Matches 327; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLNGRRLLPELSRVNASTLALALANLNGSRORSNDNLVCHARDSIAGSCLTYGLPPE 60
 Db 77 TLNGRRLLPELSRVNASTLALALANLNGSRORSNDNLVCHARDSIAGSCLTYGLPPE 136
 QY 61 KPVNISCSKNNKDLTCRWTPGAGETFLHTNYSLKTKYKRWYGODNCEHYTVGPHSCH 120
 Db 137 KPVNISCSKNNKDLTCRWTPGAGETFLHTNYSLKTKYKRWYGODNCEHYTVGPHSCH 196
 QY 121 IPKDLAFTPEIWEATNRLGARSADVLTLDIDVYTTTPPPVHVSRRVGGLEDQLSVR 180
 Db 197 IPKDLAFTPEIWEATNRLGARSADVLTLDIDVYTTTPPPVHVSRRVGGLEDQLSVR 256
 QY 181 WSPPALKDFLFQAKYQIRRYVEDSVDMKYVDVSNQTSCLAGLKPGTYFYVQVRNPF 240
 Db 257 WSPPALKDFLFQAKYQIRRYVEDSVDMKYVDVSNQTSCLAGLKPGTYFYVQVRNPF 316
 QY 241 GIGSKKAGIWMSEMSHPTAATPRSERPGGACERGPSSGYPVRELKQFLGWLKK 300

Db 317 GYSGKAGIWESEHPTASTPERSPPGACPEPGEPSGVRRELKQFLGWLK 376
 Oy 301 HAYCSNLSFRLYDQWRAMOKSHKTRNO 328
 ||||||||||||||||||||
 Db 377 HAYCSNLSFRLYDQWRAMOKSHKTRNO 404

RESULT 15

W70839

ID W70839 standard; Protein: 388 AA.

AC 17-MAR-1999 (first entry)

DE Human zcytor5 variant.

KW zcytor5; cytokinin-like receptor; down-regulation; growth factor;

KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;

KW cardiac pathology; heart enlargement; zcytor5 ligand; variant.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Misc.difference 45 /note="not specified"

PN WO9849307-A1.

PD 05-NOV-1998

PF 01-MAY-1998; U08865.

PR 13-FEB-1998; US-074721.

PR 01-MAY-1997; US-045287.

PR 01-MAY-1997; US-850030.

PR 13-FEB-1998; US-023890.

PA (ZYMO) ZYMOGENETICS INC.

PI Adams RL, Foster DC, Jelmberg AC, Lehner JM,

PI Lok S, Presnell SR, Whitmore TE;

DR WPI; 99-034662/03.

PT New mammalian cytokinin-like receptor zcytor5 - useful for, e.g.

PT down-regulating zcytor5 natural ligands or detecting cardiotrophin-1

PT in blood

PS Claim 1; Page 80-81; 55pp; English.

CC The present sequence represents a zcytor5 variant protein. zcytor5

CC is a cytokinin-like receptor. Soluble zcytor5 may be administered to

CC down-regulate the effects of a growth and/or maintenance factor in

CC thyroid, heart, and skeletal muscle for example to lessen the effect

CC of cardiotrophin-1 on cardiac pathologies, so preventing heart

CC enlargement. zcytor5 could be used to detect cardiotrophin-1 in the

CC blood, and to discover other possible zcytor5 ligands. A probe

CC comprising zcytor5 DNA or RNA can be used to determine the presence

CC and integrity of the zcytor5 gene on chromosome 19. Antibodies and the

CC anti-idiotypic antibody could be used to purify zcytor5 and the

CC therapeutically to modify zcytor5 ligand effects.

SQ Sequence 388 AA;

Query Match 93.2%; Score 1789; DB 1; Length 388;
 Best Local Similarity 99.4%; Pred. No. 5.6e-161;

Matches 326; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 TINGRRRLPELSRVNASTLALANLNGSRGSDNLVCHARDGSIAGSCLYGLPPE 60
 ||||||||||||||||||||
 Db 43 TLXGRRRLPELSRVNASTLALANLNGSRGSDNLVCHARDGSIAGSCLYGLPPE 102
 ||||||||||||||||||||
 Oy 61 KPVNISCWSKKNKDLTCMTPEAGETFLHTNYSLSKTKLRYGODNTCEETHVGPSSCH 120
 ||||||||||||||||||||
 Db 103 KPVNISCWSKKNKDLTCMTPEAGETFLHTNYSLSKTKLRYGODNTCEETHVGPSSCH 162
 ||||||||||||||||||||
 Oy 121 IPKDLALFTPEIWEATNRLGSARSDVLTLDIVVTDDPPDHVSRRVGLDQLSVR 180
 ||||||||||||||||||||
 Db 163 IPKDLALFTPEIWEATNRLGSARSDVLTLDIVVTDDPPDHVSRRVGLDQLSVR 222
 ||||||||||||||||||||
 Oy 181 WSPPALDLEFOAKYQIRYVEDSVDMKVVDVSNQTSCLAGLKPETVYFVQRCNPF 240
 ||||||||||||||||||||
 Db 223 WSPPALDLEFOAKYQIRYVEDSVDMKVVDVSNQTSCLAGLKPETVYFVQRCNPF 282
 ||||||||||||||||||||
 Oy 241 GYSGKAGIWESEHPTASTPERSPPGACPEPGEPSGVRRELKQFLGWLK 300
 ||||||||||||||||||||
 Db 283 GYSGKAGIWESEHPTASTPERSPPGACPEPGEPSGVRRELKQFLGWLK 342

Oy 301 HAYCSNLSFRLYDQWRAMOKSHKTRNO 328
 Db 343 HAYCSNLSFRLYDQWRAMOKSHKTRNO 370

Search completed: September 17, 1999, 03:08:16
 Job time: 307 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:41:09 ; Search time 53.94 Seconds

(Without Alignments)
64,033 Million cell updates/sec

Title: US-09-037-657-25

Sequence: 1 TLNGRRRLPELSTRLNASTL.....TRGSCPRADGARREVLDPDKL 350

Scoring table: BLOSUM62

Searched: 106577 seqs, 9868381 residues

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/PCITUS9.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	290.5	15.1	708	1	US-07-797-556-2
2	290.5	15.1	708	2	US-08-308-881-2
3	290.5	15.1	708	3	PCT-US95-06530-2
4	241	12.6	837	1	US-07-923-976-2
5	220.5	11.5	836	1	US-07-923-976-4
6	220.5	11.5	771	1	US-07-923-976-6
7	220.5	11.5	863	1	US-07-923-976-8
8	219.5	11.4	372	1	US-07-865-878A-4
9	219.5	11.4	372	1	US-07-676-647-2
10	219.5	11.4	372	1	US-08-448-329-2
11	219.5	11.4	372	2	US-08-445-073-2
12	219.5	11.4	372	3	PCT-US91-03896-2
13	213.5	11.1	602	2	US-08-419-652-6
14	207.5	10.8	862	2	US-08-685-118-2
15	207.5	10.8	862	2	US-08-915-485-2
16	207	10.8	572	2	US-08-418-652-5
17	196	10.2	633	1	US-08-250-859-17
18	196	10.2	633	1	US-08-490-803-17
19	196	10.2	633	1	PCT-US94-08806-17
20	196	10.2	633	3	PCT-US95-01775-17
21	196	10.2	633	3	PCT-US95-16626-7
22	190	9.9	626	3	US-08-184-327A-2
23	190	9.9	482	1	US-08-184-327A-8
24	190	9.9	482	3	PCT-US95-00670-2
25	190	9.9	482	3	PCT-US95-00670-8
26	188.5	9.8	635	1	US-08-184-327A-4
27	188.5	9.8	635	3	PCT-US95-00670-4
28	176	9.2	1001	1	US-07-797-556-6
29	176	9.2	1001	1	US-07-943-843-2
30	176	9.2	1097	1	US-07-943-843-6
31	176	9.2	1001	2	US-08-347-003-2
32	176	9.2	1097	2	US-08-347-003-6
33	166	8.7	719	1	US-07-943-843-4
34	166	8.7	719	2	US-08-347-003-4
35	161	8.4	569	1	US-08-306-231-3
36	161	8.4	960	2	US-08-355-888A-8
37	161	8.4	960	2	US-08-693-697-8
38	161	8.4	908	2	US-08-693-697-33
39	161	8.4	898	2	US-08-693-697-36

40	160	8.3	908	2	US-08-588-526-3	Sequence 3, Appl1
41	159.5	8.3	383	1	US-08-609-572-2	Sequence 2, Appl1
42	156	8.1	960	1	US-08-588-190-3	Sequence 3, Appl1
43	154.5	8.1	508	2	US-08-850-293-5	Sequence 5, Appl1
44	148	7.7	229	2	US-08-684-687-2	Sequence 2, Appl1
45	145.5	7.6	897	1	US-07-960-389-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1	US-07-797-556-2	Sequence 2, Application US/07797556	Patent No. 5262522	GENERAL INFORMATION:
APPLICANT:	Geating, David P.	RECEIPTOR FOR ONCOSTATIN M AND LEUKEMIA		
TITLE OF INVENTION:	Receptor for Oncostatin M and Leukemia			
NUMBER OF INVENTION:	Inhibitory Factor			
NUMBER OF SEQUENCES:	17			
CORRESPONDENCE ADDRESS:				
ADDRESS:	Immunex Corporation			
STREET:	51 University Street			
CITY:	Seattle			
STATE:	WA			
COUNTRY:	USA			
ZIP:	98101			
COMPUTER READABLE FORM:				
COMPUTER:	IBM PC compatible			
OPERATING SYSTEM:	PC-DOS/MS-DOS			
SOFTWARE:	PatentIn Release #1.0, Version #1.25			
CURRENT APPLICATION DATA:				
APPLICATION NUMBER:	US/07/797,556			
FILING DATE:	19911122			
CLASSIFICATION:	435			
ATTORNEY/AGENT INFORMATION:				
NAME:	Seese, Kathryn A.			
REGISTRATION NUMBER:	32,172			
REFERENCE/DOCKET NUMBER:	2607			
TELECOMMUNICATION INFORMATION:				
TELEPHONE:	206-587-0430			
TELEFAX:	206-587-0606			
INFORMATION FOR SEQ ID NO: 2:				
SEQUENCE CHARACTERISTICS:				
LENGTH:	708 amino acids			
TYPE:	AMINO ACID			
TOPOLOGY:	linear			
MOLECULE TYPE:	protein			
US-07-797-556-2				
Query Match	15.18; Score 290.5; DB 1; Length 708;			
Best Local Similarity	28.78; Pred. No. 4.6e-21;			
Matches	76; Conservative 46; Mismatches 128; Indels 15; Gaps 7;			
OY	7	LPPELSRYLNASTLALANLNGSRQSGDYLVCARQSGSLAGCLVGPPEPVNIS 66		
Db	74	IPKEQYTLNNTASSVFTDASLNLTQTCNLTFTGQLEQVNYGTTISGPEPKNLS 133		
OY	67	CMSKMKMDLTCRWTPGAGETFLTNTYSLAKKLRLMYGQDNTCEEHTVGPSCHPKDLA 126		
Db	134	CIYVNGKMKREMGGR--ETHLETNFTLKSEMAHKFAADCAKROT--PTSCYVDISTV 189		
OY	127	LFTPEIWEATNRLGARSQVLTLDLDVTTDPPDPVHSRYVGGLEDQSVRWVSPA 186		
Db	190	YFVNIWEVVEAENMLGKVTSDHINFDPPYKVPBPBHLVYINSEELSLIKMTN-PS 248		
OY	187	LKDLFLPAKYIRIRVEDSDVMKYV---DDVSNQTSCLAGLAKGYTVFOVRCNPGIT 243		
Db	249	IKSVIT-LKNIQIORTDASQSOIPPEDASTRSSFTVDLKEFTVEYFIRIC-----M 302		
OY	244	GSKRAGIWEVSHPTASTPSESRP 268		

Db 303 KEDGKGYWSDMSEASGIT-YEDRP 326

RESULT 2

US-08-308-881-2
Sequence 2, Application US/08308881
Patent No. 5783672
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-308-881-2

Query Match 15.1%; Score 290.5; DB 2; Length 708;
Best Local Similarity 28.7%; Pred. No. 4.6e-21;
Matches 76; Conservative 46; Mismatches 128; Indels 15; Gaps 7;
Db 7 LPELSVNLASTLALANLNGSRORSRSDNLYCHARDGSLAGSLYGLPPEKPVNIS 66
Db 74 IPKQYIIINRTASSVFTDIASINIOITCNIILFGOLEQNVYGITIISGLPPEKPNLS 133
QY 67 CWSNNMDELTCRMTPGAAGETFLHTNYSLSKYLKRWYGODNTCEYHTVGPCHIKDLA 126
Db 134 CYNVEGKMKCEMDGGR--ETHLETNFKSEWATKRFADCKARKDT--PTSCVYDSTV 189
QY 127 LFTPEIWEATNRLSARSADVLTLDLDVYTTDPPDVHVSFVGLDOLSVRWSPPA 186
Db 190 YFVNIIEWVAENALGVTSDFINFDVYKVPNPVHNSVINSEELSSILKLTWTN-PS 248
QY 187 LKDFLQAKQOIRRVDSVDKVV---DDVSNQTSCLAGLKPQTVYFVQRCNPFGIT 243
Db 249 IKSVTI-LKINIQYRTKDASTWQIIPEDDASTRSSFTVODLKPFLEYVFRIRC-----M 302
QY 244 GSKKAGIWMSESHPTASTPRSERP 268
Db 303 KEDGKGYWSDMSEASGIT-YEDRP 326

RESULT 3

PCT-US95-06530-2
Sequence 2, Application PC/TUS9506530
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06530
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,881
FILING DATE: 09-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-06530-2

Query Match 15.1%; Score 290.5; DB 3; Length 708;
Best Local Similarity 28.7%; Pred. No. 4.6e-21;
Matches 76; Conservative 46; Mismatches 128; Indels 15; Gaps 7;
Db 7 LPELSVNLASTLALANLNGSRORSRSDNLYCHARDGSLAGSLYGLPPEKPVNIS 66
Db 74 IPKQYIIINRTASSVFTDIASINIOITCNIILFGOLEQNVYGITIISGLPPEKPNLS 133
QY 67 CWSNNMDELTCRMTPGAAGETFLHTNYSLSKYLKRWYGODNTCEYHTVGPCHIKDLA 126
Db 134 CYNVEGKMKCEMDGGR--ETHLETNFKSEWATKRFADCKARKDT--PTSCVYDSTV 189
QY 127 LFTPEIWEATNRLSARSADVLTLDLDVYTTDPPDVHVSFVGLDOLSVRWSPPA 186
Db 190 YFVNIIEWVAENALGVTSDFINFDVYKVPNPVHNSVINSEELSSILKLTWTN-PS 248
QY 187 LKDFLQAKQOIRRVDSVDKVV---DDVSNQTSCLAGLKPQTVYFVQRCNPFGIT 243
Db 249 IKSVTI-LKINIQYRTKDASTWQIIPEDDASTRSSFTVODLKPFLEYVFRIRC-----M 302
QY 244 GSKKAGIWMSESHPTASTPRSERP 268
Db 303 KEDGKGYWSDMSEASGIT-YEDRP 326

RESULT 4

US-07-923-976-2
Sequence 2, Application US/07923976
Patent No. 5574136
GENERAL INFORMATION:
APPLICANT: Nagata, Shigekazu
APPLICANT: Fukunaga, Rikito
TITLE OF INVENTION: DNA Encoding Granulocyte
NUMBER OF SEQUENCES: 8
TITLE OF INVENTION: Colony-Stimulating Factor Receptor
CORRESPONDENCE ADDRESS:
ADDRESS: Jones, Tullar & Cooper, P.C.
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,976
FILING DATE: 19920922
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74539/1990
FILING DATE: 23-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 176629/1990
FILING DATE: 03-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP91/00375
FILING DATE: 22-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hellwege, James W.
REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 514853
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-415-1508
TELEFAX: 703-415-1508
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 837 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-923-976-2

Query Match 12.6%; Score 241; DB 1; Length 837;
Best Local Similarity 28.0%; Pred. No. 5.8e-16;
Matches 89; Conservative 45; Mismatches 112; Indels 72; Gaps 17;

QY 53 LYVGLPEKPYNISCSKNNKDLTCRTWPAHGETFLHTYSLK-YKLR---WYGDNT 107
DB 118 LHAQPPSPNLSCLMLTNSLYCQEP--ETHLPTSLKFSRSDCQYQPTI 175
QY 108 CEYHTVGRHSCHIP-KDLALFTPELWEATNRLGSARSDVLTLDIDVTTDP-- 163
DB 176 PDCAKKNONNSIPRKMLLYQYMAIVQAENMLGSESPRLCLDPADVYKLEPPMLOA 235
QY 163 ---PDVHVSRYGLEGDLQSVRWVS-PPALADFLQAKYQIRYVE-DSVDMKVVDV-S 215
DB 236 LDIGDVSYPGCL-----WLSMKWPKSEYVEQCELTQQLKGAWMTLVFLPS 288
QY 216 NOTSRLGLKPGTYVFOVRCNPFGIYSKRAIGTSEMS-----HPT-AASTPSEBPG 269
DB 289 SKDQELGSLHQAAPYTTLMRC-----IRSLPGFMSPPSLQALPIMKAPTILDT-- 342
QY 270 PGGACGEPGEPSS-----GVRRELKQFLGWLKKAHYCSNLSFRLYDQRRANQ 320
DB 342 ---WCOKHODPGRYVSLFLFWKPTPLQEDSQIQGYL-----LSWNS 380

QY 321 KSHKTRNH---RTRGSC 335
DB 381 PDHGGQDHLICNTTQLSC 398

RESULT 5
US-07-923-976-4
Sequence 4, Application US/07923976
Patent No. 5574136
GENERAL INFORMATION:
APPLICANT: Nagata, Shigekazu
APPLICANT: Fukunaga, Rikito
TITLE OF INVENTION: DNA Encoding Granulocyte
NUMBER OF SEQUENCES: 8
TITLE OF INVENTION: Colony-Stimulating Factor Receptor
CORRESPONDENCE ADDRESS:
ADDRESS: Jones, Tullar & Cooper, P.C.
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,976
FILING DATE: 19920922
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74539/1990
FILING DATE: 23-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 176629/1990
FILING DATE: 03-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP91/00375
FILING DATE: 22-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hellwege, James W.
REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 514853
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-415-1508
TELEFAX: 703-415-1508
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 836 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-923-976-4

Query Match 11.5%; Score 220.5; DB 1; Length 836;
Best Local Similarity 32.0%; Pred. No. 6.7e-14;
Matches 70; Conservative 31; Mismatches 89; Indels 29; Gaps 11;

QY 53 LYVGLPEKPYNISCSKNNKDLTCRTWPAHGETFLHTYSLK-YKLRVYGO---DNT 107
DB 117 LRAQYPPAIPNLSCLMLTNSLYCQEP--ETHLPTSLKFSRSDCQYQPTI 174
QY 108 CEYHTVGRHSCHIP-KDLALFTPELWEATNRLGSARSDVLTLDIDV-----T 158
DB 175 LDCVYKDGQSCICPRKHLILYQYMAIVQAENMLGSESPRLCLDPADVYKLEPPMRT 234
QY 159 TDPPEVHVSRYGLEGDLQSVRWVS-PPALADFLQAKYQIRYVE-DSVDMKVVDVSNQ 217
DB 235 MDPSEAPAPQAGCLQ-----LCW--EPWQPLHINOKCELHNRKQRCGEASVALYGPPLLE 288
QY 218 T-SRLGLKPGTYVFOVRCNPFGIYSKRAIGTSEMS 255

Db 289 ALOYELCGLLPATATVTLQIRCIKRWPL-----PGHMSDMS 322

RESULT 6

US-07-923-976-6
Sequence 6, Application US/07923976
Patent No. 5574136

GENERAL INFORMATION:

APPLICANT: Nagata, Shigekazu
APPLICANT: Fukunaga, Rikio
TITLE OF INVENTION: DNA Encoding Granulocyte
NUMBER OF INVENTION: Colony-Stimulating Factor Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones, Tulliar & Cooper, P.C.
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,976
FILING DATE: 19920922
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74539/1990
FILING DATE: 23-MAR-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 176629/1990
FILING DATE: 03-JUL-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP91/00375
FILING DATE: 22-MAR-1991

ATTORNEY/AGENT INFORMATION:
NAME: Hellwege, James W.
REGISTRATION NUMBER: 28,808

TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-415-1500
TELEFAX: 703-415-1508

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

LENGTH: 771 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear

MOLECULE TYPE: protein
US-07-923-976-6

Query Match 11.5%; Score 220.5; DB 1; Length 771;
Best Local Similarity 32.0%; Pred. No. 6e-14;
Matches 70; Conservative 31; Mismatches 89; Indels 29; Gaps 11;

QY 53 LVVGLPEKPKVISC-WSKNMDLTCRMTPGAHEFTLHTNSLK-YKLRWYGO---DNT 107
DB 117 LRAQVPAIPHNLSCMLNLTSSLICQWEPGP-ETHLPSTFLSKFSKRGNCOTQGDSSI 174
QY 108 CEFTVTPHSGHIP-KDIALFTPEIWEATNRLGSARSADVLTLDIDVY-----T 158
DB 175 LDCVPRKQDSHCCIPRKHLLLYONNGIWOAENALGTSMPQLCLDPMDVVKLEPMLRT 234
QY 159 TDPDPDVHSRVGLEDLSRWVSPPALKDFLOAKYQIRYRE-DSVDMKVVDDVSNQ 217
DB 235 MDPSEAPAPQAGCQ---LCW--EPWQPLHINQKCELHRKPKQGEASWALVGPLPLE 288
QY 218 T-SCRLAGLKPGTYVVOVRCNPFGIYSKRAGIWMSEWS 255
DB 289 ALOYELCGLLPATATVTLQIRCIKRWPL-----PGHMSDMS 322

RESULT 7

US-07-923-976-8
Sequence 8, Application US/07923976
Patent No. 5574136

GENERAL INFORMATION:

APPLICANT: Nagata, Shigekazu
APPLICANT: Fukunaga, Rikio
TITLE OF INVENTION: DNA Encoding Granulocyte
NUMBER OF INVENTION: Colony-Stimulating Factor Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones, Tulliar & Cooper, P.C.
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,976
FILING DATE: 19920922
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74539/1990
FILING DATE: 23-MAR-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 176629/1990
FILING DATE: 03-JUL-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP91/00375
FILING DATE: 22-MAR-1991

ATTORNEY/AGENT INFORMATION:
NAME: Hellwege, James W.
REGISTRATION NUMBER: 28,808

TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-415-1500
TELEFAX: 703-415-1508

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

LENGTH: 863 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear

MOLECULE TYPE: protein
US-07-923-976-8

Query Match 11.5%; Score 220.5; DB 1; Length 863;
Best Local Similarity 32.0%; Pred. No. 7.1e-14;
Matches 70; Conservative 31; Mismatches 89; Indels 29; Gaps 11;

QY 53 LVVGLPEKPKVISC-WSKNMDLTCRMTPGAHEFTLHTNSLK-YKLRWYGO---DNT 107
DB 117 LRAQVPAIPHNLSCMLNLTSSLICQWEPGP-ETHLPSTFLSKFSKRGNCOTQGDSSI 174
QY 108 CEFTVTPHSGHIP-KDIALFTPEIWEATNRLGSARSADVLTLDIDVY-----T 158
DB 175 LDCVPRKQDSHCCIPRKHLLLYONNGIWOAENALGTSMPQLCLDPMDVVKLEPMLRT 234
QY 159 TDPDPDVHSRVGLEDLSRWVSPPALKDFLOAKYQIRYRE-DSVDMKVVDDVSNQ 217
DB 235 MDPSEAPAPQAGCQ---LCW--EPWQPLHINQKCELHRKPKQGEASWALVGPLPLE 288
QY 218 T-SCRLAGLKPGTYVVOVRCNPFGIYSKRAGIWMSEWS 255
DB 289 ALOYELCGLLPATATVTLQIRCIKRWPL-----PGHMSDMS 322

RESULT 8

US-07-865-878A-4

Sequence 4, Application us/07865878A

Patent No. 5332672

GENERAL INFORMATION:

APPLICANT: Yancopoulos, George D. et al.

TITLE OF INVENTION: Cell Free Ciliary Neurotrophic

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/865,878A

FILING DATE: 19911202

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/801,562

FILING DATE: 02-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 6526-082

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 790-9090

TELEFAX: 212 8698864/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 372 amino acids

TYPE: AMINO ACID

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-07-865-878A-4

Query Match 11.4%; Score 219.5; DB 1; Length 372;
Best Local Similarity 26.7%; Pred. No. 2,7e-14;
Matches 86; Conservative 37; Mismatches 122; Indels 77; Gaps 16;

QY 2 LNRGRLPPELSRVNASTLALALANLNGSRORSQDNLVCHARDGSIAGS-CLYVGLPPE 60
DB 59 VNGTDLPDL---LNGSOLV-----LHGLELGHSGLYACFHRDSMHLRHQVLLHVGLP 110
QY 61 KPVNISCSKNNM-KDLTCRW-----TPGAGHGFELHTNYSLSKYLKRWYQDNCEYH 112
DB 111 EPV-LSCRSNTYPRGFCSMHLPPTIPIPTFNTVLAHSGKIM-----VCEKDP 158
QY 113 TVGPHSCHIRPDALFT--PYEIVWEATNRLSGARSVDLTLDIDVTTDPDPVHRSV 170
DB 159 AL-KNRCHI-RYMHLFSTIKKVISVSNLGH-NATAITFDEFTYKPPDPENVARPV 215
QY 171 GGLEDOLSVWVSPALKD-FLFOAKQIQRVEDSVDMKVVDDVSNQTSCLAGLPGT 229
DB 216 PSNPRRLLEVWQPTSTPDPDESPLKFFLRPLILDQWQHV-ELSDGTAHTTIDAYAGK 274
QY 230 VYEVQVPCNPFGLYSGKAGIWMSEWSHPTAASPRSERP----- 269
DB 275 EYIIQVAAK-----DNEIGTWSQMS-VAAHATPWTEEPHNLTEAQALETTSSTSSLA 327
QY 269 -----GPGGACAP 277
DB 328 PPPTTRICDPGELSGGGPCAP 349

RESULT 9
US-07-676-647-2

Sequence 2, Application us/07676647

Patent No. 5426177

GENERAL INFORMATION:

APPLICANT: Davis, Samuel

APPLICANT: Squinto, Stephen P.

APPLICANT: Furth, Mark E.

TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/676,647

FILING DATE: 19910328

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 6526-048

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 790-9090

TELEFAX: 212 8698864/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 372 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-676-647-2

Query Match 11.4%; Score 219.5; DB 1; Length 372;
Best Local Similarity 26.7%; Pred. No. 2,7e-14;
Matches 86; Conservative 37; Mismatches 122; Indels 77; Gaps 16;

QY 2 LNRGRLPPELSRVNASTLALALANLNGSRORSQDNLVCHARDGSIAGS-CLYVGLPPE 60
DB 59 VNGTDLPDL---LNGSOLV-----LHGLELGHSGLYACFHRDSMHLRHQVLLHVGLP 110
QY 61 KPVNISCSKNNM-KDLTCRW-----TPGAGHGFELHTNYSLSKYLKRWYQDNCEYH 112
DB 111 EPV-LSCRSNTYPRGFCSMHLPPTIPIPTFNTVLAHSGKIM-----VCEKDP 158
QY 113 TVGPHSCHIRPDALFT--PYEIVWEATNRLSGARSVDLTLDIDVTTDPDPVHRSV 170
DB 159 AL-KNRCHI-RYMHLFSTIKKVISVSNLGH-NATAITFDEFTYKPPDPENVARPV 215
QY 171 GGLEDOLSVWVSPALKD-FLFOAKQIQRVEDSVDMKVVDDVSNQTSCLAGLPGT 229
DB 216 PSNPRRLLEVWQPTSTPDPDESPLKFFLRPLILDQWQHV-ELSDGTAHTTIDAYAGK 274
QY 230 VYEVQVPCNPFGLYSGKAGIWMSEWSHPTAASPRSERP----- 269
DB 275 EYIIQVAAK-----DNEIGTWSQMS-VAAHATPWTEEPHNLTEAQALETTSSTSSLA 327
QY 269 -----GPGGACAP 277
DB 328 PPPTTRICDPGELSGGGPCAP 349

RESULT 10
US-08-449-329-2
Sequence 2, Application US/08449329
Patent No. 5648334
GENERAL INFORMATION:
APPLICANT: Davis, Samuel
APPLICANT: Squinto, Stephen P.
APPLICANT: Furch, Mark E.
APPLICANT: Yancopoulos, George D.
TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,329
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/700,677
FILING DATE: 15-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mastrook, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-065
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-449-329-2

Query Match 11.4%; Score 219.5; DB 1; Length 372;
Best Local Similarity 26.7%; Pred. No. 2,7e-14;
Matches 86; Conservative 37; Mismatches 122; Indels 77; Gaps 16;
DB 2 LNRRLPELSESRVNLSTALALANLNGSRSGDNLVCHARDGSIAGS-CLYVGLPPE 60
59 VNGTDLPDL---LNGSQLV---LHGLELGHSGLYACFHRDSMHLRHQVLLHVLGPPR 110
DB 61 KPNISQSMKNM-KDLICRM-----TPGAHGETFLHNTNLSKYLKRWYGQDNCEYH 112
111 EPLVLSRSMTYKRGYCSNHLPTPTPTPTNTVTLHOSKIN-----VCEKDP 158
DB 113 TVGPHSCHIRKDLALFT--PYEIVEATNRLGARSADVLTLDLDVTTDPPDVHVSRY 170
159 AL-KNNGHI-RYMHLESTIKYKISIVSNALGH-NATATITDEFITVKPDPENVARPV 215
DB 171 GGLSDLSVWVSPPLKD-FLFOAKQIRRYVEDSVDMKVVYDVSNQTSCLAGLKPCT 229
216 PSNPRRLLEVWQPTSTWPDSEPLKFLRPLILDQWQH-ELSDGTAHTITDAVAK 274
DB 230 VFVQVRCNPFGLYSGKKGIMSEWHPRTAASRSPR----- 269
275 EYIIQVAAK-----DNEIGTWSQMS-VAAHATPWTEPRHLTTEAOAETTTSTSSLA 327
QY 269 -----GPGGACEP 277

DB 328 PPPTKICDPGEISGGGCPAP 349
RESULT 11
US-08-445-073-2
Sequence 2, Application US/08445073
Patent No. 5849897
GENERAL INFORMATION:
APPLICANT: Davis, Samuel
APPLICANT: Squinto, Stephen P.
APPLICANT: Furch, Mark E.
APPLICANT: Yancopoulos, George D.
TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,073
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,647
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mastrook, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-445-073-2

Query Match 11.4%; Score 219.5; DB 2; Length 372;
Best Local Similarity 26.7%; Pred. No. 2,7e-14;
Matches 86; Conservative 37; Mismatches 122; Indels 77; Gaps 16;
DB 2 LNRRLPELSESRVNLSTALALANLNGSRSGDNLVCHARDGSIAGS-CLYVGLPPE 60
59 VNGTDLPDL---LNGSQLV---LHGLELGHSGLYACFHRDSMHLRHQVLLHVLGPPR 110
DB 61 KPNISQSMKNM-KDLICRM-----TPGAHGETFLHNTNLSKYLKRWYGQDNCEYH 112
111 EPLVLSRSMTYKRGYCSNHLPTPTPTPTNTVTLHOSKIN-----VCEKDP 158
DB 113 TVGPHSCHIRKDLALFT--PYEIVEATNRLGARSADVLTLDLDVTTDPPDVHVSRY 170
159 AL-KNNGHI-RYMHLESTIKYKISIVSNALGH-NATATITDEFITVKPDPENVARPV 215
DB 171 GGLSDLSVWVSPPLKD-FLFOAKQIRRYVEDSVDMKVVYDVSNQTSCLAGLKPCT 229
216 PSNPRRLLEVWQPTSTWPDSEPLKFLRPLILDQWQH-ELSDGTAHTITDAVAK 274
DB 230 VFVQVRCNPFGLYSGKKGIMSEWHPRTAASRSPR----- 269
275 EYIIQVAAK-----DNEIGTWSQMS-VAAHATPWTEPRHLTTEAOAETTTSTSSLA 327
QY 275 EYIIQVAAK-----DNEIGTWSQMS-VAAHATPWTEPRHLTTEAOAETTTSTSSLA 327

QY 269 -----GPGGACBP 277
DB 328 PPTTKICDPGELSGGCGCAP 349

RESULT 12

PCT-US91-03896-2
Sequence 2, Application PC/TUS9103896

GENERAL INFORMATION:

APPLICANT: Davis, Samuel
APPLICANT: Squinto, Stephen P.
APPLICANT: Furl, Mark E.
APPLICANT: Yancopoulos, George D.
TITLE OF INVENTION: The ciliary Neurotrophic Factor Receptor
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/03896
FILING DATE: 19910603
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-065-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US91-03896-2

Query Match

Best Local Similarity 11.4%; Score 219.5; DB 3; Length 372;
Matches 86; Conservative 37; Mismatches 122; Indels 77; Gaps 16;

QY 2 LNSRRRLPELRSVNASTLALALANLNGSRORSNDLVCHARDOSIAGS-CLYGLPPE 60
DB 59 VNGDLDAPD---LNGSOLV-----LNGLEIGHGSLYACHRHDSWHLRHQVLLHVGJLPPR 110
QY 61 KPNVNSCSKXNM-KDLTCRW-----TPGAGHETFLHTYSLKYLKRWGODNTCEYH 112
DB 111 EPV-LSCRSTYFGFYCSWHLPTPIYIPMTFNTVYHSGKIM-----VCKDP 158
QY 113 TVGHSCHIKDALTFT--PYEIVVENTNLSGRSVLTLDLIDVTTDPPDVHVSRY 170
DB 159 AL-KNRCHI-RYHMLFSTIKYSISVSNALGH-NATAITFDEFTYKPPPENNVARPV 215
QY 171 GGLDOLSVRWSPALKD-FLFOAKQIYRYVEDSVDMKVVDVSNQTSCLAGLKPPT 229
DB 216 PSNPRLEVTWQPTSTPDPESPFLKFLYRPLILDQWQHV-ELSDGTAHTTTDVAAGR 274
QY 230 VYVQVRCNPFGLYSGKAGIEMSEWSPHTAASPTPRSERP-----269
DB 275 EYIIQVAAK-----DNEIGTWSDMV-VAAHATPWEERPHLITTEAQAETTTSTTSSLA 347

QY 269 -----GPGGACBP 277
DB 328 PPTTKICDPGELSGGCGCAP 349

RESULT 13

US-08-419-652-6
Sequence 6, Application US/08419652

PATENT No. 5831007

GENERAL INFORMATION:

APPLICANT: Chua, Anne O
APPLICANT: Gubler, Ulrich A
TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07110-1199

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,652
FILING DATE: 11-APR-1995
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/248,532
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/094,713
FILING DATE: 19-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: Kass, Alan P.

REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: CD 9174

TELECOMMUNICATION INFORMATION:

TELEPHONE: (201) 235-4205
TELEFAX: (201) 235-3500

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 602 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Region

LOCATION: 1..602

OTHER INFORMATION: 731 of human granulocyte colony-stimulating factor-receptor.

US-08-419-652-6

Query Match

Best Local Similarity 11.1%; Score 213.5; DB 2; Length 602;
Matches 68; Conservative 31; Mismatches 86; Indels 29; Gaps 11;

QY 58 PPKPYNISG-SKNNKDLTCRWTPGAHETFLHTYSLK-YKLRWYQ---DNTCEYH 112
DB 3 PPAIPNLSCLNMLTSSICOWEPGP--ETHLPSTFLKSRSCNCGTQSGSIIDCPV 60
QY 113 TVGPHSCHRP-KDLAFTYEIVVENTNLSGRSVLTLDLIDV-----TTDPP 163
DB 61 KQGSQSCCLPRKHLHLYQNGIYVQDAENALGTSMSPOLCLDPDVKLEPPMLRTMDPSP 120
QY 164 DVHVSVGLDOLSVRWSPALKD-FLFOAKQIYRYVEDSVDMKVVDVSNQTSCLAGLKPPT 221
DB 121 EAAPQAGCLQ-----LCW--EPWQPGHINQCELRHQRQGEASWALVGPPLLEALQYE 174

```

0Y 222 LAGLKPGTVYFVQVRCNPEGIGYSKRAGINSEMS 255
      | | | | | : | | : |
Db 175 LCGLLPATAYTLQIRICIRWPL-----PGHWSBWS 203

```

RESULT 14
US-08-685-

```

; Sequence 2, Application US/08685118
; Patent No. 5840530
; GENERAL INFORMATION.

```

APPLICANT: Gubler, Ulrich A
APPLICANT: Presky, David H
TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
Inventors: "Ulrich A. Gubler, David H. Presky"
Correspondence Address: "Ulrich A. Gubler, David H. Presky"

```

? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/665,118
? FILING DATE:

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Query Match	10.8%	Score 207.5	DB 2	Length 862
Best Local Similarity	28.9%	Pred. No. 1.4e-12		
Matches 71	Conservative 32	Mismatches 104	Indels 39	Gaps 10

QY	38	LVCHAKRGSLIASCCLVYGLPEPEKPVNISCMMK--DLTCRMTPGAAGETFLTNTSLK	96
Db	103	LACINSDIICGAEIIVGAPPEOPNLSIOKEOQTVACTWGRGR--DTHLTETTLQ	160
QY	97	Y----KLRWYGO--DNTCEEYHTGV-----PASHCIPMDLAEFTPEYLVETATNTLGS	143
Db	161	LSGPKNLTMQKCKDIYC-DYLDGIMLTPESPESNFTAK-----YAVNSLGS	208
QY	144	ARGDVLFLDILDVYTTDPDPDVHNSRVNGSGLEDOLSVYVSWSPALKDFQAKVQIRRYVE	203
Db	209	SSSLPSFTFLDILRYRLPPMDIRIKFQKASVRCITLW-----RDGCLVILNLRKLRTPS	263
QY	204	DSVDKMYVDVSNQTSRGLAKGKGYIVFYQVRCNPGFIIGSKRAGIWSSEMSHPTAASP	263
Db	263	NSRLMNNVNTAKAGRHDDLDPKFTLEYEQI--SSKLHLY---KGSWSDMSSESLRAQTP	317
QY	264	RSERPG	269
Db	318	EEEPFG	323

RESULT 15

US-08-915-495-2
; Sequence 2, Application US/08915495
; Patent No. 5852176

APPLICANT: Gubler, Ulrich A
 APPLICANT: Preasky, David H
 TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hoffmann-La Roche Inc.
 STREET: 340 Kingsland street
 CITY: Nutley
 STATE: NJ
 COUNTRY: USA
 ZIP: 07110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,495
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,118
FILING DATE:

Query Match	10.88;	Score 207.5;	DB 2;	Length 862;
Best Local Similarity	28.9%;	Pred. No. 1.4e-12;		
Matches 71;	Conservative 32;	Mismatches 104;	Indels 39;	Gaps 10;

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QY      38  LVCHARDGSLIAGSLCYGLPEPEKPVNISCMSSNMK--DLTCRWTPGAGGEMFLHTNLSLK  96
Db      103  LACINSDDELQIGAGMEIFPGVAPBEPQULSIOIQGDEGQYACWMEGR--DHHLYETETLQ  100C

QY      97  Y-----KLRWYGO--DNTCSEYHTVG-----PHSCHIKRDIALFTPYEIVEATNRLGGS  143
Db      161  LSGPRNLTWOKRCKDITC-DYLDGFINLTPPESEPSNFTAK-----VTAVNSLGS  208B

QY      144  ARSDVLTLDIDVYTTTPPEPPVHVSRRVGLGDEDLTSRWSPSPALKDFLFOAKYQIRRYVE  203
Db      209  SSLSLSTFTFLDIYRPLRPMDIRKTFOKASVSCSLITYW-----RDESLVTLNFKLTRPS  262Z

QY      204  DSDVMKRVVDVYSNOTSCLAGLKGVTYFVOVACNPFQIGYSGKKAIGINSEWSHPTAASP  263S
Db      263  NSRLNNMNVYTKARGRHDLIDIKRFEYEFQI--SKTLHLX-----KGSWSDWSESLRQOTP  317H

QY      264  NSERPQ  269
Db      318  EEPPTG  323

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Search completed: September 16, 1999, 20:41:10
Job time: 5439 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:42:10 ; Search time 49.27 Seconds

(without alignments)
284.614 Million cell updates/sec

Title: US-09-037-657-25

Perfect score: 1919

Sequence: 1 TLNGRRRLPELRSVLNASTL.....TRGSCPADGAREVLPDKL 350

Scoring table: BLOSUM62

Searched: 122810 seqs, 40065486 residues

Database :
1: PIR_60.*
2: PIR1.*
3: PIR2.*
4: PIR3.*
5: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	332	17.3	622	2 A40144	prolactin receptor
2	325.5	17.0	206	2 A57018	prolactin receptor
3	316	16.5	830	2 I50455	prolactin receptor
4	313	16.3	610	2 A34631	lactogen receptor
5	313	16.3	610	2 A36116	prolactin receptor
6	313	16.3	412	2 A41070	prolactin receptor
7	313	16.3	310	2 A29884	prolactin receptor
8	309.5	16.1	303	2 I75524	prolactin receptor
9	309.5	16.1	292	2 I75525	prolactin receptor
10	309.5	16.1	608	2 I53269	prolactin receptor
11	308	16.1	831	2 J01655	prolactin receptor
12	306.5	16.0	581	2 I45971	prolactin receptor
13	306.5	15.7	616	2 A30304	prolactin receptor
14	297	15.5	917	2 I49639	prolactin receptor
15	290.5	15.1	918	2 A36337	glycoprotein 130 -
16	285	14.9	918	2 A44257	membrane glycoprot
17	263.5	13.7	630	2 I51086	interleukin-6 sign
18	241	12.6	837	2 A34898	prolactin receptor
19	226.5	11.8	372	2 I58141	granulocyte colony
20	220.5	11.5	783	2 JH0329	ciliary neurotroph
21	220.5	11.5	771	2 B38252	granulocyte colony
22	220.5	11.5	863	2 C38252	granulocyte colony
23	219.5	11.4	372	2 UHHCN	granulocyte colony
24	204	10.6	432	2 I48343	ciliary neurotroph
25	203	10.6	422	2 I37891	interleukin-11 rec
26	202	10.5	362	2 S60614	growth promoting a
27	199	10.4	156	2 A32868	prolactin receptor
28	194	10.1	625	2 S35317	hematopoietic grow
29	191	9.9	150	2 B34631	lactogen receptor
30	190	9.9	626	2 S37622	proto-oncogene - m
31	188.5	9.8	579	2 B45266	MPL-R protein prec
32	188.5	9.8	635	2 A45266	interleukin-6 rece
33	181	9.4	468	1 A41242	leukemia inhibitor
34	176	9.2	1097	2 S17308	leptin receptor (v
35	174.5	9.1	894	2 S68437	leptin receptor (v
36	174.5	9.1	900	2 S68441	leptin receptor (v
37	174.5	9.1	805	2 S68441	leptin receptor (v
38	173.5	9.0	460	2 JLO145	interleukin-6 rece
39	170	8.9	894	2 JCA797	leptin receptor pr

40	170	8.9	1162	2 PC4184	leptin receptor, O
41	170	8.9	805	3 JC4897	leptin receptor, O
42	169	8.8	265	2 S14081	erythropoietin rec
43	166	8.7	1092	2 JX0312	differentiation st
44	166	8.7	719	2 JC3181	differentiation st
45	165.5	8.6	440	2 JLO144	interleukin-6 rece

ALIGNMENTS

RESULT 1
A40144
prolactin receptor long form precursor, hepatoma and breast cancer cells - human
C/Species: Homo sapiens (man)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Sep-1998
C/Accession: A40144
R/Boutin, J.M.; Edery, M.; Shitka, M.; Jolicoeur, C.; Lesneux, L.; All, S.; Gould, D
Mol. Endocrinol. 3, 1455-1461, 1989
A/Title: Identification of a cDNA encoding a long form of prolactin receptor in human
A/Reference number: A40144; MID:90114212
A/Accession: A40144
A/Molecule type: mRNA
A/Residues: 1-622 <BOU>
A/Cross-references: GB:M31661; NID:G190361; PID:G190362
A/Genes: GDB:PRLR
A/Map position: 5p13.3-5p13.1
A/Keywords: glycoprotein; transmembrane protein
F/1-24/Domains: signal sequence #status predicted <SIG>
F/25-622/Product: prolactin receptor, long form #status predicted <AT>
F/59,104,233/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 17.38; Score 332; DB 2; Length 622;
Best Local Similarity 37.18; Pred. No. 1.8e-21;
Matches 83; Conservative 28; Mismatches 95; Indels 18; Gaps 8;

QY 47 ILAAGCLYVG-LPEKPNVISCNKNKMDLCRTPGAHGTFHTNYSKYKLRMTGQD 105
DB 15 LFLWTLCLNGQLPGKPKETFCRSPNKEFTFCWRPPTDG--LPTNYSLYHREGFTLM 72
QY 106 NTCEHYHTVGHPSCHIFPD-LALFPEIWEATNTRGASRVLTLDIDVYTTDPPD 164
DB 73 HECDDYITGPNNSCHFPKQYTSMTRTIYATNATNONGSSFSDLYDVYIVQDPDPLE 132
QY 165 VHSRVGGLDQLSVRW--SPALNDF--LFOAKYQIRYVEDSVDMKVVDDVSNQTS 219
DB 133 LAV-EVQPEDEKRPKYLWIKNSPPTLIDLKTGWTLLYELIKPEKAEME-IRFAGQTE 190
QY 220 CRLAGLRPGYTFVQVNCNPGTIGSKAKGIWSEWSHPTAASP 263
DB 191 FKILSLHPGKTLVQVCRKP-----DHGYWSMSPATRIQIP 227

RESULT 2

A57018
prolactin receptor - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-Jul-1996
C/Accession: A57018
R/Fuh, G.; Wells, J.A.
J. Biol. Chem. 270, 13133-13137, 1995
A/Title: Prolactin receptor antagonists that inhibit the growth of breast cancer cell
A/Reference number: A57018; MID:95286597
A/Accession: A57018
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-206 <RES>
A/Cross-references: GB:S78505; NID:G999114; PID:G999115

Query Match 17.0%; Score 325.5; DB 2; Length 206;
 Best Local Similarity 37.6%; Pred. No. 1.7e-21;
 Matches 80; Conservative 26; Mismatches 90; Indels 17; Gaps 7;

57 LPPEKPVNISCSKNNKDLTCRMTPGAAGETFLHTNYSLKYLKMYGODVTCCEHYTGP 116
 2 LPPEKPEFKRSNKEFTCWMKPGDGG--LPTNYSLYHNGEFLMHECPYITGCP 59
 117 HSHCHPDL-LALTPYEIWEATNRLGARSADVLTLDIVYTTDPPDVHVSNGLED 175
 60 NSCHFGQYQYSMTWTYIMVNAIOMGSSFSEDELYVDTYIVQDPPLLELAV--EVKQPED 118
 176 QLSRWV--SPALKDF--LFOAKYQIRYVEDSVDMKVVDVSNQTSCLAGLKPGTV 230
 119 RKPLMKWSPPTLIDLTGTFWTLIRLKPPEAAEME--IHFAGQOTEFKLSLHFGQK 177
 231 YFVQRCNPFGIYSGKAGIWMSESHPTAASP 263
 178 YLVQVRCR-----DHGYWSMSPATFIQIP 203

RESULT 3
 150455
 prolactin receptor - pigeon
 C:Species: Columba livia (domestic pigeon)
 C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Sep-1996
 C:Accession: 150455
 R:Chen, X.; Horseman, N.D.
 A:Endocrinology 135, 269-276, 1994
 A:Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor.
 A:Reference number: 150455; MUID:94283267
 A:Accession: 150455
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-830 <CHE>
 A:Cross-references: EMBL:U07694; NID:g466381; PID:g466382

Query Match 16.5%; Score 316; DB 2; Length 830;
 Best Local Similarity 36.6%; Pred. No. 6.8e-20;
 Matches 75; Conservative 30; Mismatches 82; Indels 18; Gaps 8;

58 PPEKPVNISCSKNNKDLTCRMTPGAAGETFLH--TNSLKYLKMYGODVTCCEHYTGP 116
 231 PPEKPTTIKCRSPKEFTTCWMKPGSDG--HPTNYSLYHNGEFLMHECPYITGAP 287
 117 HSHCH-PRDLALTPYEIWEATNRLGARSADVLTLDIVYTTDPPDV--HYSRVGGL 173
 288 NSCHYDKKHTSFMTYINITVKAINEISNSVDPLVDTYIVQDPPLVNTLELKKTYNR 347
 174 EDQLSRVNVSPPALKDF--LFOAKYQIRYVEDSVDMKVVDVSNQTSCLAGLKPGTV 230
 348 KPYLVLTW--SPPLADVSGWLTLDYELRLKPEAEEMETI--FVGOQTHYKCFSLNPGKK 405
 231 YFVQRCNPFGIYSGKAGIWMSEWS 285
 406 YIVQVRCR-----DHGWSMSEWS 424

RESULT 4
 A34631
 lactogen receptor 1 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 13-Jul-1990 #sequence_revision 09-Oct-1992 #text_change 10-Sep-1997
 C:Accession: A34631
 R:Zheng, R.; Buczo, E.; Tsai-Morris, C.H.; Hu, Z.Z.; Dufau, M.L.
 A:Biochem. Biophys. Res. Commun. 168, 415-422, 1990
 A:Title: Isolation and characterization of two novel rat ovarian lactogen receptor cDNA
 A:Reference number: A34631; MUID:90241201
 A:Accession: A34631
 A>Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-610 <2HA>

A:Cross-references: GB:M34083; NID:g205122; PID:g205123
 A:Note: the authors translated the codon GAG for residue 533 as Gly

Query Match 16.3%; Score 313; DB 2; Length 610;
 Best Local Similarity 35.0%; Pred. No. 8.4e-20;
 Matches 79; Conservative 36; Mismatches 85; Indels 26; Gaps 10;

46 SIAGSCLYGLPPEKPVNISCSKNNKDLTCRMTPGAAGETFLHTNYSLKYLKMYGOD 105
 15 SLKQGS-----PPGRPEIKHCRSPDKETTCWMNPGTGG--LPTNYSLYSKE--GEK 65
 106 NT--CEEYHTVGHSHIPD-LALTPYEIWEATNRLGARSADVLTLDIVYTTDP 162
 66 TTYECPDYKSGNSCFSSQYTSIMKTYITVNAIOMGSSSDPLVDTYIVPEEP 125
 163 PDVHVSNGLEDQLSVRWV--SPALKDF--LFOAKYQIRYVEDSVDMKVVDVSNQ 217
 126 RNLT-LVKNLKNKTYLWKMSPPTITDVKTGTFMEYELRLKPEAEEME--IHFTHQ 183
 218 TSCRLAGLKPGTYFVQVRCNPFGIYSGKAGIWMSESHPTAASP 263
 184 TQKVFVDLYPGQKYLVTQTRCKP-----DHGYWSMSSQESSVEMP 222

RESULT 5
 A36116
 prolactin receptor 2 precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 10-Sep-1997
 C:Accession: A36116
 R:Shiota, M.; Banville, D.; Ali, S.; Jolicoeur, C.; Boutin, J.M.; Edery, M.; Djiane, M.L.
 A:Endocrinol. 4, 1136-1143, 1990
 A:Title: Expression of two forms of prolactin receptor in rat ovary and liver.
 A:Reference number: A36116; MUID:91155946
 A:Accession: A36116
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-610 <SH1>
 A:Cross-references: GB:M57668; NID:g206366; PID:g206367; GB:M60728

Query Match 16.3%; Score 313; DB 2; Length 610;
 Best Local Similarity 35.0%; Pred. No. 8.4e-20;
 Matches 79; Conservative 36; Mismatches 85; Indels 26; Gaps 10;

46 SIAGSCLYGLPPEKPVNISCSKNNKDLTCRMTPGAAGETFLHTNYSLKYLKMYGOD 105
 15 SLKQGS-----PPGRPEIKHCRSPDKETTCWMNPGTGG--LPTNYSLYSKE--GEK 65
 106 NT--CEEYHTVGHSHIPD-LALTPYEIWEATNRLGARSADVLTLDIVYTTDP 162
 66 TTYECPDYKSGNSCFSSQYTSIMKTYITVNAIOMGSSSDPLVDTYIVPEEP 125
 163 PDVHVSNGLEDQLSVRWV--SPALKDF--LFOAKYQIRYVEDSVDMKVVDVSNQ 217
 126 RNLT-LVKNLKNKTYLWKMSPPTITDVKTGTFMEYELRLKPEAEEME--IHFTHQ 183
 218 TSCRLAGLKPGTYFVQVRCNPFGIYSGKAGIWMSESHPTAASP 263
 184 TQKVFVDLYPGQKYLVTQTRCKP-----DHGYWSMSSQESSVEMP 222

RESULT 6
 A41070
 prolactin receptor NB2 precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 10-Sep-1997
 C:Accession: A41070; I55417
 R:Ali, S.; Pellegrini, I.; Kelly, P.A.
 A:Biochem. Biophys. Res. Commun. 186, 266-271, 1992
 A:Title: A prolactin-dependent immune cell line (NB2) expresses a mutant form of pro-

A:Accession: A41070
 A:Molecule type: mRNA
 A:Residues: 1-412 <ALIS>
 A:Cross-references: GB:M74152; NID:g206389; PID:g206390
 J.O'Neal, K.D.; Yu-Lee, L.Y.
 J. Biol. Chem. 269, 26076-26082, 1994
 A:Title: Differential signal transduction of the short, Nb2, and long prolactin receptor
 A:Reference number: 155417; MUID:95014432
 A:Accession: 155417
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-412 <RES>
 A:Cross-references: EMBL:007567; NID:g641963; PID:g641964
 A:Experimental source: ND2-11C cell line
 C:Keywords: transmembrane protein

Query Match 16.3%; Score 313; DB 2; Length 412;
 Best Local Similarity 35.0%; Pred. No. 5, 1e-20;
 Matches 79; Conservative 36; Mismatches 85; Indels 26; Gaps 10;

46 SILAGSCLYVGLPEKPVNISCNMKDLTCRMTPGAHEFTLHNTSLKTKLRYGOD 105
 15 SLKNGS-----PPKPELHKCRSPDKETFTCMWNPDTGG--LPTNYSILYSKE--GEK 65
 106 NT--CEEHTVGPCHIPKD-LALFTPEIWEATNRLGSARSDVLTLDIDVYTTDP 162
 66 TTYECPDYKTSQPNCSFSGKQYTSIMKIYIIVNATNGSSSDPLVYVYIYEPEP 125
 163 PDVHVSRRVGLLEDLSVWV--SPPALKDF--LFQARYQIRRVSDVMKVVDDVSNQ 217
 126 RNLTL-EVKQKDKKTYLWVWSPPTITDVKTGMFTMEYELRKPEAEEME-IHFTGHQ 183
 218 TSCRLAGLPGTYVFOVNCNPGIYSGSKKAGIWMSEHPTASTP 263
 184 TORVFDLYPGQKYLIVOTRCKP-----DHGYMSRWMSQESSVEAP 222

RESULT 7
 A:Accession: A23984
 A:Molecule type: mRNA
 A:Residues: 1-310 <BOU>
 A:Cross-references: GB:M19304; NID:g206364; PID:g206365
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1989 #sequence, revision 30-Sep-1989 #text, change 20-Mar-1998
 C:Accession: A29984
 R.Boutin, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Ebery, M.; Shirota, M.; Banville
 Cell 53, 69-77, 1988
 A:Title: Cloning and expression of the rat prolactin receptor, a member of the growth ho
 A:Reference number: A29884; MUID:88165059
 A:Accession: A29884

A:Molecule type: mRNA
 A:Residues: 1-310 <BOU>
 A:Cross-references: GB:M19304; NID:g206364; PID:g206365
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1989 #sequence, revision 30-Sep-1989 #text, change 20-Mar-1998
 C:Accession: A29984
 R.Boutin, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Ebery, M.; Shirota, M.; Banville
 Cell 53, 69-77, 1988
 A:Title: Cloning and expression of the rat prolactin receptor, a member of the growth ho
 A:Reference number: A29884; MUID:88165059
 A:Accession: A29884

Query Match 16.3%; Score 313; DB 2; Length 310;
 Best Local Similarity 35.0%; Pred. No. 3, 5e-20;
 Matches 79; Conservative 36; Mismatches 85; Indels 26; Gaps 10;

46 SILAGSCLYVGLPEKPVNISCNMKDLTCRMTPGAHEFTLHNTSLKTKLRYGOD 105
 15 SLKNGS-----PPKPELHKCRSPDKETFTCMWNPDTGG--LPTNYSILYSKE--GEK 65
 106 NT--CEEHTVGPCHIPKD-LALFTPEIWEATNRLGSARSDVLTLDIDVYTTDP 162
 66 TTYECPDYKTSQPNCSFSGKQYTSIMKIYIIVNATNGSSSDPLVYVYIYEPEP 125
 163 PDVHVSRRVGLLEDLSVWV--SPPALKDF--LFQARYQIRRVSDVMKVVDDVSNQ 217
 126 RNLTL-EVKQKDKKTYLWVWSPPTITDVKTGMFTMEYELRKPEAEEME-IHFTGHQ 183

QY 218 TSCRLAGLPGTYVFOVNCNPGIYSGSKKAGIWMSEHPTASTP 263
 DB 184 TORVFDLYPGQKYLIVOTRCKP-----DHGYMSRWMSQESSVEAP 222

RESULT 8

prolactin receptor precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence, revision 02-Aug-1996 #text, change 02-Aug-1996
 C:Accession: 177524
 R.Davis, J.A.; Linzer, D.I.H.
 Mol. Endocrinol. 3, 674-680, 1989
 A:Title: Expression of multiple forms of the prolactin receptor in mouse liver.
 A:Reference number: 157699; MUID:89261824
 A:Accession: 177524
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-303 <RES>
 A:Cross-references: GB:M22958; NID:g200479; PID:g200480

Query Match 16.1%; Score 309.5; DB 2; Length 303;
 Best Local Similarity 31.4%; Pred. No. 6, 9e-20;
 Matches 82; Conservative 38; Mismatches 94; Indels 47; Gaps 10;

QY 11 LSRVNAATLALANLNGSNRSGDNVCHARDGSIAGSCLYVGLPEKPVNISCMSK 70
 DB 1 MSSALAYMLVLSILNGS-----PPGPEIHKCRSP 34
 QY 71 NKMDTCRMTPGAHEFTLHNTSLKTKLRYGODNT--CEEHTVGPCHIPKD-LAL 127
 DB 35 DKEFTCMWNPDSOG--LPTNYSILYSKE--GEKNTYECDDYTSQPNCSFSGKQYTSI 90
 QY 128 FTPEIWEATNRLGSARSDVLTLDIDVYTTDPPDVHVSRRVGLLEDLSVWV--PP 185
 DB 91 WKIITVYVNAATNGSSSDPLVYVYIYEPEPRLTL-EVKQKDKKTYLWVWSPPTITDVKTGMFTMEYELRKPEAEEME-IHFTGHQ 149
 QY 186 ALKDF--LFQARYQIRRVSDVMKVVDDVSNQTSCLAGLPGTYVFOVNCNPGI 242
 DB 150 TITDVKTGMFTMEYELRKPEAEEME-IHFTGHQTFKVFDPYGVQKYLIVOTRCKP--- 206
 QY 243 YGSKKAGIWMSEHPTASTP 263
 DB 206 ----DHGYMSRWMSQESSVEAP 222

RESULT 9

prolactin receptor precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence, revision 02-Aug-1996 #text, change 02-Aug-1996
 C:Accession: 177525
 R.Davis, J.A.; Linzer, D.I.H.
 Mol. Endocrinol. 3, 674-680, 1989
 A:Title: Expression of multiple forms of the prolactin receptor in mouse liver.
 A:Reference number: 157699; MUID:89261824
 A:Accession: 177525
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-292 <RES>
 A:Cross-references: GB:M22959; NID:g200481; PID:g200482

Query Match 16.1%; Score 309.5; DB 2; Length 292;
 Best Local Similarity 31.4%; Pred. No. 6, 6e-20;
 Matches 82; Conservative 38; Mismatches 94; Indels 47; Gaps 10;

QY 11 LSRVNAATLALANLNGSNRSGDNVCHARDGSIAGSCLYVGLPEKPVNISCMSK 70
 DB 1 MSSALAYMLVLSILNGS-----PPGPEIHKCRSP 34
 QY 71 NKMDTCRMTPGAHEFTLHNTSLKTKLRYGODNT--CEEHTVGPCHIPKD-LAL 127

Db 35 DEETFCWNNPDSG--LPTNYSLSYKE--GEKTYECPDYKTSNCSFSSKQYPSI 90
 QY 128 FTPEYEWATNRLGSARSDVLTLDLVYTTDPPEDVAVSVAGLEQOLSTRWVS--PP 185
 Db 91 WRIYITVATNEMGSSSDPLVDVTVIYVEPEPRNLTLEVKOLKDKKYLWVKWLP 149
 QY 186 ALKDF---LFOAKYQIRRVEDSVDMKVVDVSNQTSCLAGLKPGTYFVQVRCNPGI 242
 Db 150 TITDVKTGTFMEYFIRLKSSEADME--IHFGHOTQFVFPDLYGCKYLVQTRCKP--- 206
 QY 243 YGSKKAGIWEWSHPTASTP 263
 Db 206 ---DHGYSRWGQEKSEIEIP 222

RESULT 10

153269
 prolactin receptor, long form - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence revision 02-Aug-1996 #text_change 29-Jan-1999
 C:Accession: J01655
 R:Clarke, D.L.; Linzer, D.I.H.
 Endocrinology 133, 224-232, 1993
 A:Title: Changes in prolactin receptor expression during pregnancy in the mouse ovary.
 A:Reference number: 153269; MUID:93307149
 A:Accession: J01655
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-608 <RES>
 A:Cross-references: GB:L14811; NID:g9293769; PID:g9293770
 R:Moore, R.C.; Oka, T.
 Gene 134, 263-265, 1993
 A:Title: Cloning and sequencing of the cDNA encoding the murine mammary gland long-form
 A:Reference number: J06071; MUID:94085788
 A:Accession: J06071
 A:Molecule type: mRNA
 A:Residues: 1-608 <MOO>
 A:Cross-references: GB:L13593; NID:g947398; PID:g947842
 R:Edery, M.; Pezet, A.; Nandi, S.; Kelly, P.A.
 Submitted to the EMBL Data Library, June 1993
 A:Description: Isolation and nucleotide sequence of a mouse cDNA prolactin receptor.
 A:Reference number: S34336
 A:Accession: S34336
 A:Molecule type: mRNA
 A:Residues: 1-557; F:559-608 <EDE>
 A:Cross-references: EMBL:X73372; NID:g9312696; PID:g9312697
 C:Comment: Prolactin receptor have long form and short form which are resulted from alternative splicing.
 C:Keywords: receptor; transmembrane protein
 F:230-253/Domain: transmembrane #status predicted <TM>

Query Match 16.1%; Score 309.5; DB 2; Length 608;
 Best Local Similarity 31.4%; Pred. No. 1,7e-19;
 Matches 82; Conservative 38; Mismatches 94; Indels 47; Gaps 10;

QY 11 LSRVLA NSTLALANLNGSRGSDNLYCHARGSLAGSCLVGLPPEKPVNISCKSK 70
 Db 1 MSSALATVLLVLSISLNGS-----PPGKPEIRHKCRSP 34
 QY 71 NMKDLTCWTPGAGETFLATNYSLKYLKRWYGODNT--CEHYTVGPHSHIPKRD-LAL 127
 Db 35 DKFEFTCWNNPDSG--LPTNYSLSYKE--GEKTYECPDYKTSNCSFSSKQYPSI 90
 QY 128 FTPEYEWATNRLGSARSDVLTLDLVYTTDPPEDVAVSVAGLEQOLSTRWVS--PP 185
 Db 91 WRIYITVATNEMGSSSDPLVDVTVIYVEPEPRNLTLEVKOLKDKKYLWVKWLP 149
 QY 186 ALKDF---LFOAKYQIRRVEDSVDMKVVDVSNQTSCLAGLKPGTYFVQVRCNPGI 242
 Db 150 TITDVKTGTFMEYFIRLKSSEADME--IHFGHOTQFVFPDLYGCKYLVQTRCKP--- 206

QY 243 YGSKKAGIWEWSHPTASTP 263
 Db 206 ---DHGYSRWGQEKSEIEIP 222

RESULT 11

101655
 prolactin receptor precursor - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 10-Sep-1997
 C:Accession: J01655
 R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
 Biochem. Biophys. Res. Commun. 188, 490-496, 1992
 A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDN.
 A:Reference number: J01655; MUID:93075121
 A:Accession: J01655
 A:Molecule type: mRNA
 A:Residues: 1-831 <TRAN>
 A:Cross-references: DDBJ:D13154; NID:g222848; PID:d1002939; PID:g222849
 A:Experimental source: Kidney
 C:Keywords: glycoprotein; transmembrane protein
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-831/Product: prolactin receptor #status predicted <MAT>
 F:439-462/Domain: transmembrane #status predicted <TM>
 F:59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (asn) (con

Query Match 16.1%; Score 308; DB 2; Length 831;
 Best Local Similarity 34.6%; Pred. No. 3.4e-19;
 Matches 75; Conservative 28; Mismatches 96; Indels 18; Gaps 8;

QY 58 PPEKPVNISCKSKMKDLTCRWTPGAGETFLH-TNLSLKYLKRWYGODNTCEHYTVGP 116
 Db 230 PPEKPVNISCKSKMKDLTCRWTPGAGETFLH-TNLSLKYLKRWYGODNTCEHYTVGP 116
 QY 117 HSCHI-PKDLALFTPEYEWATNRLGSARSDVLTLDLVYTTDPPEDV--HVSRYGGL 173
 Db 287 NSCFDCKKHNSFWITVITVATNEMGSSSDPLVDVTVIYVQDPDVNTLEKPPINR 346
 QY 174 EDOLSVRWSPALKDF--LFOAKYQIRRVEDSVDMKVVDVSNQTSCLAGLKPGTV 230
 Db 347 KPYLVLTW-SPPPLADVRSGWLTLEYELRLKPEEGEMETI-FGQGOYQKMFSLNKGK 404
 QY 231 YFQVRCNPGIYGSKAGIWEWSHPTASTP 267
 Db 405 YFQVRCNPGIYGSKAGIWEWSHPTASTP 267

RESULT 12

145971
 prolactin receptor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 16-Aug-1996 #sequence revision 16-Aug-1996 #text_change 28-Feb-1997
 C:Accession: J01655
 R:Scott, P.; Kessler, M.A.; Schuler, L.A.
 Mol. Cell. Endocrinol. 89, 47-58, 1992
 A:Title: Molecular cloning of the bovine prolactin receptor and distribution of pro:
 A:Reference number: 145971; MUID:93246019
 A:Accession: J01655
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-581 <SCO>
 A:Cross-references: GB:L02549; NID:g163617; PID:g163618
 C:Genetics: PRLR
 A:Gene: PRLR

Query Match 16.0%; Score 306.5; DB 2; Length 581;
 Best Local Similarity 31.2%; Pred. No. 2.9e-19;
 Matches 81; Conservative 38; Mismatches 94; Indels 47; Gaps 9;
 QY 12 LSRVLA NSTLALANLNGSRGSDNLYCHARGSLAGSCLVGLPPEKPVNISCKSK 71
 Db 1 MSSALATVLLVLSISLNGS-----PPGKPEIRHKCRSP 34

Db 7 SRVFIILLFLSVSLNGOS-----PPEKPLVKCRSPG 40

QY 72 MKDLCHWTFGAGHETFLHNNYSKLYKLRWGDONTCEHYTHVPHSCHT-PRDLAFTP 130

Db 41 KEFTTCWMEPGADG--LPNNYTLTHKEGELLHECPDXTGGPNSCYSKRTSTWKM 98

QY 131 YEIWEATNRLSGARSVDLTLDIDVTTDPPDPVHVSRLVGLSDQSVRV--SPALK 188

Db 99 YVITVNNINOMGISSDPLVHYHYTYIEPPEPNLTL-ELKHPRDKRYLWIKNSPPTMT 157

QY 189 D-----FLFOAKYQIRYVEDSDVMKVVDDVSNQTSCLAGLKGTYFVQVRCNPFQIY 243

Db 158 DVKSGWFIID--YEIRLKPKEATDME-THFLKOTQKIFNLPGQYQLVQIRCKP----- 211

QY 244 GSKKAGIYSEMSHPTAASP 263

Db 211 ----DHGIWSEMSPESSIQIP 227

RESULT 13

A30304

prolactin receptor 2 precursor - rabbit

M:Alternate names: prolactin receptor, mammary gland

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Mar-1998

C:Accession: A30304; A60380

R:Deriv. M.: Jolicœur, C.; Levl-Meyrueis, C.; Dusanter-Fourt, I.; Petridou, B.; Boutin, Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116, 1989

A:Title: Identification and sequence analysis of a second form of prolactin receptor by

A:Reference number: A30304; MID:89184578

A:Accession: A30304

A:Molecule type: mRNA

A:Residues: 1-616 <EDB>

A:Cross-references: GB:J04510; NID:g165669; PID:g165670

R:Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I. Int. J. Biochem. 22, 1089-1095, 1990

A:Title: Purification and partial sequence of the rabbit mammary gland prolactin receptor

A:Reference number: A60380; MID:9116782

A:Accession: A60380

A:Molecule type: protein

A:Residues: 41-98, 'X', 60-66; 90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108; 150-164, 'XX', 167

A:Note: the amino end of the mature protein was blocked

C:Keywords: blocked amino end; glycoprotein; transmembrane protein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-616/Product: prolactin receptor 2 #status predicted <MAT>

F:235-256/Domain: transmembrane #status predicted <TM>

F:59,104,132,347,389,411/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.7%; Score 300.5; DB 2; Length 616;

Best Local Similarity 35.4%; Pred. No. 1,4e-18;

Matches 75; Conservative 29; Mismatches 91; Indels 17; Gaps 7;

QY 58 PPEKPLVNSCSNMKDLRCRMTGAGHETFLHNNYSKLYKLRWGDONTCEHYTHVPH 117

Db 27 PPEKPLVNSCSNMKDLRCRMTGAGHETFLHNNYSKLYKLRWGDONTCEHYTHVPH 84

QY 118 SCHI-PRDLAFTPPEIWEATNRLSGARSVDLTLDIDVTTDPPDPVHVSRLVGLSDQ 176

Db 85 SCVFSKSHNSIMWITITVATNOMSGSSVDDPRVVDYTYIEPPEPNLTL-EKXHEDR 143

QY 177 LSVRWVS--PPALKDF--LFQAKYQIRYVEDSDVMKVVDDVSNQTSCLAGLKGTY 231

Db 144 KPLVWYKMLPPLVDVSGWLTQYERLKPKEAWE-THFAQOQOFKILSLXPQKY 202

QY 232 FVQVRCNPFQIYSEMSHPTAASP 263

Db 203 LVOYRCKP-----DHGIWSEMSPESSIQIP 227

C:Species: Mus musculus (house mouse)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 07-Feb-1997

C:Accession: I49699; I48370

R:Salto, M.; Yoshida, R.; Hibi, M.; Taga, T.; Kishimoto, T. J. Immunol. 148, 4066-4071, 1992

A:Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp

A:Reference number: I48370; MID:9221552

A:Accession: I49699

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-917 <RES>

A:Cross-references: GB:M83336; NID:g193591; PID:g193592

A:Accession: I48370

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-917 <RE2>

A:Cross-references: EMBL:X62646; NID:g840816; PID:g840817

C:Genetics:

A:Gene: gp130

C:Keywords: glycoprotein

Query Match 15.5%; Score 297; DB 2; Length 917;

Best Local Similarity 30.5%; Pred. No. 3.6e-18;

Matches 83; Conservative 45; Mismatches 124; Indels 20; Gaps 9;

QY 3 NGRRLPELRSVZINASTLALANLNGSRQSGDNLYCHARDGSLIAGSCLYVGLPPEKP 62

Db 70 NHAAPREGQVTAIRNTSSVTFIDVPLVSQVLCNLSFQIQNYYGVYMLSGFPDPK 129

QY 63 VNISCSNMKDLTCRTTPAHBETFLHNNYSKLYKLRWGD-NTCEHYTHVPHSCHT 121

Db 130 TNLTCIYNENKNNMCCMDPCR--EYILEYNTLKSE--WATERFPDQSKHGK---SCWV 182

QY 122 PKDLAFTPEIWEATNRLSGARSVDLTLDIDVTTDPPDPVHVSRLVGLSDQSVRW 181

Db 183 SYMTYVTVLEVVEALNAGKVSSEINFDVQKAPDPYMLSVTNSELSILKLSW 242

QY 182 VSPPALNDFLFOAKYQIRYVEDSDVMKVV--DVSNGTSCLAGLKGTYFVQVRCN 238

Db 243 VSSGL--GGLDLKSDIQYTKRASNIGVPLDITSPRSFTVQDLKPELEVYRIR-- 299

QY 239 PFGIYSGKRAKGIYSEMSHPTAASP--PRSERP 268

Db 299 --SIKDSGK-GYMSDSEASGTYEDRPSRP 327

RESULT 15

A36337

membrane glycoprotein gp130 precursor - human

C:Species: Homo sapiens (man)

C>Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-Sep-1998

C:Accession: A36337

R:Hibi, M.; Murakami, M.; Salto, M.; Hirano, T.; Taga, T.; Kishimoto, T. Cell 63, 1149-1157, 1990

A:Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.

A:Reference number: A36337; MID:91084844

A:Accession: A36337

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-918 <HIB>

A:Cross-references: GB:M57230; NID:g186353; PID:g186354

C:Genetics:

A:Gene: GDB:IL6ST; GP130

A:Cross-references: GDB:126725; OMIM:600694

A:Map position: 5q11-5q11

C:Keywords: glycoprotein; membrane protein

Query Match 15.1%; Score 290.5; DB 2; Length 918;

Best Local Similarity 28.7%; Pred. No. 1.4e-17;

Matches 76; Conservative 46; Mismatches 128; Indels 15; Gaps 7;

RESULT 14

I49699

glycoprotein 130 - mouse

```

Oy 7 LPPELSRYLNASTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLPPEKPNIS 66
Db 74 IPKEQYTIINRTASSVTFTDIASLNIQJTCNLTLEGGOLEQNVYGTITISGLPPEKPKLIS 133
Oy 67 CWSKMKDLTCRMTPGAHGETFLHTNYSIAKYKLRWYGODNTCEEHVGPCHIPKDLA 126
Db 134 CIVNCGKKMRCEWGGGR--ETHLETFILKSEMAIHKFADCKAKRDT--PTSCIVDYSTV 189
Oy 127 LFTPEIWEATNRLGSARSDVLTLDLIDVTTDPPDPVHVSRYVGLEDQLSVRWVSPPA 186
Db 190 YFVNIEVWEAENALGKVTSDHINFDPPYKVPNPNHLSVINSELSILKLTMTN-PS 246
Oy 187 LKDFLFAKQIRYRVEDSVDMKVY--DVSNOTSCLAGLAPGITYFVOVRCNPGITY 243
Db 249 IKSIVIT-LKINIQYRTKDASTWSQIPPEDASTRSSFTYODLKPFTEYFRIRC----M 302
Oy 244 GSKRAGIWEWSHPTASTPRSERP 268
Db 303 KEDGKGYSWDSSEASGIT-YEDRP 326

```

Search completed: September 16, 1999, 20:42:10
 Job time: 5403 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 17, 1999, 03:10:14 ; Search time 35.09 Seconds
(without alignments)
281,958 Million cell updates/sec

Title: US-09-037-657-25
Sequence: 1 TLNGRRLPELSEVLAASLT.....TNGSCPADGARREVLPRDL 350

Scoring table: BLOSUM62

Database: 77977 seqs, 28268293 residues
SwissProt_37.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	332	17.3	622	1	PLR_HUMAN
2	316	16.5	830	1	PLR_COILI
3	313	16.3	610	1	PLR_RAT
4	309.5	16.1	608	1	PLR_MOUSE
5	308	16.1	831	1	PLR_CHICK
6	307	16.0	831	1	PLR_MEIGA
7	306.5	16.0	581	1	PLR_BOVIN
8	304	15.8	581	1	PLR_CEREL
9	300.5	15.7	616	1	PLR_RABIT
10	297	15.5	917	1	IL6_MOUSE
11	290.5	15.1	918	1	IL6_HUMAN
12	285	14.9	918	1	IL6_RAT
13	263.5	13.7	630	1	PLR_ORENI
14	241	12.6	837	1	GCSR_MOUSE
15	226.5	11.8	372	1	CNTR_RAT
16	220.5	11.5	836	1	GCSR_HUMAN
17	217.5	11.3	372	1	CNTR_HUMAN
18	202	10.5	362	1	TPO_MOUSE
19	194	10.1	625	1	TPO_MOUSE
20	188.5	9.8	635	1	TPO_MOUSE
21	181	9.4	468	1	IL6_HUMAN
22	176	9.2	1097	1	IL6_MOUSE
23	174.5	9.1	1162	1	IL6_MOUSE
24	173.5	9.0	460	1	IL6_MOUSE
25	171.5	8.9	462	1	IL6_MOUSE
26	166	8.7	1092	1	IL6_MOUSE
27	165.5	8.6	638	1	GHR_MOUSE
28	161.5	8.4	508	1	GHR_RABIT
29	161	8.4	1165	1	GHR_HUMAN
30	158.5	8.3	638	1	GHR_HUMAN
31	158	8.2	507	1	GHR_PIG
32	156	8.1	507	1	EPOR_RAT
33	153	8.0	638	1	EPOR_MOUSE
34	146	7.6	638	1	GHR_HUMAN
35	145.5	7.6	897	1	GHR_RAT
36	145.5	7.6	897	1	CYB_HUMAN
37	145	7.6	380	1	GHR_HUMAN
38	143.5	7.5	424	1	GHR_SHEEP
39	142.5	7.4	1131	1	GHR_MOUSE
40	141.5	7.4	888	1	UFO_MOUSE
41	141.5	7.4	650	1	GHR_MOUSE
42	139.5	7.3	297	1	GHR_MOUSE
43	138.5	7.2	662	1	GHR_HUMAN
			608	1	GHR_CHICK

ALIGNMENTS

RESULT	ID	Query Match	Score	DB	Length	Description
1	PLR_HUMAN	17.3	332	1	622	PLR_HUMAN
2	PLR_HUMAN	16.5	316	1	830	PLR_COILI
3	PLR_HUMAN	16.3	313	1	610	PLR_RAT
4	PLR_HUMAN	16.1	309.5	1	608	PLR_MOUSE
5	PLR_HUMAN	16.1	308	1	831	PLR_CHICK
6	PLR_HUMAN	16.0	307	1	831	PLR_MEIGA
7	PLR_HUMAN	16.0	306.5	1	581	PLR_BOVIN
8	PLR_HUMAN	15.8	304	1	581	PLR_CEREL
9	PLR_HUMAN	15.7	300.5	1	616	PLR_RABIT
10	PLR_HUMAN	15.5	297	1	917	IL6_MOUSE
11	PLR_HUMAN	15.1	290.5	1	918	IL6_HUMAN
12	PLR_HUMAN	14.9	285	1	918	IL6_RAT
13	PLR_HUMAN	13.7	263.5	1	630	PLR_ORENI
14	PLR_HUMAN	12.6	241	1	837	GCSR_MOUSE
15	PLR_HUMAN	11.8	226.5	1	372	CNTR_RAT
16	PLR_HUMAN	11.5	220.5	1	836	GCSR_HUMAN
17	PLR_HUMAN	11.3	217.5	1	372	CNTR_HUMAN
18	PLR_HUMAN	10.5	202	1	362	TPO_MOUSE
19	PLR_HUMAN	10.1	194	1	625	TPO_MOUSE
20	PLR_HUMAN	9.8	188.5	1	635	TPO_MOUSE
21	PLR_HUMAN	9.4	181	1	468	IL6_HUMAN
22	PLR_HUMAN	9.2	176	1	1097	IL6_MOUSE
23	PLR_HUMAN	9.1	174.5	1	1162	IL6_MOUSE
24	PLR_HUMAN	9.0	173.5	1	460	IL6_MOUSE
25	PLR_HUMAN	8.9	171.5	1	462	IL6_MOUSE
26	PLR_HUMAN	8.7	166	1	1092	IL6_MOUSE
27	PLR_HUMAN	8.6	165.5	1	638	GHR_MOUSE
28	PLR_HUMAN	8.4	161.5	1	508	GHR_RABIT
29	PLR_HUMAN	8.4	161	1	1165	GHR_HUMAN
30	PLR_HUMAN	8.3	158.5	1	638	GHR_HUMAN
31	PLR_HUMAN	8.2	158	1	507	GHR_PIG
32	PLR_HUMAN	8.1	156	1	507	EPOR_RAT
33	PLR_HUMAN	8.0	153	1	638	EPOR_MOUSE
34	PLR_HUMAN	7.6	146	1	638	GHR_HUMAN
35	PLR_HUMAN	7.6	145.5	1	897	GHR_RAT
36	PLR_HUMAN	7.6	145.5	1	897	CYB_HUMAN
37	PLR_HUMAN	7.6	145	1	380	GHR_HUMAN
38	PLR_HUMAN	7.5	143.5	1	424	GHR_SHEEP
39	PLR_HUMAN	7.4	142.5	1	1131	GHR_MOUSE
40	PLR_HUMAN	7.4	141.5	1	888	UFO_MOUSE
41	PLR_HUMAN	7.4	141.5	1	650	GHR_MOUSE
42	PLR_HUMAN	7.3	139.5	1	297	GHR_MOUSE
43	PLR_HUMAN	7.2	138.5	1	662	GHR_HUMAN
	PLR_HUMAN				608	GHR_CHICK

Query Match: 17.38; Score 332; DB 1; Length 622;
Best Local Similarity: 37.18; Pred. No. 4,7e-21;
Matches: 83; Conservative: 28; Mismatches: 95; Indels: 18; Gaps: 8;

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FT1 CARBOHYD 132 132 POTENTIAL.
FT2 CARBOHYD 263 263 POTENTIAL.
FT3 CARBOHYD 304 304 POTENTIAL.
FT4 CARBOHYD 316 316 POTENTIAL.
FT5 CARBOHYD 336 336 POTENTIAL.
SQ SEQUENCE 830 AA: 94507 MW: 56FAD051 CRC32;

Query Match 16.5%; Score 316; DB 1; Length 830;
Best Local Similarity 36.6%; Pred. No. 1.6e-19;
Matches 75; Conservative 30; Mismatches 82; Indels 18; Gaps

QY 58 PEKRVINISCKSNKADLTCTWTPGACGETLH-TNLSLKYKLWYGQDNTCEEYHTVGP 116
DB 231 PEKRTIITKCSPEKETCTCWMKKGSDG---HPTNTLLYSKEGGEVYECPPDYKTAP 287
QY 117 HSCHE-PRDLLEFPFEYETWETATNRIGARSQVLTLDIVTTPDPEDPV--HYSRKGGL 173
DB 288 NSCYDKRHHTSFMTIYNTVAATNEIGSNNSDPYVDTYIVOTDPPEVNTLEIKTKVNR 347
QY 174 EDQSVNRYSPSPALKDF--LDAQYQIRRVEDSVYMKVVDVYSNOTSCRLAGLPGTV 230
DB 348 KPYVLTLW-SPPPLADVNSGWLTDYDELRLKPEAEEMETI-FVGQQTHTKMSLNGKR 405
QY 231 YFYVQRCNPFQIYSGSKAGTSEMS 255
DB 406 IYVQIHCKP-----DHRGSEMS 424

RESULT 3
PRLR_RAT STANDARD; PRT; 610 AA.
ID POS710; Q63451; Q63723; Q62832; Q64274; Q63479;
AC 01-NOV-1988 (REL. 09, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DE 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (LACTOGEN RECEPTOR).
GN PRLR.
OS RATUS NORVEGICUS (RAT).
OC EDARUOTA; METAQOA; CHORATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ROENTIA; SCUROGNATHI; MURIDAE; MORINAE; RATTUS.
[1]
RA SEQUENCE FROM N.A.
RA MEDLINE, 91155946.
RA SHIROTA M., BANVILLE D., ALI S., JOLICOEUR C., BOUTIN J.M.,
RA EDERY M., DUJANE J., KELLY P.A.;
RA "Expression of two forms of prolactin receptor in rat ovary and
RA 11ver.";
RA MOL. ENDOCRINOL. 4:1136-1143(1990).
[2]
RA SEQUENCE FROM N.A. (LONG FORM AND SHORT FORM).
RA STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY;
RA MEDLINE, 90241201.
RA ZHANG R., BOCZKO E., TSAI-MORRIS C.H., HU Z.Z., DUFRAU M.L.;
RA "Isolation and characterization of two novel rat ovarian lactogen
RA receptor cDNA species.";
RA BIOCHEM. BIOPHYS. RES. COMMUN. 168:415-422(1990).
[3]
RA SEQUENCE OF 281-610 FROM N.A.
RA BANVILLE D., STOCO R., MURPHY K.K., BOIE Y., KELLY P.A.;
RA SUBMITTED (MAR-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
[4]
RA SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (MEDIUM FORM).
RA TISSUE-LIVER;
RA MEDLINE, 88163059.
RA BOUTIN J.-M., JOLICOEUR C., OKAMURA H., GAGNON J., EDERY M.,
RA SHIROTA M., BANVILLE D., DUSANIER-FOURT I., DUJANE J., KELLY P.A.;
RA "Cloning and expression of the rat prolactin receptor, a member of
RA the growth hormone/prolactin receptor gene family.";
RA CELL 53:69-77(1988).
[5]
RA SEQUENCE FROM N.A. (FORM NB2).
RA TISSUE-LYMPHOMA;

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Best Match      16.38; Score 313; DB 1; Length 610;
Query Local Similarity 35.08; Pred. No. 2e-19;
Matches 79; Conservative 36; Mismatches 85; Indels 26; Gaps 10;

OY 46 SLAGSCLVGLPPEKPVNISCNSKNNKDLGCMTGAGHGETLHNYSISKYLRMGCD 105
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 15 SLNGGS-----PPGRKEIHKRCSPDEETTCMMNNGTDDG--LPTNYSILYSKE--GEK 65

OY 106 NT--CEEHYHVGPHSCHIPRD-LALFPEIWEATNRLGARSADVLTDIIDVYTTDPP 162
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 66 TTYECPPKTSIGPSCFSGKQYSIMKIIYITNAINQNGSSSDLYIVDYIYEPEPP 125

OY 163 PDVHVSRYGLEDQLSTRWY--SPPLKDF--LFQAKYQIRYVEDSYDMKRVVDVSNQ 217
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 126 RNLTL-EVKOLDKRKTYLWYKMSPPITTDVTKGMFMEYEIRLKPENAEWE-IHFTGHQ 183

OY 218 TSCRLAGLPGTYFYOVRCNPGIISGKAGYSWHSIPTLAASP 263
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 184 TORKVDLYIRGOKYLVQIRCKP-----DHGYMSWMSQSSSEVP 222

RESULT 4
PRLR MOUSE STANDARD. PRT: 608 AA.
ID PRLR MOUSE STANDARD. PRT: 608 AA.
AC 008501; Q62099; P15213; P15212;
DT 01-APR-1990 (REL. 14, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; MUS.
RN (1)
RP SEQUENCE FROM N.A. (FORM PRL-R3).
RC STRAIN=C3H; TISSUE=MAMMARY GLAND;
RX MEDLINE; 94085788.
RA MOORE R.C., OKA T.;
RT "Cloning and sequencing of the cDNA encoding the murine mammary gland
RN long-form prolactin receptor."
RT GENE 134:263-265(1993).
RN (2)
RP SEQUENCE FROM N.A. (FORM PRL-R3).
RC STRAIN=SWISS WEBSTER; TISSUE=LIVER;
RX MEDLINE; 93307149.
RA CLARKE D.L., LINZER D.I.H.;
RT "Changes in prolactin receptor expression during pregnancy in the
RN mouse ovary."
RT GENE 133:224-232(1993).
RN (3)
RP SEQUENCE FROM N.A. (FORM PRL-R3).
RA SASAKI M.;
RN (4)
RP SUBMITTED (JUL-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
RN (5)
RP SEQUENCE FROM N.A. (FORM PRL-R3).
RC STRAIN=BALB/C; TISSUE=MAMMARY GLAND;
RA EDERY M., PEZET A., NANDI S., KELLY P.A.;
RN SUBMITTED (JUN-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
RP SEQUENCE FROM N.A. (FORM PRL-R2 AND PRL-R1).
RC STRAIN=SWISS WEBSTER; TISSUE=LIVER;
RA MEDLINE; 89261824.
RA DAVIS J.A., LINZER D.I.H.;
RT "Expression of multiple forms of the prolactin receptor in mouse
RN liver."
RN (6)
RP ENDOCRINOLOGY 133:674-680(1989).
RN (7)
RP FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
RN PROLACTIN, AS WELL AS PLACENTAL LACTOGEN I AND II.
RN (8)
RP SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
RN (9)
RP ALTERNATIVE PRODUCTS: THREE FORMS, PRL-R1, PRL-R2 AND PRL-R3
RN (SHOWN HERE) ARE PRODUCED BY ALTERNATIVE SPLICING OF THE PRLR
RN GENE.
RN (10)
RP SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS

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CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL; L13593; G347842; -
DR EMBL; L14811; G293770; -
DR EMBL; D10214; G220576; -
DR EMBL; X73372; G312697; -
DR EMBL; M22959; G200482; -
DR EMBL; M22958; G200480; -
DR PIR; J10671; J10671; -
DR MGI; MGI:97763; PRLR.
DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; FALSE_NEG.
DR PFAM; PF00041; fn3; 2.
DR HSSP; P16471; 1BP3.
KM RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT;
KW ALTERNATIVE SPLICING.
FT SIGNAL 1 19
FT CHAIN 20 608
FT TRANSMEM 20 229
FT TRANSMEM 230 253
FT DOMAIN 254 608
FT DOMAIN 20 117
FT DOMAIN 119 222
FT DISULFID 31 41
FT DISULFID 70 81
FT CARBOHYD 54 54
FT CARBOHYD 99 99
FT CARBOHYD 127 127
FT VASPLIC 281 292
FT VASPLIC 293 608
FT VASPLIC 281 303
FT VASPLIC 304 608
FT CONFLICT 558 558
FT SEQUENCE 608 AA; 68240 MW; AA401B67 CRC32;

Query Match 16.1%; Score 309.5; DB 1; Length 608;
Best Local Similarity 31.4%; Pred. No. 4e-19;
Matches 82; Conservative 38; Mismatches 94; Indels 47; Gaps 10;

OY 11 LSRVNSTALALANLNGSRGSDNVCARDGSIAGSLCYGLPPEKFNISCMK 70
DB 1 MSALALMLVLSILNQS-----PPKFEIHKCNSP 34
OY 71 NKKDLTCRWTPGAGHETFLHNYSLKYLKMYGQDNT--CEEYHVGPHSCHIPRD-LAL 127
DB 35 DKETFCWMNPSDGG--LPTNYSLYSKE--GEKNTYCPDYKTSGRNSCFKSYTSI 90
OY 128 FPEYELWVATNRLGASRSDVLTLDLVYTTDPPDVAVSKVGLDQLSTRVYS--PP 185
DB 91 WKIYITVATNEMSGSDPLVYDVYIYEPEPPNLT-L-EVKDLKKKTYLWAKWLP 149
OY 186 ALKDF---LEQAKYQIRYVEDSVDRKVVVDVSNQTSCLAGLQPTVYFVQVRCNPEFI 242
DB 150 TITDVATGFTMEYERLRKSEADENE-IHFGHQGFVFPDLYPQAKLYVTRCKP--- 206
OY 243 YGSKKAGIWEWSHPTAASP 263
DB 206 ---DHGYSRWGOEKSEIEIP 222

RESULT 5
PRLR_CHICK STANDARD; PRT; 831 AA.

AC 004594;
DE 01-JUN-1994 (REL. 29, CREATED)
DE 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DE 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (CPRLP).
GN PRLR.
OS GALLUS GALLUS (CHICKEN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
OC NOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LEBHORN; TISSUE-KIDNEY;
RX MEDLINE; 93075121.
RA TANAKA M., MAEDA K., OKUBO T., NAKASHIMA K.;
RT "Double antenna structure of chicken prolactin receptor deduced from
RT the cDNA sequence";
RL BIOCHEM. BIOPHYS. RES. COMMUN. 188:490-496(1992).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D13154; G222849; -
DR PIR; J01655; J01655.
DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 2.
DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 2.
DR PFAM; PF00041; fn3; 4.
DR HSSP; P16471; 1BP3.
KM RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
FT SIGNAL 1 23
FT CHAIN 24 831
FT TRANSMEM 24 438
FT TRANSMEM 439 459
FT DOMAIN 460 831
FT DOMAIN 25 122
FT DOMAIN 123 225
FT DOMAIN 228 325
FT DOMAIN 326 428
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 91 91
FT CARBOHYD 100 100
FT CARBOHYD 112 112
FT CARBOHYD 132 132
FT CARBOHYD 262 262
FT CARBOHYD 303 303
FT CARBOHYD 315 315
FT CARBOHYD 335 335
FT SEQUENCE 831 AA; 94102 MW; B977BE07 CRC32;

Query Match 16.1%; Score 308; DB 1; Length 831;
Best Local Similarity 34.6%; Pred. No. 7.9e-19;
Matches 75; Conservative 28; Mismatches 96; Indels 18; Gaps 8;

OY 58 PPEKFNISCMKNNKDLTCRWTPGAGHETFLH-TNYSLKYLKMYGQDNTCEEYHYVCP 116
DB 230 PPEKFTIICKRSPEKETFTCWKPKDIDGG---HPTNYLLSKSDEEYVCEPDYRTAGP 286
OY 117 HSCCH-PKDALFPPYELWVATNRLGASRSDVLTLDLVYTTDPPDV--HYSRVGL 173
DB 287 NSCYDKRHTSFMTYITNVTATNEMSGNSSDPHVYDVYIYVQDPVAVYLELKKPINR 346

```


OY 174 EDQSVRWSPALNDF---LFOAKYQIRRYEDSVDMKVVDVNSQTSCLAGKPGTV 230
 DB 347 KPYLWLTW-SPPPLADVBSGWLTLDELKPEEGEWEI-FVGOQOTQYKMFSLNPKK 404
 OY 231 YFQVRCNPFQIYSGKAGIWSHPTAASPRESR 267
 DB 405 YIIOIHCNP-----DHGWSWSESENYIPIPNDR 435

RESULT 6
 ID PRLR.MELGA
 ID PRLR.MELGA STANDARD; PRT; 831 AA.
 Q91094; Q91091; Q91092;
 01-NOV-1997 (REL. 35, CREATED)
 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 PROLACTIN RECEPTOR PRECURSOR (PRL-R) (TPRLR).
 PRLR.
 MELAGRIS GALLOPANO (COMMON TURKEY).
 EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
 NEOGNATHAE; GALLIFORMES; MELEGRIDIDAE; MELEGRIS.
 [1]
 SEQUENCE FROM N.A.
 TISSUE-KIDNEY;
 ZHOU J.F.; ZADWORN D.; GUENNE D.; KUNHEIN U.;
 SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 [2]
 SEQUENCE OF 82-121 AND 473-522 FROM N.A.
 TISSUE-OVARY;
 PITTS G.R.; YOU S.K.; FOSTER D.N.; EL HALAWANI M.E.;
 SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 [1]
 FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 PROLACTIN.
 [1]
 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 [1]
 SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 [1]
 SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

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EMBL: L76587; G1345365;
 EMBL: U22947; G973165;
 PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 2.
 PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 2.
 PFAM: PF00041; fn3; 4.
 HSP: P16471; 1BP3.
 RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
 SIGNAL 1 23
 CHAIN 24 831
 DOMAIN 24 438
 TRANSSEM 439 459
 DOMAIN 460 831
 DOMAIN 25 122
 DOMAIN 123 225
 DOMAIN 228 325
 DOMAIN 326 428
 DISULFID 36 46
 CARBOHYD 75 59
 CARBOHYD 91 91
 CARBOHYD 100 100
 CARBOHYD 112 112
 CARBOHYD 132 132
 CARBOHYD 262 262
 CARBOHYD 303 303
 CARBOHYD 315 315
 CARBOHYD 335 335

SO SEQUENCE 831 AA; 94394 MW; FB71SC98 CRC32;
 Query Match 16.0%; Score 307; DB 1; Length 831;
 Best Local Similarity 35.0%; Pred. No. 9,6e-19;
 Matches 76; Conservative 26; Mismatches 97; Indels 18; Gaps 8;

OY 58 PERKVNISCKSKNMKLLCMTWPGANGFELH-TNYSLKTKLWYGODTCEGHTVGP 116
 DB 230 PERKVTTCRSPERKFTTWMKPGIDG---HPTNVTLLKSGEGEQVIECPDRTAGP 286
 OY 117 HSCHI-PKDALFTPEIWEATNRRGSARSDVLLDIDVTTDPDPV--HYSRVGL 173
 DB 287 NSCYFDKHTSEFTYVNTNYKATNGSNSDPHYVDVYIYQPDPPANVTLELKPINR 346
 OY 174 EDQSVRWSPALNDF---LFOAKYQIRRYEDSVDMKVVDVNSQTSCLAGKPGTV 230
 DB 347 KPYLWLTW-SPPPLADVBSGWLTLDELKPEEGEWEI-FVGOQOTQYKMFSLNPKK 404
 OY 231 YFQVRCNPFQIYSGKAGIWSHPTAASPRESR 267
 DB 405 YIIOIHCNP-----DHGWSWSESENYIPIPNDR 435

RESULT 7
 ID PRLR.BOVIN
 ID PRLR.BOVIN STANDARD; PRT; 581 AA.
 Q28172;
 01-NOV-1997 (REL. 35, CREATED)
 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 PROLACTIN RECEPTOR PRECURSOR (PRL-R).
 PRLR.
 BOS TAURUS (BOVINE).
 EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 ARTIODACTYLA; RUMINANTIA; PECORA; BOVIDAE; BOVINAE; BOS.
 [1]
 SEQUENCE FROM N.A.
 TISSUE-ENDOMETRIUM;
 RA MEDLINE; 93246019.
 SCOTT P.; KESSLER M.A.; SCHULER L.A.;
 RT "Molecular cloning of the bovine prolactin receptor and distribution
 of prolactin and growth hormone receptor transcripts in fetal and
 utero-placental tissues."
 RT MOL. CELL. ENDOCRINOL. 89:47-58(1992).
 [1]
 FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 PROLACTIN.
 [1]
 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 [1]
 SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 [1]
 SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

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EMBL: L02549; G163618;
 PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
 PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 PFAM: PF00041; fn3; 2.
 HSP: P14787; 1AN3.
 RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
 SIGNAL 1 24
 CHAIN 25 581
 DOMAIN 25 234
 TRANSSEM 235 258
 DOMAIN 259 581
 DOMAIN 25 122
 DOMAIN 123 227
 DISULFID 36 46

EMBL: L02549; G163618;
 PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
 PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 PFAM: PF00041; fn3; 2.
 HSP: P14787; 1AN3.
 RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
 SIGNAL 1 24
 CHAIN 25 581
 DOMAIN 25 234
 TRANSSEM 235 258
 DOMAIN 259 581
 DOMAIN 25 122
 DOMAIN 123 227
 DISULFID 36 46

FT DISULFID 75 86 BY SIMILARITY.
 FT CARBOHYD 59 59 POTENTIAL.
 FT CARBOHYD 132 132 POTENTIAL.
 SO SEQUENCE 581 AA: 65153 MW; CORCA0A2 CRC32;

Query Match
 Best Local Similarity 31.2%; Score 306.5; DB 1; Length 581;
 Matches 81; Conservative 38; Mismatches 94; Indels 47; Gaps 9;

12 SRVLAALALANLNGSRSGNDLVCHARDGSLAGSLVGLPPEKPNISCSWSN 71
 7 SRVFLILLFLSVSLNGOS-----PPEKPKLVKCRSPG 40

72 MKDLTCRWTPGAGETFLHNTYSLKRYKRYGDNCEHTYVPSCHI-PKDLALFPP 130
 41 KEFTLWMEWEGADGG--LPTNYTLTYHKEGETLIHEDCPDITGSPNSCFSKHSTWKM 98

131 YEIWEATNRLGARSVDLTLDVYTTDPPDVHVSRYVGLDLSVWV--SSPALK 188
 99 YVTVNAINOMGISSDPLVHTYIYEPPANLPL-ELKHEDRKPIMIKSPPTW 157

189 D-----FLFOAKYQIRYVEDSVDMKVVDSVNOTSCLAGLPGYTYVQVNCNPFGL 243
 158 DVKSGMFIQ--YEIRLKPPEKATDME-THTLKTOTLKIRINLYPGKRYLVQIRCKP----- 211

244 GSKKAGINSEMSHPTASTP 263
 211 ---DHGYMSEMSPESSIOIP 227

RESULT 8
 PRLR_CEREL STANDARD; PRT; 581 AA.
 ID PRLR_CEREL Q28235;

DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUN-1998 (REL. 36, LAST ANNOTATION UPDATE)

DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
 GN PRLR.
 OS CERVUS ELAPHUS (RED DEER).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC ARTIODACTYLA; RUMINANTIA; PECORA; CERVOIDEA; CERVIDAE; CERVINAE;
 CC CERVUS.

[1]
 RN SEQUENCE FROM N.A.
 RP TISSUE-LIVER.
 RC MEDLINE; 96030711.
 RA CLARKE L.A., EDERY M., LOUDON A.S., RANDALL V.A., POSTEL-VINAY M.C.,
 RA KELLY P.A., JABBOUR H.N.;

*Expression of the prolactin receptor gene during the breeding and
 RT non-breeding seasons in red deer (Cervus elaphus): evidence for the
 RT expression of two forms in the testis.*

RL J. ENDOCRINOLOGY, 146:313-321(1995).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

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 CC or send an email to license@isb-sib.ch).

CC EMBL: X94953; E218406;
 CC DR PROSITE: P80044; RECEPTOR_CYTOKINES_1; 1.
 CC DR PROSITE: P80040; RECEPTOR_CYTOKINES_2; 1.
 CC DR PFAM: PF00041; fn3; 2.
 CC DR HSP; P14787; IAN3.

KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
 FT SIGNAL 1 24 BY SIMILARITY.
 FT CHAIN 25 581 PROLACTIN RECEPTOR.
 FT DOMAIN 25 234 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 235 258 POTENTIAL.
 FT DOMAIN 259 581 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 125 122 FIBRONECTIN TYPE-III.
 FT DISULFID 123 227 FIBRONECTIN TYPE-III.
 FT DISULFID 36 46 FIBRONECTIN TYPE-III.
 FT DISULFID 75 86 BY SIMILARITY.
 FT CARBOHYD 59 59 BY SIMILARITY.
 FT CARBOHYD 132 132 POTENTIAL.
 FT CARBOHYD 233 233 POTENTIAL.
 SO SEQUENCE 581 AA: 65159 MW; 721F0366 CRC32;

Query Match
 Best Local Similarity 33.2%; Score 304; DB 1; Length 581;
 Matches 75; Conservative 37; Mismatches 92; Indels 22; Gaps 8;

44 DGSILAGSLVGLPPEKPNISCSWSNKKDLTCRWTPGAGETFLHNTYSLKRYLWYG 103
 18 NMSLNGOS-----PGRKRIIKRSPGKETFLCWMEPSDGG--LPTNYTLTYHKEGET 70

104 QDNCEHTYVPSCHI-PKDLALFPEIYVATNRLGARSVDLTLDVYTTDPP 162
 71 LIHECPDYKTGTPNCTYFSKHTSIKRIYIVTNAINOMGVSSDPLVYDYIYEPEP 130

163 PDVHVSRYVGLDLSVWV--SPALKDF--LFOAKYQIRYVEDSVDMKVVDSVNG 217
 131 ANLTL-ELKHEDRKPIMIKSPPTWLVKSGWMIQIETIRKPEATDME-IHRAKQ 188

218 TSCRLAGLPGYTYVQVNCNPFGLTSCRWTPGAGETFLHNTYSLKRYLWYG 263
 189 TQKITSIVPGKRYLVQIRCKP-----DHGYMSEMSPESSIOIP 227

RESULT 9
 PRLR_RABIT STANDARD; PRT; 616 AA.
 ID PRLR_RABIT P14787;

DT 01-APR-1990 (REL. 14, CREATED)
 DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
 GN PRLR.
 OS ORCTOLOGUS CUNICULUS (RABBIT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC LAGOMORPHA; LEPORIDAE; ORCTOLOGUS.

[1]
 RN SEQUENCE FROM N.A.
 RP TISSUE-MAMMARY GLAND;
 RC MEDLINE; 89184578.
 RA EDERY M., JOLICOEUR C., LEVI-MEYREUETS C., DUSANTER-FOURT I.,
 RA PETRIDOU B., BOUIN J.M., LESUEUR L., KELLY P.A., DIANE J.,

*Identification and sequence analysis of a second form of prolactin
 RT receptor by molecular cloning of complementary DNA from rabbit
 RT mammary gland.*

RL PROC. NATL. ACAD. SCI. U.S.A. 86:2112-2116(1989).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

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DB 103 SYMPYINIEWEAEANALGVSESEINFDPVDKVKPTPPNLSVTNSELSILKLSW 242
OY 102 VSPPLAKPFLQAKQIQRVEDSDVKVY---DDVSNQTSCLAGLPGVYFVOVRCN 238
DB 243 VSSGL- GGLDLKSDIDYRKDASTWIOVPLEDTMSPTSTVODLKFTEYFRIR-- 299
OY 239 PEGYSGKAGIMSEMSHPTAST--PRSERP 268
DB 299 --SINDSGK-GYWSDMSEASGTIEDRPSR 327

RESULT 11
IL6B_HUMAN STANDARD: PRT: 918 AA.
AC P40189;
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130) (ONCOSTATIN M
DE RECEPTOR (CDM130) (CD130 ANTIGEN).
GN IL6ST.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CAVIARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-MELOMA, AND PLACENTA;
RX HIRI M., MURAKAMI M., SAITO M., HIRANO T., TAGA T., KISHIMOTO T.;
RT "Molecular cloning and expression of an IL-6 signal transducer,
RT gp130."
RT Cell 63:1149-1157(1990).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.
RX MEDLINE; 98169383.
RA BRAVO J., STANTON D., HEATH J.K., JONES E.Y.;
RT "Crystal structure of a cytokine-binding region of gp130."
RT EMBD J. 17:1665-1674(1998).
CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
CC IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
CC EMERSONIC DEVELOPMENT (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: FOUND IN ALL THE TISSUES AND CELL LINES.
CC EXAMINED. EXPRESSION NOT RESTRICTED TO IL-6 RESPONSIVE CELLS.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC ONE IG-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- DATABASE: NAME-PROW; NOTE-CD guide CD130 entry;
CC WWW-"http://www.ncbi.nlm.nih.gov/prov/ncd/cd130.htm"
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M57230; G186354;
DR PIR; A36337; A36337.
DR PDB; 1B0U; 26-AUG-98.
DR MIM; 600694;
DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
DR PFAM; PF00041; fn3; 3.
KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
KW REPEAT; 3D-STRUCTURE.

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FT SIGNAL 1 22
FT CHAIN 23 918
FT DOMAIN 23 619
FT TRANSMEM 620 641
FT DOMAIN 642 916
FT DOMAIN 120 120
FT DOMAIN 124 222
FT DOMAIN 223 324
FT DOMAIN 325 423
FT DOMAIN 424 517
FT DOMAIN 518 613
FT DOMAIN 725 755
FT DISULFID 134 144
FT DISULFID 172 182
FT CARBOHYD 43 43
FT CARBOHYD 83 83
FT CARBOHYD 131 131
FT CARBOHYD 137 137
FT CARBOHYD 227 227
FT CARBOHYD 379 379
FT CARBOHYD 383 383
FT CARBOHYD 390 390
FT CARBOHYD 553 553
FT CARBOHYD 564 564
FT SEQUENCE 918 AA; 103522 MW; 7CC06F05 CRC32;

Query Match 15.1% Score 290.5; DB 1; Length 918;
Best Local Similarity 28.7% Pred. No. 2.8e-17;
Matches 76; Conservative 46; Mismatches 128; Indels 15; Gaps 7;

OY 7 LPEELSRVNLSTALALANLNGSRORSNDLVCHARDGSLVGLVGPPEKPVNIS 66
DB 74 IPKEGYTIINFTASSVTTDIALSNIGLTCNIFRGLEQNVYGTIISGLPEKPKNLS 133
OY 67 CWSKMKKLTCTKATPGANGFELHTNYSLKRLKRGDNTCEHTYGPCHPKDLA 126
DB 134 CIVNEGKMKREBMOGR--ETHLETFNFKLSMATHKPADCKAKKDT--PTSCIVDYSTV 189
OY 127 LETPEIWEATNRNGSARSDVLTLDIDVVTDPPEVHYSRVGLGLEDQLSVRWVSPA 186
DB 130 YFVNIEWEAEANALGKTSDBINDPVYKKPNPMLSYNSELSILKLTWTN-PS 248
OY 187 LKDFLEQAKQIQRVEDSDVKVY---DDVSNQTSCLAGLPGVYFVOVRCNPFGLY 243
DB 249 IKSVIY-LKYNQYKTRDASTWSQIPEDTASTRESFTVODLKFTEYFRIR-----M 302
OY 244 GSKKAGIMSEMSHPTASTPRSERP 268
DB 303 KEDGKYWSDMSEASGTI-YEDRP.326

RESULT 12
IL6B_RAT STANDARD: PRT: 918 AA.
AC P40190;
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).
GN IL6ST.
OS RATUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCITROGNATHI; MORIDAE; MORINAE; RATIUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER;
RX MEDLINE; 93052397.
RA WANG Y., NESBITT J.E., FUENTES N.L., FULLER G.M.;
RT "Molecular cloning and characterization of the rat liver IL-6 signal
RT transducing molecule, gp130."
RT GENOMICS 14:666-672(1992).

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CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
CC IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GPI30 FOR INITIATING
CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES.
CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
CC EMBRYONIC DEVELOPMENT (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS
CC AND ENDOTHELIAL CELLS.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC ONE IG-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: M93340; NOT_ANNOTATED_CDS.
CC
CC PIR: A44257; A44257.
CC DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
CC DR PFAM: PF00041; fn3; 3.
CC DR HSP: P40189; 1BQU.
CC
CC REPEAT: TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
CC
CC SIGNAL 1 22
CC CHAIN 23 918
CC DOMAIN 23 618 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
CC TRANSMEM 641 918 EXTRACELLULAR (POTENTIAL).
CC DOMAIN 26 120 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 124 221 IG-LIKE C2-TYPE DOMAIN.
CC DOMAIN 222 323 FIBRONECTIN TYPE-III.
CC DOMAIN 324 422 FIBRONECTIN TYPE-III.
CC DOMAIN 423 516 FIBRONECTIN TYPE-III.
CC DOMAIN 517 612 FIBRONECTIN TYPE-III.
CC DOMAIN 724 754 SER-RICH.
CC DISULFID 134 144 BY SIMILARITY.
CC DISULFID 172 181 BY SIMILARITY.
CC CARBOHYD 43 43 POTENTIAL.
CC CARBOHYD 61 61 POTENTIAL.
CC CARBOHYD 83 83 POTENTIAL.
CC CARBOHYD 131 131 POTENTIAL.
CC CARBOHYD 157 157 POTENTIAL.
CC CARBOHYD 205 205 POTENTIAL.
CC CARBOHYD 226 226 POTENTIAL.
CC CARBOHYD 382 382 POTENTIAL.
CC CARBOHYD 389 389 POTENTIAL.
CC CARBOHYD 477 477 POTENTIAL.
CC CARBOHYD 552 552 POTENTIAL.
CC SQ 918 AA; 102450 MW; E6EFD00 CRC32;

```

Query Match 14.9%; Score 285; DB 1; Length 918;
 Best Local Similarity 30.5%; Pred. No. 8.4e-17;
 Matches 81; Conservative 46; Mismatches 121; Indels 18; Gaps 9;

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7 LPBELSVNLASTLALALANLUNGSRSGDNLVCHARDGSLAGSCLYVGLPKPVNIS 66
74 VPREQVTVIRKTSVFTVQVNVOLTCNLSFGQIEQNVGIIITLSGYPDPINLS 133
67 CWSKNNKMDLTCRWTGAGETFLHTNYSKYLKMYGOD-NTCEYHYVGHSHIRKDL 125
134 CYNKGNMMLCOLDPRG-ETYLENTNLKSE-WATEKPPDCYTKH-GISSCWMTYTP 187
126 ALTPPEIWEATNRLGARSADVLTLDIDVYTTDPPDVHVSFVGLDQLSVRWYSP 185
188 IYFNIEMVWEAEALANLNVSEPIINFDVPVKRSPPHNLSVTNSELSLKLAWNSG 247

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OY 186 ALKDLPAKAYOIRRVSDVMKTV---DVSNOTSCLAGKAGTYIVQVRCNPGCI 242
DB 248 L--DSLRLKSDIQRTDASTWIDVPLEDVPSPRTSFTVODLKFEYVERIR-----SI 301
OY 243 YGSKRAGIMSEVSHPTASTPSESP 268
DB 302 KENGR-GVWSMDSE-EASGTYEDNP 325

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RESULT 13
PRLR.ORENI
ID PRLR.ORENI STANDARD; PRT: 630 AA.
AC 091513;
DE 01-NOV-1997 (REL. 35, CREATED)
DE 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DE 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS OROCHROMIS NILOTICUS (NILE TILAPIA) (TILAPIA NILOTICA).
CC EUKARYOTA; METAZOA; CHORDATA; VERTebrATA; ACTINOPTERYGII; NEOPTERYGII;
CC TELEOSTEI; EUTELEOSTEI; ACANTHOPTERYGII; PERCOMORPHA; PERCIFORMES;
CC LARROIDEI; CICHLIDAE; TILAPIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-KIDNEY;
RX MEDLINE; 95320210.
RA SANDRA O., SOHM F., DE LUZE A., PRUNET P., EDERY M., KELLY P.A.;
RT "Expression cloning of a cDNA encoding a fish prolactin receptor."
RL PROC. NATL. ACAD. SCI. U.S.A. 92:6037-6041(1995).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: L34783; G903847;
CC DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
CC DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
CC DR PFAM: PF00041; fn3; 2.
CC DR HSP: P16471; 1BP3.
CC
CC RECEPTOR: TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT.
CC
CC SIGNAL 1 23
CC CHAIN 24 630
CC DOMAIN 24 234 PROLACTIN RECEPTOR.
CC TRANSMEM 235 258 EXTRACELLULAR (POTENTIAL).
CC DOMAIN 259 630 POTENTIAL.
CC DOMAIN 124 123 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 124 228 FIBRONECTIN TYPE-III.
CC DISULFID 37 47 FIBRONECTIN TYPE-III.
CC DISULFID 76 87 BY SIMILARITY.
CC CARBOHYD 92 92 BY SIMILARITY.
CC CARBOHYD 101 101 POTENTIAL.
CC SQ 630 AA; 70810 MW; E9AAE553 CRC32;

```

Query Match 13.7%; Score 263.5; DB 1; Length 630;
 Best Local Similarity 32.7%; Pred. No. 3.7e-15;
 Matches 70; Conservative 27; Mismatches 94; Indels 23; Gaps 9;

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OY 59 PERPVNISCWSKNNKMDLTCRWTGAGETFLHTNYSKYLKMYGODNCEYHYTVGPHS 118
DB 29 PGRPTLTKKSPKPEFTKMKRGSOG--LPFTTALYTRKESDVVHECPDYHTAGKNS 86
OY 119 CHIPKDLAL-FTPEIWEATNRLGARSADVLTLDIDVYTTDPPDVHVSFVGLDQ- 177

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Db 87 CEFKNNLTVWSNITVATNALGKTYSPDQIDVITYIOPHPPELETF---VKMDQG 143
 QY 177 ---LSVRWSPALKDF---LFOAKYQIRYVED-SYDMKVVDDVSNQSCRLAGLPQT 229
 Db 144 WPEFLKWSM-BPPKADTRSGMITLILYELRVKLEDESESEME-NHAGQCKNFENIFSLASGG 201
 QY 230 VYFVQVNCNFGIYSGKAKIWSMESHPTAASP 263
 Db 202 TYLIQVACKP-----DHGFWSMSTSYKVP 228

RESULT 14
 GCSR_MOUSE STANDARD: PRT; 837 AA.

AC P40223;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE GRANULOCYTE COLONY STIMULATING FACTOR RECEPTOR PRECURSOR (G-CSF-R).
 GN CSF3R OR CSFGR.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIURGNATHI; MURIDAE; MURINAE; MUS.
 RP [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 90235283.
 RA FUKUNAGA R., ISHIZAKA-IKEDA E., SETO Y., NAGATA S.;
 RT "Expression cloning of a receptor for murine granulocyte colony-
 RT stimulating factor.";
 RL CELL 61:341-350(1990).
 RN [2]
 RP STRUCTURE BY NMR OF 225-333.
 RX MEDLINE: 97333327.
 RA YAMASAKI K., NAITO S., ANAGUCHI H., OHKUBO T., OTA Y.;
 RT "Solution structure of an extracellular domain containing the WxWS
 RT motif of the granulocyte colony-stimulating factor receptor and its
 RT interaction with ligand.";
 RL NAT. STRUCT. BIOL. 4:498-504(1997).
 CC -1- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR. IN
 CC ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION EVENTS AT
 CC THE CELL SURFACE.
 CC -1- SUBUNIT: DIMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: FOUND IN BONE MARROW.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -----
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 CC -----
 CC EMBL: M58288; G193455;
 DR PIR: A34898; A34898.
 DR PDB: 1GCF: 22-OCT-97.
 DR PDB: 1GTO: 22-OCT-97.
 DR MGD: MGI:88533; CSFGR.
 DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
 DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR PFAM: PF00041; fn3, 3.
 KN RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
 KW REPEAT: 3D-STRUCTURE.
 FT SIGNAL 1 25
 FT CHAIN 26 837
 FT DOMAIN 26 626
 FT TRANSMEM 627 650
 FT POTENTIAL.
 FT GRANULOCYTE COLONY STIMULATING FACTOR
 FT RECEPTOR.
 FT EXTRACELLULAR (POTENTIAL).
 FT POTENTIAL.

FT DOMAIN 651 837 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 26 118 IG-LIKE C2-TYPE DOMAIN.
 FT DOMAIN 122 228 FIBRONECTIN TYPE-III.
 FT DOMAIN 229 333 FIBRONECTIN TYPE-III.
 FT DOMAIN 334 431 FIBRONECTIN TYPE-III.
 FT DOMAIN 432 528 FIBRONECTIN TYPE-III.
 FT DOMAIN 529 624 FIBRONECTIN TYPE-III.
 FT DISULFID 132 143 BY SIMILARITY.
 FT DISULFID 249 296 BY SIMILARITY.
 FT DISULFID 267 310 BY SIMILARITY.
 FT CARBOHYD 51 51 POTENTIAL.
 FT CARBOHYD 34 54 POTENTIAL.
 FT CARBOHYD 129 129 POTENTIAL.
 FT CARBOHYD 186 186 POTENTIAL.
 FT CARBOHYD 279 279 POTENTIAL.
 FT CARBOHYD 392 392 POTENTIAL.
 FT CARBOHYD 408 408 POTENTIAL.
 FT CARBOHYD 474 474 POTENTIAL.
 FT CARBOHYD 487 487 POTENTIAL.
 FT CARBOHYD 582 582 POTENTIAL.
 FT CARBOHYD 613 613 POTENTIAL.
 SQ SEQUENCE 837 AA; 93406 MW; D55F8AD4 CRC32;

Query Match 12.6%; Score 241; DB 1; Length 837;
 Best Local Similarity 28.0%; Pred. No. 4,5e-13;
 Matches 89; Conservative 45; Mismatches 112; Indels 72; Gaps 17;

QY 53 LVGLPPEPVPVISC-WSNMMDLCRMTGPGHGEFTLTNSLK-YKLR--WIGDNT 107
 Db 118 LHAGYPPASPSPNLSCLMHLTNSLYCOWMEGP--ETHLPTSLKFSRRAQCQYGDRI 175
 QY 108 CEYHTVGPSPHSCHIP-KDIALFTPEIYEATNRBSARSADVLTDLVVTDP----- 163
 Db 176 POCVAKRRNNKNSIPKRNLLIYOYAIWQAEMTGLSSSPFLCDPMDVVKLEPMLQA 235
 QY 163 ----PDVHYSRVGLLEDQLSVKWS-PPALKDFLFOAKYQIRYVE-DSVDMKVVDDV-S 215
 Db 236 LDIGPDVYSHQPGCL-----WLSWKPKPKPSEVMEQEGELNYPQLKGNANTLVPHLHS 288
 QY 216 NOTSRLAGLAKCTYTFVOVRCNPFPGIYSGKAGIWSWS-----HPT-AASTPSERPG 269
 Db 289 SKDQELGLGMAQAPYTTQMRC-----IRSSLPGEWSPSPQLQRLPTKAPTRIDT-- 342
 QY 270 PGGACEPRGGEPS-----GPVRELRKQFGLKHKHAYCNLSRLDQNRAMQ 320
 Db 342 ----WCQRKQLDPGVSVQVLTFFKPPPLQDSQIOGYL-----LSWNS 380
 QY 321 KSKHTRNCH--RTGSC 335
 Db 381 PDHOGQDIHLACNTQLSC 398

RESULT 15
 CNTR_RAT STANDARD: PRT; 372 AA.
 AC 008406;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE CILIARY NEUROTROPHIC FACTOR RECEPTOR ALPHA PRECURSOR (CNTFR ALPHA).
 GN CNTFR.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIURGNATHI; MURIDAE; MURINAE; RATTUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RP TISSUE-BRAIN:
 RX MEDLINE: 93152175.
 RA IP N.Y., MCCLAIR J., BARREZUELA N.X., ALDRICH T.H., PAN L., LI Y.,
 RA WIGGAND S.J., FRIEDMAN B., DAVIS S., YACOPoulos G.D.;
 RT "The alpha component of the CNTF receptor is required for signaling
 and defines potential CNTF targets in the adult and during

```

RT development."
RL NEURON 10:89-102(1993).
RN [2]
RP SEQUENCE OF 185-277 FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
RX MEDLINE; 93211934.
RA CLATTERBUCK R.E., PRICE D.L., KOLATOS V.E.;
RT "Ciliary neurotrophic factor prevents retrograde neuronal death in
the adult central nervous system."
PROC. NATL. ACAD. SCI. U.S.A. 90:2222-2226(1993).
CC -1- FUNCTION: BINDS TO CNTF (GPA). THE ALPHA CHAIN PROVIDES THE
RECEPTOR SPECIFICITY.
CC -1- SUBUNIT: HETEROMER OF THE ALPHA CHAIN, LIFR AND GPI30.
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
CC -1- TISSUE SPECIFICITY: NERVOUS SYSTEM.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
ONE IG-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 FIBROBLAST TYPE IIR-LIKE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC -----
DR EMBL; S54212; G265056; -
DR EMBL; S57711; G299332; -
DR PIR; A47387; A47387.
DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; FALSE_NEG.
DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
DR PFAM; PF00041; fn3; 1.
DR PFAM; PF00047; 19; 1.
DR RECEPTOR; GPI-ANCHOR; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL.
KW SIGNAL.
FT CHAIN 1 20 POTENTIAL.
FT FT 21 336 CILIARY NEUROTROPHIC FACTOR RECEPTOR
FT FT 337 372 ALPHA.
FT FT 39 96 REMOVED IN MATURE FORM (POTENTIAL).
FT FT 201 302 IG-LIKE DOMAIN.
FT FT 46 89 FIBROBLAST TYPE-III.
FT FT 60 60 POTENTIAL.
FT FT 70 70 POTENTIAL.
FT FT 142 142 POTENTIAL.
FT FT 190 190 POTENTIAL.
FT FT 261 261 POTENTIAL.
FT FT 336 336 POTENTIAL.
FT FT 261 261 GPI-ANCHOR (POTENTIAL).
FT FT 261 261 N -> D (IN REF. 2).
FT Q SEQUENCE 372 AA; 40822 MW; B63000CA CRC32;

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Query Match 11.8%; Score 226.5; DB 1; Length 372;
Best Local Similarity 28.4%; Pred. No. 2.9e-12;
Matches 90; Conservative 34; Mismatches 128; Indels 65; Gaps 16;

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1 Y 2 LNGRRRLPELSRYLNASTLALANNGSRGSDNYLCAABGSLIAGS-CLYVGLPPE 60
1b 59 VNGTDLAPL-----LNGSOLINSLGLHS-----GLYACFHRSWMLRQVLLHVGLPFR 110
1Y 61 KPVNISGSKNM-KDLTCRW-----TPGAGETFLHNYSLKYKLRMWYGQNTGEEYH 112
1b 111 EPV-LSCRSNTYPRKGYGCMHLSAPYIINTFNVTYVLHSGSKM-----VGEKDP 158
1Y 113 TVGPHSCHLPKDLAFT--PYELWEATNRLGARSADVLTLDIVYTTDPPDVAVSRV 170
1b 159 AL-KNMCRI-RYMHLFSTIKYKYSISVNALGH-NTAITPDEFITVKRDPENYVAPRY 215
1Y 171 GLEDDLSYRWVSPALXD-FLQAKYQIRYREDSDWKVYDDVSNQTSCLAGLPGT 229
1b 216 PSNPRLEVTWOTPSWPDSPFLKFLRYRPLLDQOHV-ELSNGAHTTTDAYACK 274

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QY 230 VPEVYRCNPFGLYSSKKGINSMS-----HPTASTPERSRP 268
DB 275 EYIQVAAT-----DNEIGTWSWVAHAATPWTEPRHLTTETAQAPETTTSTSLAP 328
QY 269 GREGGACERGPSPSSG 285
DB 329 PPTTKCDP--GELSSG 343

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Search completed: September 17, 1999, 03:10:14
Job time: 294 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:40:09 ; Search time 68.96 Seconds
(Without alignments)
312.359 Million cell updates/sec

Title: US-09-037-657-25

Sequence: 1 TLNGRRLLPELRLSVLNASTL.....TRGSCPRADGARREVLDPDL 350

Scoring table: BLOSUM62

Searched: 201082 seqs, 61543640 residues

Database:

SPTREMBL_10:.*
1: sp_archea:.*
2: sp_bacteria:.*
3: sp_fungi:.*
4: sp_human:.*
5: sp_invertebrate:.*
6: sp_mammal:.*
7: sp_mhc:.*
8: sp_organelle:.*
9: sp_phase:.*
10: sp_plant:.*
11: sp_protent:.*
12: sp_virus:.*
13: sp_vertebrate:.*
14: sp_unclassified:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1800	93.8	422	4	075462	075462 homo sapien
2	327	17.0	881	13	057519	057519 xenopus lae
3	325.5	17.0	206	4	016354	016354 homo sapien
4	309.5	16.1	581	6	046561	046561 ovis aries
5	306.5	16.0	296	6	018880	018880 bos taurus
6	270.5	14.1	346	13	093404	093404 oreochromis
7	235.5	12.3	217	6	046386	046386 mustela vis
8	231.5	12.1	198	6	018985	018985 cervus elap
9	225.5	11.8	335	6	P79203	P79203 ovis aries
10	217.5	11.3	372	11	088507	088507 mus musculu
11	207.5	10.8	862	4	099665	099665 mus musculu
12	204	10.6	432	11	064385	064385 mus musculu
13	203	10.6	422	4	016542	016542 homo sapien
14	195	10.2	432	11	P70225	P70225 mus musculu
15	193.5	10.1	874	11	P97378	P97378 mus musculu
16	192.5	10.0	710	13	057520	057520 xenopus lae
17	178	9.3	316	11	035545	035545 rattus norv
18	174	9.1	1165	6	002671	002671 mus musculu
19	165.5	8.6	440	11	000343	000343 mus musculu
20	163.5	8.5	895	11	062960	062960 rattus norv
21	161	8.4	958	4	092920	092920 homo sapien
22	161	8.4	1165	4	092921	092921 homo sapien
23	161	8.4	958	4	013592	013592 homo sapien
24	161	8.4	906	4	013593	013593 homo sapien
25	161	8.4	896	4	013594	013594 homo sapien
26	161	8.4	896	4	092919	092919 homo sapien
27	159.5	7.9	383	11	088786	088786 mus musculu
28	152.5	7.3	229	6	027950	027950 mus musculu
29	152.5	7.9	229	6	028206	028206 bos taurus

30	149	7.8	1093	11	070535	070535 rattus norv
31	148.5	7.7	228	11	035228	035228 mus musculu
32	148	7.7	229	4	075269	075269 homo sapien
33	146	7.6	279	11	064236	064236 rattus norv
34	141.5	7.4	86	6	018853	018853 mustela put
35	141.5	7.4	890	11	0921A0	0921A0 cavla porce
36	140	7.3	229	4	014213	014213 mus musculu
37	137.5	7.2	634	6	046600	046600 bos taurus
38	137.5	7.2	269	6	P79195	P79195 macaca mula
39	137	7.1	396	4	014631	014631 homo sapien
40	137	7.1	420	4	014633	014633 homo sapien
41	137	7.1	333	4	015459	015459 homo sapien
42	135	7.0	896	11	064146	064146 rattus norv
43	134.5	7.0	427	4	095646	095646 mus musculu
44	133	6.9	971	11	070458	070458 mus musculu
45	133	6.9	970	11	088821	088821 mus musculu

ALIGNMENTS

RESULT 1
ID 075462 PRELIMINARY; PRT; 422 AA.
AC 075462;
DT 01-NOV-1998 (TREMREL.08, Created)
DT 01-NOV-1998 (TREMREL.08, Last sequence update)
DT 01-MAY-1999 (TREMREL.10, Last annotation update)
DE CYTOKINE-LIKE FACTOR-1 PRECURSOR.
GN CLF-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA ELSON G.C.A., GRABER P., LOSBERGER P., HERREN S., GRETNER D.,
RA MENON D.L.N., WELLS T.N.C., KOSCO-VILBOIS M.H., GAUCHAT J.F.;
RT CLF-1, a Novel Soluble Protein Shares Homology With Members of the
RT Cytokine Type-1 Receptor Family.
RL J. Immunol. 0:0-0(1998).
DR EMBL; AF059293; AAC2835.1;
DR PIRAM; PF00041; fn3; 2.
KW signal.
FT signal.
FT CHAIN 38 422 POTENTIAL.
FT CHAIN 38 422 CYTOKINE-LIKE FACTOR-1.
SQ SEQUENCE 422 AA; 46301 MW; 87799BC9 CRC32.

Query Match 93.8%; Score 1800; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 6.6e-159;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TLNGRRLLPELRLSVLNASTLALANINSGRSGDNVCHARDGSLIAGCLYGLPPE	60
DB	77	TLNGRRLLPELRLSVLNASTLALANINSGRSGDNVCHARDGSLIAGCLYGLPPE	136
QY	61	KPVNISCSKMDLFCRPTGAGHGFHTNYSIKYKLRWQDNVCEHYHVGSHCS	120
DB	137	KPVNISCSKMDLFCRPTGAGHGFHTNYSIKYKLRWQDNVCEHYHVGSHCS	196
QY	121	IPFDLALFPYEIWEATNRLGARSVDVLTLDVVTITDPPDVASRYGLEDLSVR	180
DB	197	IPFDLALFPYEIWEATNRLGARSVDVLTLDVVTITDPPDVASRYGLEDLSVR	256
QY	181	WSPPLKDELPAQKQIKRYVEDSDYKRVVDVSNQISCRLAGLPGTVYFVQVNCNF	240
DB	257	WSPPLKDELPAQKQIKRYVEDSDYKRVVDVSNQISCRLAGLPGTVYFVQVNCNF	316
QY	241	GIYSGKAGIWSHPTASTPRSERPGGACPRGSGSSGVVRELKQFGLWKL	300
DB	317	GIYSGKAGIWSHPTASTPRSERPGGACPRGSGSSGVVRELKQFGLWKL	376
QY	301	HAYCSNLSFRLYDQWRAVAMOKSHKTRNO	328

Db 377 HAYCSNLSFRLYDQWRAMQKSHTRNQ 404

RESULT 2
ID 057519 PRELIMINARY; PRT; 881 AA.

AC 057519; 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DE 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
GN GP130P1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae;
OC Xenopus.
RN (1)
RP SEQUENCE FROM N.A.
RA CHEN J., GRACE A., CHIEN K.R.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF041845; AAC03531.1;
PFAM; PF00041; fn3; 4.
SQ SEQUENCE 881 AA; 99003 MM; 647E152E CRC32;

Query Match 17.0%; Score 327; DB 13; Length 881;
Best Local Similarity 30.7%; Pred. No. 4.7e-22;
Matches 91; Conservative 39; Mismatches 118; Indels 48; Gaps 10;

QY 2 LNCRLPPELSRYNASTALALANINGSRQSGDNLVGHARDGSIAGSCLYGSLPERK 61
DB 65 VKGKVPETQYELNOTTSVFENLTINSPLTCNMAAGVAAVLYGIFLGLPDK 124
QY 62 PVNISCSNMKDLGCRWTPGANGETLHTNYSLSKYLKLM-----YGDNTCEHYT 113
DB 125 PNLITCTYNODNLCTMPGR--PTNLPTNTLSH--KNAHFGANYCGAANSC----- 176
QY 114 VGHSCHPKDLALFTPYEIVWEATNRLGSASDVLTLDLVYTTDPDVHVSAGL 173
DB 176 ---THSP--GQFYIDTFQVEATNMLGQSEITLIPVKNRPOLSLISL 230
QY 174 EDGLSRWVSPALKDFLEQAKQIRYEDSVDMKV---DVSQTSCLAGLKPVT 230
DB 231 PNLKLEMKNPIT--NAENLKYNIRYKVTQDMVPEEDTASHRDFTLQDLIPNTV 287
QY 231 YFVQVRCNPFGIYGSKKAGIWSMSHPTAASPRSERPGGACPRGEPSSCP 286
DB 288 YEVSINC-----IHKDGHGFSWMSLKKQVTP--EAP-----PSRGP 323

RESULT 3
ID 016354 PRELIMINARY; PRT; 206 AA.

AC 016354; 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE PROLACTIN RECEPTOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homindae; Homo.
RN (1)
RP SEQUENCE FROM N.A.
RA MEDLINE; 95286597.
RA FUH G., WELLS J.A.;
RT "Prolactin receptor antagonists that inhibit the growth of breast cancer cell lines."
RT J. Biol. Chem. 270:13133-13137 (1995).
RL EMBL; S78505; AAB34470.1;
DR PFAM; PF00041; fn3; 2.
FT NON_TER 1
SQ SEQUENCE 206 AA; 23950 MM; D7E57266 CRC32;

Query Match 17.0%; Score 325.5; DB 4; Length 206;
Best Local Similarity 37.6%; Pred. No. 1e-22;
Matches 80; Conservative 26; Mismatches 90; Indels 17; Gaps 7;

QY 57 LPPEKPVNISCSNMKDLGCRWTPGANGETLHTNYSLSKYLKMWGADNTCEHYTGP 116
DB 2 LPPEKPEIKRCSNPKEFTGMMRPOTDGC--LPTNYSLYHREGFTLHNECPDYLITGP 59
QY 117 HSCHPKDLALFTPYEIVWEATNRLGSASDVLTLDLVYTTDPDVHVSAGLGD 175
DB 60 NSCHFGKQYTSKMRITVMVNAINQSSFSDELVDVYIYQPPPLAV--EVKQPD 118
QY 176 QLSVRV--SPALNDF--LFOAKQIRYREDSVDMKVVDVSNQTSCLAGLKPVT 230
DB 119 RKPYLMIKSPPTLIDKLGWFTLXELKKEKAENE--TFAGQOTEFKILSLHGGK 177
QY 231 YFVQVRCNPFGIYGSKKAGIWSMSHPTAASP 263
DB 178 YLVQVRCRP-----DHGYWSAMSPATFIQIP 203

RESULT 4
ID 046561 PRELIMINARY; PRT; 581 AA.

AC 046561; 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DE 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE PROLACTIN RECEPTOR LONG FORM PRECURSOR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Caprine; Ovis.
RN (1)
RP SEQUENCE FROM N.A.
RA MEDLINE; 98001468.
RA BIGNON C., BIVART N., ORMANDY C., SCHULER L.A., KELLY P.A.,
RA DJANE J.;
RT "Long and short forms of the ovine prolactin receptor: cDNA cloning and genomic analysis reveal that the two forms arise by different alternative splicing mechanisms in ruminants and in rodents."
RT J. Mol. Endocrinol. 19:109-120 (1997).
RN (2)
RP SEQUENCE FROM N.A.
RA BIGNON C., DJANE J.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF041257; AAB96795.1;
DR PFAM; PF00041; fn3; 2.
KW signal.
FT SIGNAL 1
FT CHAIN 25
FT CHAIN 581
SQ SEQUENCE 581 AA; 65235 MM; 6792A7C7 CRC32;

Query Match 16.1%; Score 309.5; DB 6; Length 581;
Best Local Similarity 32.2%; Pred. No. 1.2e-20;
Matches 83; Conservative 33; Mismatches 99; Indels 43; Gaps 8;

QY 12 SHVLNASTLALANINGSRQSGDNLVGHARDGSIAGSCLYGSLPERKPVNISCSKN 71
DB 7 SHVLILLLFLFASLLNQS-----PPKPKILICRSFG 40
QY 72 MDLTCRWTPGANGETLHTNYSLSKYLKMWGADNTCEHYTGVHSCHPKDLALFTP 130
DB 41 KETFCWMEPGADGC--LPTNTLYRKGEFTLHNECPDKYKGCNSCYFSKYSIMWM 98
QY 131 YFVQVRCNPFGIYGSASDVLTLDLVYTTDPDVHVSAGLEOLSRWV--SPALK 188
DB 99 YITVSAINQSSSDPIYDVYIYVEPEPVNLT--ELKHPEDRKPYLWKMSPTLT 157
QY 189 DF--LFOAKQIRYREDSVDMKVVDVSNQTSCLAGLKPVTYFVQVRCNPFGIYS 245

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Db 158 DVSQWSEIYELRKEKATDWE-THFAPKRLQKLFNFYGGKYLVOIRCKP----- 211
QY 246 KKAGIWSMHPPTAASP 263
    |||||
Db 211 -DHGIWSEMSPESSIQIP 227

RESULT 5
ID 018880 PRELIMINARY; PRT; 296 AA.
AC 018880;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DE 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE PROLACTIN RECEPTOR SHORT FORM.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN (1)
RP SEQUENCE FROM N.A.
RA MEDLINE; 97375450.
RA SCHULER L.A., NAGEL R.J., GAO J., HONSEMAN N.D., KESSLER M.A.;
RT "Prolactin receptor heterogeneity in bovine fetal and maternal
    tissues."
RT Endocrinology 138:3187-3194(1997).
DR EMBL; AF027403; AAB8399.1;
DR PFAM; PF00041; fn3; 2.
SQ SEQUENCE 296 AA; 33854 MW; 8B40CCD8 CRC32;

Query Match 16.0%; Score 306.5; DB 6; Length 296;
Best Local Similarity 31.2%; Pred. No. 9.4e-21;
Matches 81; Conservative 38; Mismatches 94; Indels 47; Gaps 9;

QY 12 SRVNASLALALANLNGSRQSGDNLVCHARDGSIAGSCIYVGLPPEKPYNISCSKN 71
    |||||
Db 7 SRVAFILLFLFSVSLNGS-----PPEKRLVKRSRG 40

QY 72 MKDLCRMTPGNGHGFPLHTNYSLKYLKRWYGODNCEHYHVGPHSCHT-PKDALFTFP 130
    |||||
Db 41 KETLCWMEPGADGG--LPTNTYLLYHKKEGTLIHCCPDYKKGPGSCYFCKHKTSMK 98

QY 131 YEIWEATNRUGSARSVDLTLDLVTTDPPPDVHVSARGLEDDLSRWV--SPALK 188
    |||||
Db 99 YVITVNAIINQGISSDDPLYVHTVIVEEPANLTL-ELKHPEDKRPYLWKWSPTWT 157

QY 189 D-----FLFOAKYQIRYVEDSVDRKVVDDVSNQTSCLAGLPGTYVFOYRCNPFGLY 243
    |||||
Db 158 DVKSGWFTIQ--YEIRLKPKEATDWE-THFTLKQTKQKLFNFYGGKYLVOIRCKP----- 211

QY 244 GSKKAGIWSMHPPTAASP 263
    |||||
Db 211 ---DHGIWSEMSPESSIQIP 227

RESULT 6
ID 093404 PRELIMINARY; PRT; 346 AA.
AC 093404;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DE 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE PROLACTIN RECEPTOR (FRAGMENT).
OS Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Perciformes;
OC Perciformes; Labroidae; Cichlidae; Tilapia.
RN (1)
RP SEQUENCE FROM N.A.
RA TISSUE-GITL;
RA SHIRAIISHI K., MATSUDA M., MORI T., TETSUYA H.;

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RT "Expression of prolactin and cortisol receptor gene in early-life
RT stages of tilapia (Oreochromis mossambicus)."
RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF080247; AAC31825.1;
DR PFAM; PF00041; fn3; 2.
FT NON_TER 346
SQ SEQUENCE 346 AA; 39203 MW; 1E8A63B9 CRC32;

Query Match 14.1%; Score 270.5; DB 13; Length 346;
Best Local Similarity 32.7%; Pred. No. 2.5e-17;
Matches 70; Conservative 29; Mismatches 92; Indels 23; Gaps 9;

QY 59 PERPVNISCSKNKDDTCMTGARGFELHTNYSIKYLKRWYGODNCEHYHVGPHS 118
    |||||
Db 29 PGKPTLETCSRSPKEFTCWKRGSDGG--LPTTALYKESDVAHCEPDHTGKNS 86

QY 119 CHLPK-DLALFTYELWEATNRUGSARSVDLTLDLVTTDPPPDVHVSARGLEDDQ- 177
    |||||
Db 87 CFENKNDTLIWSINVTAVATNALGRTSPVDIDVYIVKPPPERKLEYT--VAKDQ 143

QY 177 ---LSYRWSPPALKDF--LEQAKYQIRYVED-SVDRKVVDDVSNQTSCLAGLPGT 229
    |||||
Db 144 WPLRLXSW-EPRHKADTRSGWITLITELRYKLEDESEWE-NHAAQOKWFTLSRSG 201

QY 230 VYFVOYRCNPFGLYGSKKAGIWSMHPPTAASP 263
    |||||
Db 202 TYLIQVRCRP-----DHGFSEMSSTSYVVP 228

RESULT 7
ID 046386 PRELIMINARY; PRT; 217 AA.
AC 046386;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DE 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE PROLACTIN RECEPTOR (FRAGMENT).
RN PRLR.
OS Muscula vison (American mink).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Placentalia; Mustelidae; Mustela.
RN (1)
RP SEQUENCE FROM N.A.
RA TISSUE-TESTIS;
RA DODDAS D.A., SONG J.-H., HONDE A., MURPHY B.D.;
RT Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF039294; AAB88899.1;
DR PFAM; PF00041; fn3; 1.
FT NON_TER 217
FT NON_TER 217
SQ SEQUENCE 217 AA; 24850 MW; F77A3B9D CRC32;

Query Match 12.3%; Score 235.5; DB 6; Length 217;
Best Local Similarity 32.3%; Pred. No. 2.4e-14;
Matches 61; Conservative 30; Mismatches 81; Indels 17; Gaps 7;

QY 81 PGHGETFLHNTYSIKYLKRWYGODNCEHYHVGPHSCHT-PKDALFTYELWEATN 139
    |||||
Db 2 PEGDGG--LPTKTYLLYKKEGTLIHCCPDYITSGPNSCYFNKHTSIWYITINNTN 59

QY 140 RUGSARSVDLTLDLVTTDPPPDVHVSARGLEDDLSRWV--SPALDF--LEQA 194
    |||||
Db 60 EMGSSSDPRVYTLTYIYEPFPVNLIS-ELKQPEDKRTYIMIKWYPTPLDVASGWLTL 118

QY 195 KYQIRYVEDSVDRKVVDDVSNQTSCLAGLPGTYVFOYRCNPFGLYGSKKAGIWSM 254
    |||||
Db 119 QYERLKPKEATDWE-THFAGLQTKQKLFNFYGGKYLVOIRCKP-----DHGFSEW 170

QY 255 SHPTAASP 263
    |||||
Db 171 SPKRSTQIP 179

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RESULT 8
ID 018985 PRELIMINARY; PRT: 198 AA.
AC 018985:
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE SOLUBLE PROLACTIN RECEPTOR.
OS Ceruus elaphus nelsoni (American elk).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
OC Cervinae; Cervus.
RN [1]
RP SEQUENCE FROM N.A.
RA JABHOUR H.N.;
RU Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; Y14753; CAA75048.1;
DR PFAM; PF00041; fn3; 1.
SQ SEQUENCE 198 AA; 22652 MW; COABAB0 CRC32;

Query Match
Best Local Similarity 12.1%; Score 231.5; DB 6; Length 198;
Matches 61; Conservative 32; Mismatches 76; Indels 15; Gaps 7;

QY 44 DCSILAGSCLYGLPPEKPVNISCMKMKDLTCRWTPGAHGTEFLHTNYSIKYLRWYG 103
DB 18 NASLNGS-----PPGRKIIICRSPGKETCTCWEPSDGG--LPVYITLTTHKEGET 70
QY 104 QNTEERYHTVGPSCSHI-PKDLAETPYEIWEATNRLSGARSVDLTLDIDVYTTDP 162
DB 71 LIHECPDYTGTPNTCYFSKHTSIKVIYVYNAINQGVSSDPLDYVYIYEPEEP 130
QY 163 PNVHNSRVGLDGLSVKVS--PPLKDF--LPQAKQIKRVEDSYDMKVVDDVSNQ 217
DB 131 ANLTTL-ELKHEDRKRYLWKWPPPLTLTVKSGWFMIOYEIRLKPETALDWE-HDHLHP 188
QY 218 TSCR 221
DB 189 TSCR 192

RESULT 9
ID P79203 PRELIMINARY; PRT: 335 AA.
AC P79203:
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE PROLACTIN RECEPTOR (FRAGMENT).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae; Bovidae;
OC Caprinae; Ovis.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-M22/80; TISSUE-ANTERIOR PITUITARY.
RA TORPONSE D.T., BROOKS J., INGLETON P., MCNEILLY A.S.;
RU Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; Y10518; CAA71597.1;
DR PFAM; PF00041; fn3; 1.
FT NON-TER 1
FT NON-TER 335
SQ SEQUENCE 335 AA; 38326 MW; 88A05AB1 CRC32;

Query Match
Best Local Similarity 11.8%; Score 225.5; DB 6; Length 335;
Matches 57; Conservative 29; Mismatches 68; Indels 31; Gaps 7;

QY 85 GEFLLHTNYSIKYLRWYGQDNTCEYHVGPHSCHIPPQD-LALFTPIYIWEATNRLGS 143

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DB 8 GEFLLH-----ECPDYKTCGNSCFSCSKYSIMKMYITVSAINOMGI 51
QY 144 ASDVLTLDIDVYTTDPPDVHVSRLVGLDQSVRW--SPALKDF--LFOAKIOI 198
DB 52 SSSDPLVDVYIVPEPPVNLTL-ELKHEDRKRYLWKWPPPLTLTVKSGWFSIOYPI 110
QY 199 RYRVEDSYDMKVVDDVSNQTSCLAGLKPQYFYOVRCNPPGIYSKAGIWMESHPT 258
DB 111 RAKPEKADWE-THRAPLITQAKINFLVPGQKYLVOIRKP-----DHGIWSEKSPS 162
QY 259 AASTP 263
DB 163 FICIP 167

RESULT 10
ID 088507 PRELIMINARY; PRT: 372 AA.
AC 088507:
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE CILIARY NEUROTROPHIC FACTOR RECEPTOR ALPHA PRECURSOR.
GN CNFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-BRAIN, SKELETAL MUSCLE;
RA MAEDA M., YAGUCHI N., HANYU C., NAKATA Y., ONODA N., TULIN E.E.,
RA KOJIMA T., HASEGAWA M., KIKUCHI Y., NOMURA H.;
RU "Mouse homolog of human ciliary neurotrophic factor receptor."
RU Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF068615; AAC25711.1;
DR PFAM; PF00041; fn3; 1.
DR PFAM; PF00047; 1g; 1.
DR SIGNAL.
FT SIGNAL 1
FT CHAIN 21 20 POTENTIAL.
FT CHAIN 21 336 CILIARY NEUROTROPHIC FACTOR RECEPTOR
FT CHAIN 21 336 ALPHA.
SQ SEQUENCE 372 AA; 40831 MW; 9A40FE12 CRC32;

Query Match
Best Local Similarity 11.3%; Score 217.5; DB 11; Length 372;
Matches 88; Conservative 35; Mismatches 129; Indels 67; Gaps 16;

QY 2 LNGRLPPELSEVYNASTLALANLNGSRQSGDNVCHARDGSLAGS-CLVYGLPPE 60
DB 59 VNGTDLADL---LNGSOLILRSLGHS-----GLYACFHDSNHLRQVILLVGLPPE 110
QY 61 KPVNISCMKMK-KDLTGRW-----TPGAGTEFLHTNYSIKYLRWYGQDNTCEYH 112
DB 111 EPV-LSCRSNTYPRKGYCSWHLPTPIYIPNFENVVLHSGKIM-----VCEKDP 158
QY 113 TVGPHSCHIPPDLAFT--PYEIWEATNRLSGASVDLTLDIDVYTTDPPDVHVSRY 170
DB 159 AL-KRCHI-RYMHLESTIKRYKVSISVSNAIGH-WTALTDEFTIVRDPENYVARPV 215
QY 171 GLEDELQSVRWSPALPD-FLFOAKQIORYVEDSYDMKVVDDVSNQTSCLAGLKPQT 229
DB 216 PSNPRRLVYVOTPESTWDPDEFPLAKFLRKRPPLLDWMQHY-ELSDGTAHITTAAYACK 274
QY 220 VYFVOVRCNPPGIYSKAGIWMESH-----HPTAASPTPSERP 268
DB 275 EYIIQVAAK-----DNEIGTWSDMVSAHAHPTTEPRHLTTEQAPETTSTSLAP 328
QY 269 GPGGACGP---RGERS 283
DB 329 PPTTKICDPGELSGGSGPS 347

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RESULT 11
ID 099665 PRELIMINARY: PRT: 862 AA.
AC 099665; (TREMblrel. 03, Created)
DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE IL-12 RECEPTOR BETA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA PRESKY D.H., YANG H., MINETTI L.J., CHUA A.O., NABAVI N., WOU C.Y.,
RA GATELY M.K., GUBER U.,
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U64198; AAB36675.1;
DR PFM: PF00041; fn3; 3.
SQ SEQUENCE 862 AA; 97134 MW; 5FEAFBD5 CRC32;

Query Match 10.8%; Score 207.5; DB 4; Length 862;
Best Local Similarity 28.9%; Pred. No. 5.4e-11;
Matches 71; Conservative 32; Mismatches 104; Indels 39; Gaps 10;
OY 38 LVCHARDGSLAGSCLYGLPPEKPVNISCWSKMK-DLTCRTPGAHGTEFLHTNYSLK 96
DB 103 LACINSDIQLGAEIFGVAPQPNLSCIOGEGVACWTERGR-DTHLYETYLQ 160
OY 97 Y-----KLRWYGO--DNTCEHYTVG-----PHSHIRKDALALPPEIWEATNRLCS 143
DB 161 LSGPNLWQOKCKIYIC-DYDDEGINLTPESPESNFTAK-----VYAVNSLGS 208
OY 144 ARSDVLIDLDVYTTDPDPVHVRVGLDQLSVRWSPALAKFLQAKQIYRYE 203
DB 209 SSSLEPTFDIYAPLPMDIRIRFOKASVRCILY-----HDEGLVILNRLKTRPS 262
OY 204 DSVMKVVDVDSNOTSCLAGLPGCTVYFVQRCNPFGLYSGKAGIWSHPTAASP 263
DB 263 NSRLMNVNWKAKGRHDLDLKPFTEYEFQI-SSKLHLX-----KGSWSDMESLRAQTP 317
OY 264 RSEKRG 269
DB 318 EEEPTG 323

RESULT 12
ID 064385 PRELIMINARY: PRT: 432 AA.
AC 064385; (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 1 PRECURSOR (NR1) (ETL2)
DE (IL-11ALPHA) (IL11RA1).
DE IL11RA1 OR IL11RA OR ETL2 OR ETL2/IL11 REC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6 X CBA; TISSUE-LIVER;
RX MEDLINE: 95045367.
RA HILTON D.J., HILTON A.A., RAICEVIC A., RAKR S., HARRISON-SMITH M.,
RA GOUGH N.M., BEGLEY C.G., METCALF D., NICOLA N.A., WILSON T.A.;
RT Cloning of a murine IL-11 receptor alpha-chain; requirement for
RT gp130 for high affinity binding and signal transduction.;
RL EXBO J. 13:4765-4775(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C AND C57BL/6; TISSUE-EMBRYO;
RA NEUHAUS H., BETTENHAUSEN B., BILINSKI P., SIMON-CHAZOTTES D.,

RA GUENET J.L., GOSSLER A.;
RL Dev. Biol. 166:521-542(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C AND C57BL/6;
RA GOSSLER A.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97129000.
RA BILINSKI P., HALL M.A., NEUHAUS H., GISSEL C., HEATH J.K.,
RA GOSSLER A.;
RT "Two differentially expressed interleukin-11 receptor genes in the
RT mouse genome."
RL Biochem. J. 320:359-363(1996).
CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11.
CC BINDS TO IL-11 WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A
CC SIGNAL.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
CC -1- SIMILARITY: BELONGS TO THE IMMNOGLOBULIN SUPERFAMILY.
CC CONTAINS ONE IG-LIKE DOMAIN.
DR EMBL: X74953; CAA52908.1; -
DR EMBL: U14412; AAB33248.1; -
DR EMBL: X94162; CAA63873.1; -
DR EMBL: X94163; CAA63873.1; JOINED.
DR MGD: MGI:107426; IL11RA1.
DR PFM: PF00041; fn3; 2.
DR PFM: PF00047; fn3; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin fold; Signal.
FT SIGNAL 1 23
FT CHAIN 1 23
FT DOMAIN 24 432
FT TRANSMEM 24 367
FT DOMAIN 368 393
FT DOMAIN 394 432
FT DOMAIN 41 102
FT CARBOHD 127 127
FT CARBOHD 194 194
SQ SEQUENCE 432 AA; 46655 MW; F5B3060 CRC32;

Query Match 10.6%; Score 204; DB 11; Length 432;
Best Local Similarity 25.4%; Pred. No. 4.7e-11;
Matches 71; Conservative 43; Mismatches 109; Indels 56; Gaps 13;
OY 39 VCHARDGSLAGSCLYGLPPEKPVNISCWSKMKDLTCRTPGAHGTEFLHTNYSLYK 98
DB 93 VCGITDVGSGKMTIKLFPARP-EVSCQAVDVENFSCWSPGO--VSGLPTRYLTSTR 149
OY 99 LHWGQDNTCEHYHVPSPHSCHIPD-----LALTPYEIWEATNRLGSASRD 147
DB 150 KTLPGASQRESSTGWPCC--PDPLASRCVYHGAETSEIRINTEVNPUG-ASTC 206
OY 148 VLTLDLDVYTTDPDPVHVRVGLDQLSVRWSPALAK--DLFOAKYQIRYVED 204
DB 207 LLDVRLGSLRPPDPGCRVSEVPGYRRLHASTYPSWNRQHFLL--KFRLOYRPAQ 264
OY 205 SVDMKVVDVDSN--TSCRLAGLPGTYVYFVQRCNPFGLYSGKAGIWSHPTAASP 262
DB 265 HPANSTVEPDLSEYITDAVAGLP-----HAYVSARDF-----LDAGTWSAWS-PEA--- 312
OY 263 PRSERPGGACGACPESSGPPVRELKQFLMKLK 301
DB 312 -----WGTSSTGLDGEIRD--WSSGH 331
RESULT 13
ID 016542 PRELIMINARY: PRT: 422 AA.
AC 016542; 014626;
DT 01-NOV-1996 (TREMblrel. 01, Created)

Db 265 HPAMSTVEPIGLEVITDVAGLP-----HAVVSARDF-----LDAGTWSAMS-PEAMGT 314
QY 263 P 263
Db 315 P 315

RESULT 15

P97378 PRELIMINARY; PRT; 874 AA.
AC P97378;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE INTERLEUKIN 12 RECEPTOR, BETA 2 (IL-12 RECEPTOR BETA2).
GN IL12RB2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA PRESKY D.H., YANG H., MINETTI L.J., CHUA A.O., NABAVI N., WOD C.Y.,
RA GATELY M.K., GUBLER U.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U64199; AAB36676.1;
DR MGD: MGI:1270861; IL12RB2.
DR PFM: PFM0041; fn3; 4.
SQ SEQUENCE 874 AA; 98196 MW; 9B90EB47 CRC32;

Query Match 10.18; Score 193.5; DB 11; Length 874;

Best Local Similarity 27.68; Pred. No. 1.1e-09;

Matches 75; Conservative 42; Mismatches 110; Indels 45; Gaps 13;

QY 13 RVLNAST-LALALANLNGSR-QRSGDNLYCHARDSILAGSCLYGLPPEKPVNISCMK 70
Db 98 QVNLSLGMLTFCKLNCNSQKKPVVC-----GVEISYGAPEPPONISCVQE 148
QY 71 NMR-DLTCRWTPGAHGEFLHTNTSLKYLKRWYGDN-TCE-EYHTVGRHSC-----H 120
Db 149 GENGTVACSMNSGR--VTYLTNTYTLQS-----GPNLTCKQCFSDNRQNCNRLDGIN 202
QY 121 IPRDLELFTPEYEVETNRLGARSQVLDLIDVYTTDPPDVHVSRYGLDQLSVR 180
Db 203 LSPDLA-ESRFIVAVTAINDGNSSLPHTFTFDIYIPLEPMDIRINFLNAGSRTIQ 261
QY 181 WSPPALKDFLFQAKYQIRYRVEDSVDMKYVDVSNQTSRLAGLKGTYFVQVRCNPF 240
Db 262 W-----EDGGVYVNLNLRQYOPLNSTSMNVNATNAKGYDLRLDRPTEYEFQI----- 311
QY 241 GYGSK---KAGIMSEWSHPTASTPSEKRG 269
Db 311 ---SKLHLGSGSMNSNSESRLRTPPEEPVG 339

Search completed: September 16, 1999, 20:40:09
Job time: 5560 sec


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GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-308-881-2

Query Match
Best Local Similarity 13.3%; Score 133.5; DB 2; Length 708;
Matches 35; Conservative 22; Mismatches 66; Indels 5; Gaps 2;

QY 2 PILLGSSIQATCSIHG---DTPGATAGLYTFNGRRLPSLSRLNTSTLALANLN 58
DB 36 PVOQLHSNFTAVCYLKEKCMDFHVNANYIWKTNHFTIPKEQYIINRTASSVFTDIA 95
QY 59 GSROOSGDLVCHARDGSLAGSCLYGLPPEKPNISGSMNMDLTCRWTPGAGET 118
DB 96 SNIQITCITILFGQLEONVIGITISGLPPEKPNLSCLVNEGKRCMDGGR--ETH 153
QY 119 LHTNYSLK 126
DB 154 LETNFTLK 161

RESULT 3
PCT-US95-06530-2
Sequence 2, Application PC/TUS9506530
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06530
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,881
FILING DATE: 09-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-06530-2

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Query Match
Best Local Similarity 13.3%; Score 133.5; DB 3; Length 708;
Matches 35; Conservative 22; Mismatches 66; Indels 5; Gaps 2;

QY 2 PILLGSSIQATCSIHG---DTPGATAGLYTFNGRRLPSLSRLNTSTLALANLN 58
DB 36 PVOQLHSNFTAVCYLKEKCMDFHVNANYIWKTNHFTIPKEQYIINRTASSVFTDIA 95
QY 59 GSROOSGDLVCHARDGSLAGSCLYGLPPEKPNISGSMNMDLTCRWTPGAGET 118
DB 96 SNIQITCITILFGQLEONVIGITISGLPPEKPNLSCLVNEGKRCMDGGR--ETH 153
QY 119 LHTNYSLK 126
DB 154 LETNFTLK 161

RESULT 4
US-07-797-556-6
Sequence 6, Application US/07797556
Patent No. 5262522
GENERAL INFORMATION:
APPLICANT: Geating, David P.
TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/797,556
FILING DATE: 19911122
CLASSIFICATION: 435

```


ATTORNEY/AGENT INFORMATION:

NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2607
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
TELEFAX: 206-587-0606
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1001 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-943-843-6

Query Match 11.4%; Score 115; DB 1; Length 1001;
Best Local Similarity 23.4%; Pred. No. 0.00016;
Matches 36; Conservative 28; Mismatches 46; Indels 44; Gaps 7;

1 DPTLLIGSSLAQTCSI-----HGDTPGAAGELVTFNGRRLLPSELRLNLTSTL 50
258 DKVILVGSDFITFCVSOEKVLSALIGHTNCPLIHLDG-----ENV 297
51 ALALANLNGSRQSGDNLYCHARDGSLIAGSCLYGLPPEKPFNISCWSRNMKDLTCRMT 110
298 AIKIRNISVS-ASSGIVNVFTTEDN--IFGTIVFAGYPPDTPQOLNCEETHDKETICSMN 354
111 PG-----AHGETFLHTNYSLSKYLRLVRSE 135
355 PGRVTLVGPRASTYTLVE-SFSGKY-VRLKRAE 386

RESULT 5

US-07-943-843-2
Sequence 2, Application US/07943843
Patent No. 5284755

GENERAL INFORMATION:

APPLICANT: Gearing, David P.
APPLICANT: Beckmann, M. P.
TITLE OF INVENTION: Leukemia Inhibitory Factor Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/943,843
FILING DATE: 19920911
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2606-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
TELEFAX: 206-587-0606
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1001 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
S-07-943-843-2

Query Match 11.4%; Score 115; DB 1; Length 1001;
Best Local Similarity 23.4%; Pred. No. 0.00016;
Matches 36; Conservative 28; Mismatches 46; Indels 44; Gaps 7;

1 DPTLLIGSSLAQTCSI-----HGDTPGAAGELVTFNGRRLLPSELRLNLTSTL 50
258 DKVILVGSDFITFCVSOEKVLSALIGHTNCPLIHLDG-----ENV 297
51 ALALANLNGSRQSGDNLYCHARDGSLIAGSCLYGLPPEKPFNISCWSRNMKDLTCRMT 110
298 AIKIRNISVS-ASSGIVNVFTTEDN--IFGTIVFAGYPPDTPQOLNCEETHDKETICSMN 354
111 PG-----AHGETFLHTNYSLSKYLRLVRSE 135
355 PGRVTLVGPRASTYTLVE-SFSGKY-VRLKRAE 386

RESULT 6

US-07-943-843-6
Sequence 6, Application US/07943843
Patent No. 5284755

GENERAL INFORMATION:

APPLICANT: Gearing, David P.
APPLICANT: Beckmann, M. P.
TITLE OF INVENTION: Leukemia Inhibitory Factor Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/943,843
FILING DATE: 19920911
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2606-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
TELEFAX: 206-587-0606
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1097 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-943-843-6

Query Match 11.4%; Score 115; DB 1; Length 1097;
Best Local Similarity 23.4%; Pred. No. 0.00018;
Matches 36; Conservative 28; Mismatches 46; Indels 44; Gaps 7;

1 DPTLLIGSSLAQTCSI-----HGDTPGAAGELVTFNGRRLLPSELRLNLTSTL 50
258 DKVILVGSDFITFCVSOEKVLSALIGHTNCPLIHLDG-----ENV 297
51 ALALANLNGSRQSGDNLYCHARDGSLIAGSCLYGLPPEKPFNISCWSRNMKDLTCRMT 110
298 AIKIRNISVS-ASSGIVNVFTTEDN--IFGTIVFAGYPPDTPQOLNCEETHDKETICSMN 354
111 PG-----AHGETFLHTNYSLSKYLRLVRSE 135

DB 355 PGRVTAIVGPRATSYTIVE-SFSGKY-VRLKRAE 386

RESULT 7

US-08-347-003-2

Sequence 2, Application US/08347003

Patent No. 5785967

GENERAL INFORMATION:

APPLICANT: Gearling, David P.

APPLICANT: Beckmann, M. P.

TITLE OF INVENTION: Leukemia Inhibitory Factor Receptors

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/347,003

FILING DATE: 29-NOV-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/943,843

FILING DATE: 11-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Seese, Kathryn A.

REGISTRATION NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 2606-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-587-0430

TELEFAX: 206-587-0606

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1001 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-347-003-2

Query Match 11.4%; Score 115; DB 2; Length 1001;

Best Local Similarity 23.4%; Pred. No. 0.00016; Mismatches 46; Indels 44; Gaps 7;

Matches 36; Conservative 28; Mismatches 46; Indels 44; Gaps 7;

DB 1 DPTLLIGSSLOATCSI-----HGDTPGATAGLYMTFNGRRPLPSELRLINTSTL 50

DB 258 DKVILVSDITFCVSOEKVLSALIGHNCPILHLDG-----ENV 297

QY 51 ALAANLNGSRQSGDNLVCHARDGSIAGSCLVGLPPEKPFNISCNRMKDLTCWT 110

DB 298 AIKIRINISVS-ASSGTVNFTEDN--IFGVIFAGYPPDPPOQINCETHDKKEICSWN 354

QY 111 PG-----AHGETPLHTNYSLKVKRLVRS 135

DB 355 PGRVTAIVGPRATSYTIVE-SFSGKY-VRLKRAE 386

RESULT 8

US-08-347-003-6

Sequence 6, Application US/08347003

Patent No. 5785967

GENERAL INFORMATION:

APPLICANT: Gearling, David P.

APPLICANT: Beckmann, M. P.

TITLE OF INVENTION: Leukemia Inhibitory Factor Receptors

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/347,003

FILING DATE: 29-NOV-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/943,843

FILING DATE: 11-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Seese, Kathryn A.

REGISTRATION NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 2606-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-587-0430

TELEFAX: 206-587-0606

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 1097 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-347-003-6

Query Match 11.4%; Score 115; DB 2; Length 1097;

Best Local Similarity 23.4%; Pred. No. 0.00018; Mismatches 46; Indels 44; Gaps 7;

Matches 36; Conservative 28; Mismatches 46; Indels 44; Gaps 7;

DB 1 DPTLLIGSSLOATCSI-----HGDTPGATAGLYMTFNGRRPLPSELRLINTSTL 50

DB 258 DKVILVSDITFCVSOEKVLSALIGHNCPILHLDG-----ENV 297

QY 51 ALAANLNGSRQSGDNLVCHARDGSIAGSCLVGLPPEKPFNISCNRMKDLTCWT 110

DB 298 AIKIRINISVS-ASSGTVNFTEDN--IFGVIFAGYPPDPPOQINCETHDKKEICSWN 354

QY 111 PG-----AHGETPLHTNYSLKVKRLVRS 135

DB 355 PGRVTAIVGPRATSYTIVE-SFSGKY-VRLKRAE 386

RESULT 9

US-07-943-843-4

Sequence 4, Application US/07943843

Patent No. 5284755

GENERAL INFORMATION:

APPLICANT: Gearling, David P.

APPLICANT: Beckmann, M. P.

TITLE OF INVENTION: Leukemia Inhibitory Factor Receptors

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

OY 156 ----GPHSLXDLGSGHSP 171
DB 194 SNTAKVTAVNSLGSSSLP 213

RESULT 12

US-08-915-495-2
Sequence 2, Application US/08915495
Patent No. 5852176
GENERAL INFORMATION:
APPLICANT: Gubler, Ulrich A
APPLICANT: Presky, David H
TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,495
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,118
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Robert A.
REGISTRATION NUMBER: 35,682
REFERENCE/DOCKET NUMBER: CD 9195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-2863
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 862 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-915-495-2

Query Match 11.0%; Score 110.5; DB 2; Length 862;
Best Local Similarity 21.5%; Pred. No. 0.00042;
Matches 43; Conservative 36; Mismatches 62; Indels 59; Gaps 10;
OY 4 LILGSSLAQATCSHGDTPGATAGLY-----WTF-----NGRRLPELSRL-L 45
DB 41 ILIGSVNTVCSL-----KPGGCFHYSRNNLLIYKDRIRINFGHSLNSQVGLPL 94
OY 46 NSTLALALANLNGSRQSGDNLYCHARDGSIAGSCLYVGLPPEKPFNISCSRMK-D 104
DB 95 GTLLFVCKLACINSDEIQ-----ICGELIVGVAPPEPQNLSCIQKEQGT 140
OY 105 LITKRWTPGAGETFLHTNLSLKYKLVLNVSEKMXGVPCPESLMPY-----PQGP- 156
DB 141 VACTWRGR--DTHLYTEYLQ-----LSGPKNLTWQKCKDIYCYLDGFINLTPESPE 193
OY 156 ----GPHSLXDLGSGHSP 171
DB 194 SNTAKVTAVNSLGSSSLP 213

RESULT 13

US-07-923-976-4

Sequence 4, Application US/07923976

Patent No. 5574136
GENERAL INFORMATION:
APPLICANT: Nagata, Shigekazu
APPLICANT: Fukunaga, Rikio
TITLE OF INVENTION: DNA Encoding Granulocyte
NUMBER OF SEQUENCES: 8
TITLE OF INVENTION: Colony-Stimulating Factor Receptor
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones, Tullar & Cooper, P.C.
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,976
FILING DATE: 19920922
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74539/1990
FILING DATE: 23-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 176629/1990
FILING DATE: 03-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP91/00375
FILING DATE: 22-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Helwege, James W.
REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 514853
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-415-1508
TELEFAX: 703-415-1508
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 836 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-923-976-4

Query Match 9.9%; Score 100; DB 1; Length 836;
Best Local Similarity 26.7%; Pred. No. 0.0061;
Matches 51; Conservative 27; Mismatches 87; Indels 26; Gaps 11;
OY 2 PILLIGSSLAQATCSHGDTPGATAE-GLYWTNGRRLPELSRLN--TSTLALANLN 58
DB 34 PIVHGDPTTASCIIKONSHLDPEQILMRGAELQPGRGORLSDGOESITLPHLN 93
OY 59 GSRQSGDNLVCHARDG---TLASCLYVGLPPEKPFNISCSRMKMDICRWTPGKH 114
DB 94 HTQA---FLSCCLMWNLSLQILDOVELRAGTPPAIPNLSCIMLTSSLCOMEPGP- 149
OY 115 GETFLHTNYSLK-YKLR--LVKSEKHXKGV-----HC---EPSLMPYQGPGLHSLX 162
DB 149 -ETHLPSTFLKFSRNGCQTOGSDILDVCFKDKDSHCCIRKHLILY-QNMGITWQAE 206
OY 163 DIGSGHSPRL 173
DB 207 NALGTSMSPOL 217

RESULT 14

US-07-923-976-6
Sequence 6, Application US/07923976
Patent No. 5574136

GENERAL INFORMATION:

APPLICANT: Nagata, Shigekazu
 TITLE OF INVENTION: DNA Encoding Granulocyte
 TITLE OF INVENTION: Colony-Stimulating Factor Receptor
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones, Tullar & Cooper, P.C.
 STREET: P.O. Box 2266 Eads Station
 CITY: Arlington
 STATE: Virginia
 ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/923,976
 FILING DATE: 19920922
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 74539/1990
 FILING DATE: 23-MAR-1990
 APPLICATION NUMBER: JP 176629/1990
 FILING DATE: 03-JUL-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP91/00375
 FILING DATE: 22-MAR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Heliwege, James W.
 REGISTRATION NUMBER: 28,808
 REFERENCE/DOCKET NUMBER: 514853
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-415-1500
 TELEFAX: 703-415-1508

INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 771 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein

S-07-923-976-6

Query Match 9.9%; Score 100; DB 1; Length 771;
 Best Local Similarity 26.7%; Pred. No. 0.0054;

Matches 51; Conservative 27; Mismatches 87; Indels 26; Gaps 11;

2 PTLIGSSLAQATCSIHGDTPGATAE-GLYWTNGRRRLPSELRLN--TSLALALANLN 58
 34 PIVHGDPTTASCIIKONSHDPEPOLMRGAELQPGROQRSDGTQESITLPHLN 93
 59 GSROOSGDNLVCHARDG---ILASCLYVGLPPEKPFNISC-WSRNKMDLTCRWTPGAH 114
 94 HTQA---FLSCCLMWGNSLQILDVELEAGYPAIPHNLSCLIMULTTSSLICQWEPGP- 149
 115 GETFLHTNYSK-YKLR--LYRSEKHXMGV-----HC---EPLMTPQCPGPHLSIX 162
 149 -ETHLPSTLSTLSEKRNCGTQSGSILDCVAKDQSHCCIPRKHLILY-QNMGIWVOAE 206
 163 DLGGSHPRL 173
 207 NALGTSMSPOL 217

ESUIT 15
 S-07-923-976-8

Sequence 8, Application US/07923976
 Patent No. 5574136
 GENERAL INFORMATION:
 APPLICANT: Nagata, Shigekazu

APPLICANT: Fukunaga, Rikio
 TITLE OF INVENTION: DNA Encoding Granulocyte
 TITLE OF INVENTION: Colony-Stimulating Factor Receptor
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones, Tullar & Cooper, P.C.
 STREET: P.O. Box 2266 Eads Station
 CITY: Arlington
 STATE: Virginia
 ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/923,976
 FILING DATE: 19920922
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 74539/1990
 FILING DATE: 23-MAR-1990
 APPLICATION NUMBER: JP 176629/1990
 FILING DATE: 03-JUL-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP91/00375
 FILING DATE: 22-MAR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Heliwege, James W.
 REGISTRATION NUMBER: 28,808
 REFERENCE/DOCKET NUMBER: 514853
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-415-1500
 TELEFAX: 703-415-1508

INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 863 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-923-976-8

Query Match 9.9%; Score 100; DB 1; Length 863;
 Best Local Similarity 26.7%; Pred. No. 0.0063;

Matches 51; Conservative 27; Mismatches 87; Indels 26; Gaps 11;

2 PTLIGSSLAQATCSIHGDTPGATAE-GLYWTNGRRRLPSELRLN--TSLALALANLN 58
 34 PIVHGDPTTASCIIKONSHDPEPOLMRGAELQPGROQRSDGTQESITLPHLN 93
 59 GSROOSGDNLVCHARDG---ILASCLYVGLPPEKPFNISC-WSRNKMDLTCRWTPGAH 114
 94 HTQA---FLSCCLMWGNSLQILDVELEAGYPAIPHNLSCLIMULTTSSLICQWEPGP- 149
 115 GETFLHTNYSK-YKLR--LYRSEKHXMGV-----HC---EPLMTPQCPGPHLSIX 162
 149 -ETHLPSTLSTLSEKRNCGTQSGSILDCVAKDQSHCCIPRKHLILY-QNMGIWVOAE 206
 163 DLGGSHPRL 173
 207 NALGTSMSPOL 217

Search completed: September 16, 1999, 20:41:11
 Job time: 5440 sec

RESULT 2
ID W55011 standard; Protein: 413 AA.
AC W55011;
DE 29-SEP-1998 (first entry)
KW Novel haemopoietin receptor NR6.1 protein.
KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
KW cell survival; therapeutic; neuronal proliferation; drug screening;
KW Mouse.
OS Mus sp.
PN WO9811225-A2.
PD 19-MAR-1998.
PF 11-SEP-1997; G02479.
PR 11-SEP-1996; AU-002246.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PA (DZIE/) DZIEGLEWSKA H E.
PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willison T,
PI Zhang J.
DR WPI: 98-260970/23.
DR N-PSDB: V27140.
PT New isolated haemopoietin receptor - used for developing products
PT for modulating proliferation, differentiation and survival of cells,
PT e.g. neuronal cells
PS Claim 14; Page 77-81; 182pp; English.
CC The haemopoietin receptor (HR) NR6.1 is a form of the novel HR NR6.
CC Interaction between the novel HR and a ligand facilitates proliferation,
CC differentiation and survival of a wide variety of cells. The HR and its
CC derivatives can be used for modulating the activity of the receptors e.g.
CC to regulate development, maintenance or regeneration in an array of
CC different cells and tissues in vitro and in vivo. They can be present in
CC therapeutics used for modulating neuronal proliferation, differentiation
CC and survival. The products can also be used for detection and diagnosis,
CC e.g. for cancers or predisposition to cancers, or for drug screening.
SQ Sequence 413 AA;

Query Match 69.5%; Score 699; DB 1; Length 413;
Best Local Similarity 90.5%; Pred. No. 9.7e-67;
Matches 134; Conservative 0; Mismatches 8; Indels 6; Gaps 2;
QY 1 DPTLLIGSSLOATCSIHGTPGATAGLWTFNGRRRLPSELRLNTSTLALANLNGS 60
DB 50 DPTLLIGSSLOATCSIHGTPGATAGLWTFNGRRRLPSELRLNTSTLALANLNGS 109
QY 61 ROOSGDNLVCHARDGSIILAGSLVYGLPPEKPFNISCWSRNKMDLCRTWPAHGETFLH 120
DB 110 ROOSGDNLVCHARDGSIILAGSLVYGLPPEKPFNISCWSRNKMDLCRTWPAHGETFLH 169
QY 121 TNYSLKYRL-----VREXMKGVPH 143
DB 170 TNYSLKYRLMYGDNTECEYHTVG-PH 196
RESULT 3
ID W55012 standard; Protein: 425 AA.
AC W55012;
DE 29-SEP-1998 (first entry)
KW Novel haemopoietin receptor NR6.2 protein.
KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
KW cell survival; therapeutic; neuronal proliferation; drug screening;
KW Mouse.
OS Mus sp.
PN WO9811225-A2.
PD 19-MAR-1998.
PF 11-SEP-1997; G02479.
PR 11-SEP-1996; AU-002246.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PA (DZIE/) DZIEGLEWSKA H E.
PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willison T,

PI Zhang J.
DR WPI: 98-260970/23.
DR N-PSDB: V27141.
PT New isolated haemopoietin receptor - used for developing products
PT for modulating proliferation, differentiation and survival of cells,
PT e.g. neuronal cells
PS Claim 15; Page 84-87; 182pp; English.
CC The haemopoietin receptor (HR) NR6.2 is a form of the novel HR NR6.
CC Interaction between the novel HR and a ligand facilitates proliferation,
CC differentiation and survival of a wide variety of cells. The HR and its
CC derivatives can be used for modulating the activity of the receptors e.g.
CC to regulate development, maintenance or regeneration in an array of
CC different cells and tissues in vitro and in vivo. They can be present in
CC therapeutics used for modulating neuronal proliferation, differentiation
CC and survival. The products can also be used for detection and diagnosis,
CC e.g. for cancers or predisposition to cancers, or for drug screening.
SQ Sequence 425 AA;

Query Match 69.5%; Score 699; DB 1; Length 425;
Best Local Similarity 90.5%; Pred. No. 1e-66;
Matches 134; Conservative 0; Mismatches 8; Indels 6; Gaps 2;
QY 1 DPTLLIGSSLOATCSIHGTPGATAGLWTFNGRRRLPSELRLNTSTLALANLNGS 60
DB 50 DPTLLIGSSLOATCSIHGTPGATAGLWTFNGRRRLPSELRLNTSTLALANLNGS 109
QY 61 ROOSGDNLVCHARDGSIILAGSLVYGLPPEKPFNISCWSRNKMDLCRTWPAHGETFLH 120
DB 110 ROOSGDNLVCHARDGSIILAGSLVYGLPPEKPFNISCWSRNKMDLCRTWPAHGETFLH 169
QY 121 TNYSLKYRL-----VREXMKGVPH 143
DB 170 TNYSLKYRLMYGDNTECEYHTVG-PH 196

RESULT 4
ID W59804 standard; Protein: 425 AA.
AC W59804;
DE 26-OCT-1998 (first entry)
KW Nucleotide sequence of the murine U4 protein.
KW Murine; U4 protein; haematopoietin receptor superfamily;
KW cell proliferation; immune response; antibody; cell differentiation;
KW autoimmune disease; cancer; allergy.
OS Mus sp.
PN WO9831813-A1.
PD 23-JUL-1998.
PF 15-JAN-1998; U00334.
PR 16-JAN-1997; US-784863.
PA (GENY) GENETICS INST INC.
PI Collins M, Donaldson DD, Neben T, Whitters M;
PI WPI: 98-414109/35.
DR N-PSDB: V41688.
PT New nucleic acid encoding U4 haematopoietin receptor superfamily
PT chain - potentially useful, e.g. for modulating cell proliferation
PT or immune response, for treating cancer and autoimmune disease
PS Claim 9; Pages 26-27; 38pp; English.
CC This is the amino acid sequence of the murine U4 protein from the
CC haematopoietin receptor superfamily, used in the method of the
CC invention for the modulation of cell proliferation, or the immune
CC response. Transformed mammalian cells are used to produce recombinant
CC U4 protein. The U4 protein is used to screen for specific binding
CC agents, raise antibodies. It is also used as reagents for assays and
CC in pharmaceutical compositions which may modulate cell proliferation,
CC cell differentiation, and the immune system (e.g. for treating immune
CC deficiency, inherited or the result of infection, autoimmune diseases,
CC cancer, and allergy).
SQ Sequence 425 AA;

Query Match 69.1%; Score 695; DB 1; Length 425;

Best Local Similarity 89.9%; Pred. No. 2,7e-66;
Matches 133; Conservative 0; Mismatches 9; Indels 6; Gaps 2;

OY 1 DPTLLIGSSLOATCSHGTGPGATAGLWTFNGRRLPSELRLNTSTLALANLNGS 60
DB 50 DPTLLIGSSLOATCSHGTGPGATAGLWTFNGRRLPSELRLNTSTLALANLNGS 109
OY 61 ROOSGDNLVCHARDGSIAGSCLYVGLPPEKPFNISCSWRNKKDLTCRWTPGAAGETFLH 120
DB 110 ROOSGDNLVCHARDGSIAGSCLYVGLPPEKPFNISCSWRNKKDLTCRWTPGAAGETFLH 169
OY 121 TNYSLKYKRL-----VRSEKHXKGVPH 143
DB 170 TNYSLKYKRLWYGQDNTCEYHTVG-PH 196

RESULT 5

W70841
ID W70841 standard; Protein: 385 AA.
AC W70841;
DE 17-MAR-1999 (first entry)
DM Human zcytor5 variant.
KW zcytor5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
KW cardiac pathology; heart enlargement; zcytor5 ligand; variant.
OS Homo sapiens.
PN MO9849307-1.
PD 05-NOV-1998.
PF 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
PI MPI: 99-034662/03.
PT New mammalian cytokinin-like receptor zcytor5 - useful for, e.g.
PT down-regulating zcytor5 natural ligands or detecting cardiostrophin-1
PT in blood
PS Claim 1; Page 83-84; 55pp; English.
CC The present sequence represents a zcytor5 variant protein. zcytor5
CC is a cytokinin-like receptor. Soluble zcytor5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC thyroid, heart, and skeletal muscle for example to lessen the effect
CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
CC enlargement. zcytor5 could be used to detect cardiostrophin-1 in the
CC blood, and to discover other possible zcytor5 ligands. A probe
CC comprising zcytor5 DNA or RNA can be used to determine the presence
CC and integrity of the zcytor5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify zcytor5 and
CC therapeutically to modify zcytor5 ligand effects.
SQ Sequence 385 AA;

Query Match 69.0%; Score 694; DB 1; Length 385;
Best Local Similarity 89.9%; Pred. No. 3e-66;
Matches 133; Conservative 0; Mismatches 9; Indels 6; Gaps 2;

OY 1 DPTLLIGSSLOATCSHGTGPGATAGLWTFNGRRLPSELRLNTSTLALANLNGS 60
DB 10 DPTLLIGSSLOATCSHGTGPGATAGLWTFNGRRLPSELRLNTSTLALANLNGS 69
OY 61 ROOSGDNLVCHARDGSIAGSCLYVGLPPEKPFNISCSWRNKKDLTCRWTPGAAGETFLH 120
DB 70 ROOSGDNLVCHARDGSIAGSCLYVGLPPEKPFNISCSWRNKKDLTCRWTPGAAGETFLH 129
OY 121 TNYSLKYKRL-----VRSEKHXKGVPH 143
DB 130 TNYSLKYKRLWYGQDNTCEYHTVG-PH 156

RESULT 6

W70862
ID W70862 standard; Protein: 425 AA.
AC W70862;
DE 17-MAR-1999 (first entry)
DM Rat zcytor5 protein.
KW zcytor5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
KW cardiac pathology; heart enlargement; zcytor5 ligand.
OS Rattus sp.
PN MO9849307-1.
PD 05-NOV-1998.
PF 01-MAY-1998; U08865.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
PI MPI: 99-034662/03.
PT New mammalian cytokinin-like receptor zcytor5 - useful for, e.g.
PT down-regulating zcytor5 natural ligands or detecting cardiostrophin-1
PT in blood
PS Claim 1; Page 75-76; 55pp; English.
CC The present sequence represents a protein designated zcytor5, which is
CC a cytokinin-like receptor. Soluble zcytor5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC thyroid, heart, and skeletal muscle for example to lessen the effect
CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
CC enlargement. zcytor5 could be used to detect cardiostrophin-1 in the
CC blood, and to discover other possible zcytor5 ligands. A probe
CC comprising zcytor5 DNA or RNA can be used to determine the presence
CC and integrity of the zcytor5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify zcytor5 and
CC therapeutically to modify zcytor5 ligand effects.
SQ Sequence 425 AA;

Query Match 69.0%; Score 694; DB 1; Length 425;
Best Local Similarity 89.9%; Pred. No. 3.5e-66;
Matches 133; Conservative 0; Mismatches 9; Indels 6; Gaps 2;

OY 1 DPTLLIGSSLOATCSHGTGPGATAGLWTFNGRRLPSELRLNTSTLALANLNGS 60
DB 50 DPTLLIGSSLOATCSHGTGPGATAGLWTFNGRRLPSELRLNTSTLALANLNGS 109
OY 61 ROOSGDNLVCHARDGSIAGSCLYVGLPPEKPFNISCSWRNKKDLTCRWTPGAAGETFLH 120
DB 110 ROOSGDNLVCHARDGSIAGSCLYVGLPPEKPFNISCSWRNKKDLTCRWTPGAAGETFLH 169
OY 121 TNYSLKYKRL-----VRSEKHXKGVPH 143
DB 170 TNYSLKYKRLWYGQDNTCEYHTVG-PH 196

RESULT 7

W55014
ID W55014 standard; Protein: 278 AA.
AC W55014;
DE 02-OCT-1998 (first entry)
DM Protein sequence of products generated by 5N race of brain cDNA.
KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
KW cell survival; therapeutic; neuronal proliferation; drug screening;
KW Mouse.
PN MO9811225-A2.
PD 19-MAR-1998.
PF 11-SEP-1997; G02479.
PR 11-SEP-1996; AU-002246.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PA (DZIEV) DZIELEWSKA H E.
PI Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,

PI Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
 PI Zhang J;
 DR WPI: 98-260970/23.
 DR N-PSDB: V27143.
 PT New isolated haemopoietin receptor - used for developing products
 for modulating proliferation, differentiation and survival of cells,
 e.g. neuronal cells
 PS Claim 17; Page 93-95; 182pp; English.
 CC The protein sequence was generated by a 5N RACE of brain cDNA using
 NR6 specific primers. NR6 is a novel Haemopoietin receptor (HR).
 CC Interaction between the novel HR and a ligand facilitates proliferation,
 differentiation and survival of a wide variety of cells. The HR and its
 derivatives can be used for modulating the activity of the receptors e.g.
 CC to regulate development, maintenance or regeneration in an array of
 different cells and tissues in vitro and in vivo. They can be present in
 CC therapeutics used for modulating neuronal proliferation, differentiation
 CC and survival. The products can also be used for detection and diagnosis,
 e.g. for cancers or predisposition to cancers, or for drug screening.
 SQ Sequence 278 AA;

Query Match 68.9%; Score 693; DB 1; Length 278;
 Best Local Similarity 90.5%; Pred. No. 2.5e-66;
 Matches 133; Conservative 0; Mismatches 8; Indels 6; Gaps 2;

OY 2 PTLIGSSLOATCSIHGDPGATAGLYTFNGRRLPSELRLNTSTLALANLNGSR 61
 DB 1 PTLIGSSLOATCSIHGDPGATAGLYTFNGRRLPSELRLNTSTLALANLNGSR 60
 OY 62 QOSGDNLYCHARDGSIILAGSCLYVGLPEKPEPNISCSRMKMDLTCRMTPGAHGETFLH 121
 DB 61 QOSGDNLYCHARDGSIILAGSCLYVGLPEKPEPNISCSRMKMDLTCRMTPGAHGETFLH 120
 OY 122 TNSLKYKRL-----VRSEKHXKGVPH 143
 DB 121 TNSLKYKRLMYGQDNCEHYHTVG-PH 146

RESULT 8
 ID W59805
 AC W59805 standard; Protein; 408 AA.
 DT 26-OCT-1998 (first entry)
 DE Amino acid sequence of the human U4 protein.
 KW Human U4 protein; haematopoietin receptor superfamily;
 KW cell proliferation; immune response; antibody; cell differentiation;
 KW autoimmune disease; cancer; allergy.
 OS Homo sapiens.
 PN WC9831811-A1.
 PF 23-JUL-1998.
 PF 15-JAN-1998; U00334.
 PF 16-JAN-1997; US-784863.
 PA (GENY) GENETICS INST INC.
 PI Collins M, Donaldson DD, Neben T, Whitters M;
 DR WPI: 98-414109/35.
 DR N-PSDB: V41689.
 PT New nucleic acid encoding U4 haematopoietin receptor superfamily
 PT chain - potentially useful, e.g. for modulating cell proliferation
 PT or immune response, for treating cancer and autoimmune disease
 PS Claim 9; Pages 29-30; 38pp; English.
 CC This is the amino acid sequence of the human U4 protein from the
 CC haematopoietin receptor superfamily, used in the method of the
 CC invention for the modulation of cell proliferation, or the immune
 CC response. Transformed mammalian cells are used to produce recombinant
 CC U4 protein. The U4 protein is also used as reagents for assays and
 CC agents, raise antibodies. It is also used as reagents for assays and
 CC as tissue markers for isolation of cognate ligands and receptors, and
 CC in pharmaceutical compositions which may modulate cell proliferation,
 CC cell differentiation, and the immune system (e.g. for treating immune
 CC deficiency, inherited or the result of infection, autoimmune diseases,
 CC cancer, and allergy).
 SQ Sequence 408 AA;

Query Match 65.4%; Score 658; DB 1; Length 408;
 Best Local Similarity 84.5%; Pred. No. 2.3e-62;
 Matches 125; Conservative 4; Mismatches 13; Indels 6; Gaps 2;

OY 1 DPTLLIGSSLOATCSIHGDPGATAGLYTFNGRRLPSELRLNTSTLALANLNGS 60
 DB 33 DPTLLIGSSLOATCSIHGDPGATAGLYTFNGRRLPSELRLNTSTLALANLNGS 92
 OY 61 QOSGDNLYCHARDGSIILAGSCLYVGLPEKPEPNISCSRMKMDLTCRMTPGAHGETFLH 120
 DB 93 QOSGDNLYCHARDGSIILAGSCLYVGLPEKPEPNISCSRMKMDLTCRMTPGAHGETFLH 152
 OY 121 TNSLKYKRL-----VRSEKHXKGVPH 143
 DB 153 TNSLKYKRLMYGQDNCEHYHTVG-PH 179

RESULT 9
 ID W70848
 AC W70848 standard; Protein; 389 AA.
 DT 17-MAR-1999 (first entry)
 DE Human zcyto5 variant.
 KW Zcyto5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 KW cardiac pathology; heart enlargement; zcyto5 ligand; variant.
 OS Homo sapiens.
 PN WC9849307-A1.
 PF 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PF 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams KL, Foster DC, Gilbert T, Jeinberg AC, Leher JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcyto5 - useful for e.g.
 PT down-regulating zcyto5 natural ligands or detecting cardiostrophin-1
 PT in blood
 PS Claim 1; Page 92-93; 55pp; English.
 CC The present sequence represents a zcyto5 variant protein. Zcyto5
 CC is a cytokinin-like receptor. Soluble zcyto5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcyto5 could be used to detect cardiostrophin-1 in the
 CC blood, and to discover other possible zcyto5 ligands. A probe
 CC comprising zcyto5 DNA or RNA can be used to determine the presence
 CC and integrity of the zcyto5 gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcyto5 and the
 CC therapeutically to modify zcyto5 ligand effects.
 SQ Sequence 389 AA;

Query Match 65.4%; Score 658; DB 1; Length 389;
 Best Local Similarity 84.5%; Pred. No. 2.2e-62;
 Matches 125; Conservative 4; Mismatches 13; Indels 6; Gaps 2;

OY 1 DPTLLIGSSLOATCSIHGDPGATAGLYTFNGRRLPSELRLNTSTLALANLNGS 60
 DB 10 DPTLLIGSSLOATCSIHGDPGATAGLYTFNGRRLPSELRLNTSTLALANLNGS 69
 OY 61 QOSGDNLYCHARDGSIILAGSCLYVGLPEKPEPNISCSRMKMDLTCRMTPGAHGETFLH 120
 DB 70 QOSGDNLYCHARDGSIILAGSCLYVGLPEKPEPNISCSRMKMDLTCRMTPGAHGETFLH 129
 OY 121 TNSLKYKRL-----VRSEKHXKGVPH 143
 DB 130 TNSLKYKRLMYGQDNCEHYHTVG-PH 156

RESULT 10
W70849 ID W70849 standard; Protein; 389 AA.
AC W70849; 17-MAR-1999 (first entry)
DE Human zcytoxin-like receptor; down-regulation; growth factor;
KM zcytoxin; cytoxin-like receptor; skeletal muscle; cardiostrophin-1;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
OS cardiac pathology; heart enlargement; zcytoxin ligand; variant.
PN Homo sapiens.
MO9849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; US-074721.
PR 13-FEB-1998; US-074721.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.
PR 13-FEB-1998; US-023890.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
PI MPI; 99-034662/03.
PT New mammalian cytoxin-like receptor zcytoxin - useful for, e.g.
PT down-regulating zcytoxin natural ligands or detecting cardiostrophin-1
in blood
PS Claim 1: Page 94-95; 55pp; English.
CC The present sequence represents a zcytoxin variant protein. zcytoxin
is a cytoxin-like receptor. Soluble zcytoxin may be administered to
down-regulate the effects of a growth and/or maintenance factor in
thyroid, heart, and skeletal muscle for example to lessen the effect
of cardiostrophin-1 on cardiac pathologies, so preventing heart
enlargement. zcytoxin could be used to detect cardiostrophin-1 in the
blood, and to discover other possible zcytoxin ligands. A probe
comprising zcytoxin DNA or RNA can be used to determine the presence
and integrity of the zcytoxin gene on chromosome 19. Antibodies and the
anti-idiotypic antibody could be used to purify zcytoxin and
therapeutically to modify zcytoxin ligand effects.
SO Sequence 389 AA.

Query Match 65.4%; Score 658; DB 1; Length 389;
Best Local Similarity 84.5%; Pred. No. 2.2e-62;
Matches 125; Conservative 4; Mismatches 13; Indels 6; Gaps 2;

QY 1 DPTLLGSSIAQATCSHGDPTAGTAEGLVTFNGRRRLPSELSTLNTSTLALANLNGS 60
DB 10 DPTLLGSSIAQATCSHGDPTAGTAEGLVTFNGRRRLPSELSTLNTSTLALANLNGS 69
QY 61 ROOSGNLVCHARDGSLIAGSCLVGLPPEKPNISCSNMMDLTCRTPGAHGETFLH 120
DB 70 ROOSGNLVCHARDGSLIAGSCLVGLPPEKPNISCSNMMDLTCRTPGAHGETFLH 129
QY 121 TNSLTKYKRL-----VRSEKHXKGVPH 143
DB 130 TNSLTKYKRLRWYGQDWTCEHYHTVG-PH 156

RESULT 11
W70850 ID W70850 standard; Protein; 389 AA.
AC W70850; 17-MAR-1999 (first entry)
DE Human zcytoxin variant.
KM zcytoxin; cytoxin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
OS cardiac pathology; heart enlargement; zcytoxin ligand; variant.
PN Homo sapiens.
MO9849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; US-074721.
PR 13-FEB-1998; US-045287.
PR 01-MAY-1997; US-850030.
PR 01-MAY-1997; US-045287.
PR 01-MAY-1997; US-850030.

PR 13-FEB-1998; US-023890.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
PI MPI; 99-034662/03.
PT New mammalian cytoxin-like receptor zcytoxin - useful for, e.g.
PT down-regulating zcytoxin natural ligands or detecting cardiostrophin-1
in blood
PS Claim 1: Page 95-96; 55pp; English.
CC The present sequence represents a zcytoxin variant protein. zcytoxin
is a cytoxin-like receptor. Soluble zcytoxin may be administered to
down-regulate the effects of a growth and/or maintenance factor in
thyroid, heart, and skeletal muscle for example to lessen the effect
of cardiostrophin-1 on cardiac pathologies, so preventing heart
enlargement. zcytoxin could be used to detect cardiostrophin-1 in the
blood, and to discover other possible zcytoxin ligands. A probe
comprising zcytoxin DNA or RNA can be used to determine the presence
and integrity of the zcytoxin gene on chromosome 19. Antibodies and the
anti-idiotypic antibody could be used to purify zcytoxin and
therapeutically to modify zcytoxin ligand effects.
SO Sequence 389 AA.

Query Match 65.4%; Score 658; DB 1; Length 389;
Best Local Similarity 84.5%; Pred. No. 2.2e-62;
Matches 125; Conservative 4; Mismatches 13; Indels 6; Gaps 2;

QY 1 DPTLLGSSIAQATCSHGDPTAGTAEGLVTFNGRRRLPSELSTLNTSTLALANLNGS 60
DB 10 DPTLLGSSIAQATCSHGDPTAGTAEGLVTFNGRRRLPSELSTLNTSTLALANLNGS 69
QY 61 ROOSGNLVCHARDGSLIAGSCLVGLPPEKPNISCSNMMDLTCRTPGAHGETFLH 120
DB 70 ROOSGNLVCHARDGSLIAGSCLVGLPPEKPNISCSNMMDLTCRTPGAHGETFLH 129
QY 121 TNSLTKYKRL-----VRSEKHXKGVPH 143
DB 130 TNSLTKYKRLRWYGQDWTCEHYHTVG-PH 156

RESULT 12
W70851 ID W70851 standard; Protein; 389 AA.
AC W70851; 17-MAR-1999 (first entry)
DE Human zcytoxin variant.
KM zcytoxin; cytoxin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
OS cardiac pathology; heart enlargement; zcytoxin ligand; variant.
PN Homo sapiens.
MO9849307-A1.
PD 05-NOV-1998.
PF 01-MAY-1998; US-074721.
PR 13-FEB-1998; US-045287.
PR 01-MAY-1997; US-850030.
PR 01-MAY-1997; US-023890.
PR 13-FEB-1998; US-023890.
PA (ZYMO) ZYMOGENETICS INC.
PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
PI Lok S, Presnell SR, Whitmore TE;
PI MPI; 99-034662/03.
PT New mammalian cytoxin-like receptor zcytoxin - useful for, e.g.
PT down-regulating zcytoxin natural ligands or detecting cardiostrophin-1
in blood
PS Claim 1: Page 96-97; 55pp; English.
CC The present sequence represents a zcytoxin variant protein. zcytoxin
is a cytoxin-like receptor. Soluble zcytoxin may be administered to
down-regulate the effects of a growth and/or maintenance factor in
thyroid, heart, and skeletal muscle for example to lessen the effect
of cardiostrophin-1 on cardiac pathologies, so preventing heart
enlargement. zcytoxin could be used to detect cardiostrophin-1 in the
blood, and to discover other possible zcytoxin ligands. A probe
comprising zcytoxin DNA or RNA can be used to determine the presence

CC and integrity of the zcytors gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcytors and
 CC therapeutically to modify zcytors ligand effects.
 SQ Sequence 389 AA;

Query Match 65.4%; Score 658; DB 1; Length 389;
 Best Local Similarity 84.5%; Pred. No. 2.2e-62;

Matches 125; Conservative 4; Mismatches 13; Indels 6; Gaps 2;

QY 1 DPTLLIGSLQATCSIHGDTPGATAGLYWTFNGRRLPELSRLNTSTLALALANLNGS 60
 DB 10 DPTLLIGSLQATCSVHGDPGATAGLYWTFNGRRLPELSRVNASTLALALANLNGS 69
 QY 61 ROOSGDNLYCHARDGSIILAGSCLYVGLPPEKPNISCSRNKMDLTCRTPGAHGETFLH 120
 DB 70 ROOSGDNLYCHARDGSIILAGSCLYVGLPPEKPNISCSRNKMDLTCRTPGAHGETFLH 129
 QY 121 TNSLKYKRLR-----VRSEKHXMGVPH 143
 DB 130 TNSLKYKRLRWYGQDNTCEYHTVG-PH 156

RESULT 13

ID W70852 standard; Protein; 389 AA.

AC W70852, 17-MAR-1999 (first entry)
 DE Human zcytors variant.
 KW zcytors; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 KW cardiac pathology; heart enlargement; zcytors ligand; variant.
 OS Homo sapiens.
 PN MO9849307-AL.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE,
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcytors - useful for, e.g.
 PT down-regulating zcytors natural ligands or detecting cardiostrophin-1
 PT in blood
 PS Claim 1; Page 98-99; 55pp; English.
 CC The present sequence represents a zcytors variant protein. zcytors
 CC is a cytokinin-like receptor. Soluble zcytors may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcytors could be used to detect cardiostrophin-1 in the
 CC blood, and to discover other possible zcytors ligands. A probe
 CC comprising zcytors DNA or RNA can be used to determine the presence
 CC and integrity of the zcytors gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcytors and
 CC therapeutically to modify zcytors ligand effects.
 SQ Sequence 389 AA;

Query Match 65.4%; Score 658; DB 1; Length 389;
 Best Local Similarity 84.5%; Pred. No. 2.2e-62;

Matches 125; Conservative 4; Mismatches 13; Indels 6; Gaps 2;

QY 1 DPTLLIGSLQATCSIHGDTPGATAGLYWTFNGRRLPELSRLNTSTLALALANLNGS 60
 DB 10 DPTLLIGSLQATCSVHGDPGATAGLYWTFNGRRLPELSRVNASTLALALANLNGS 69
 QY 61 ROOSGDNLYCHARDGSIILAGSCLYVGLPPEKPNISCSRNKMDLTCRTPGAHGETFLH 120
 DB 70 ROOSGDNLYCHARDGSIILAGSCLYVGLPPEKPNISCSRNKMDLTCRTPGAHGETFLH 129

QY 121 TNSLKYKRLR-----VRSEKHXMGVPH 143
 DB 130 TNSLKYKRLRWYGQDNTCEYHTVG-PH 156

RESULT 14

ID W70853 standard; Protein; 389 AA.

AC W70853, 17-MAR-1999 (first entry)
 DE Human zcytors variant.
 KW zcytors; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 KW cardiac pathology; heart enlargement; zcytors ligand; variant.
 OS Homo sapiens.
 PN MO9849307-AL.
 PD 05-NOV-1998.
 PF 01-MAY-1998; U08865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jelmeberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE,
 DR WPI: 99-034662/03.
 PT New mammalian cytokinin-like receptor zcytors - useful for, e.g.
 PT down-regulating zcytors natural ligands or detecting cardiostrophin-1
 PT in blood
 PS Claim 1; Page 99-100; 55pp; English.
 CC The present sequence represents a zcytors variant protein. zcytors
 CC is a cytokinin-like receptor. Soluble zcytors may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. zcytors could be used to detect cardiostrophin-1 in the
 CC blood, and to discover other possible zcytors ligands. A probe
 CC comprising zcytors DNA or RNA can be used to determine the presence
 CC and integrity of the zcytors gene on chromosome 19. Antibodies and the
 CC anti-idiotypic antibody could be used to purify zcytors and
 CC therapeutically to modify zcytors ligand effects.
 SQ Sequence 389 AA;

Query Match 65.4%; Score 658; DB 1; Length 389;
 Best Local Similarity 84.5%; Pred. No. 2.2e-62;

Matches 125; Conservative 4; Mismatches 13; Indels 6; Gaps 2;

QY 1 DPTLLIGSLQATCSIHGDTPGATAGLYWTFNGRRLPELSRLNTSTLALALANLNGS 60
 DB 10 DPTLLIGSLQATCSVHGDPGATAGLYWTFNGRRLPELSRVNASTLALALANLNGS 69
 QY 61 ROOSGDNLYCHARDGSIILAGSCLYVGLPPEKPNISCSRNKMDLTCRTPGAHGETFLH 120
 DB 70 ROOSGDNLYCHARDGSIILAGSCLYVGLPPEKPNISCSRNKMDLTCRTPGAHGETFLH 129
 QY 121 TNSLKYKRLR-----VRSEKHXMGVPH 143
 DB 130 TNSLKYKRLRWYGQDNTCEYHTVG-PH 156

RESULT 15

ID W70840 standard; Protein; 392 AA.

AC W70840, 17-MAR-1999 (first entry)
 DE Human zcytors variant.
 KW zcytors; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 KW cardiac pathology; heart enlargement; zcytors ligand; variant.
 OS Homo sapiens.
 PN MO9849307-AL.

PD 05-NOV-1998.
 PF 01-MAY-1998; 008865.
 PR 13-FEB-1998; US-074721.
 PR 01-MAY-1997; US-045287.
 PR 01-MAY-1997; US-850030.
 PR 13-FEB-1998; US-023890.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Foster DC, Gilbert T, Jernberg AC, Lehner JM,
 PI Lok S, Presnell SR, Whitmore TE;
 DR MPI: 99-034662/03
 PT New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
 PT down-regulating Zcytor5 natural ligands or detecting cardiotrophin-1
 PT in blood
 PS Claim 1: Page 81-82; 55pp; English.
 CC The present sequence represents a Zcytor5 variant protein. Zcytor5
 CC is a cytokinin-like receptor. Soluble Zcytor5 may be administered to
 CC down-regulate the effects of a growth and/or maintenance factor in
 CC thyroid, heart, and skeletal muscle for example to lessen the effect
 CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
 CC enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the
 CC blood, and to discover other possible Zcytor5 ligands. A probe
 CC comprising Zcytor5 DNA or RNA can be used to determine the presence
 CC and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the
 CC anti-Idiotypic antibody could be used to purify Zcytor5 and
 CC therapeutically to modify Zcytor5 ligand effects.
 SQ Sequence 392 AA;

Query Match 65.4%; Score 658; DB 1; Length 392;
 Best Local Similarity 84.5%; Pred. No. 2.2e-62;
 Matches 125; Conservative 4; Mismatches 13; Indels 6; Gaps 2;

QY 1 DPTLLIGSSLOATCSIHGDPGATAGLTYTFNGRRPSELSTRLNTSTALALANLNGS 60
 DB 13 DPTLLIGSSILATCSVHGDPGATAGLTYTFNGRRPSELSTRLNTSTALALANLNGS 72
 QY 61 ROOSGDNLYCHARDGSIAGSCLYVGLPPEKPFNISCWSRNMKDLTCRMTPGAHEFELH 120
 DB 73 ROSSGDNLYCHARDGSIAGSCLYVGLPPEKPFNISCWSRNMKDLTCRMTPGAHEFELH 132
 QY 121 TNYSLKYLRL-----VRSEKHXKGVPH 143
 DB 133 TNYSLKYLRLRWYGODNTCEEYHTVG-PH 159

Search completed: September 17, 1999, 03:08:16
 Job time: 307 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:42:10 ; Search time 49.27 Seconds

(Without alignments)
151.252 Million cell updates/sec

Title: US-09-037-657-29
Perfect score: 1006

Sequence: 1 DPTLLIGSSLSQATCSIRHGT.....SHQSPRLSKIXCPHTGCPGR 186

Scoring table: BLOSUM62

Searched: 122810 seqs, 40065486 residues

Database :
1: PIR_60:*
2: PIR_2:*
3: PIR_3:*
4: PIR_4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	144	14.3	917	2	glycoprotein 130 -
2	133.5	13.3	918	2	membrane glycoprot
3	130	12.9	918	2	interleukin-6 sign
4	115	11.4	1097	2	leukemia inhibitor
5	112.5	11.2	1092	2	differentiation-st
6	112.5	11.2	719	2	differentiation-st
7	107.5	10.7	422	2	interleukin-11 rec
8	101.5	10.1	622	2	prolactin receptor
9	100	9.9	771	2	granulocyte colony
10	100	9.9	771	2	granulocyte colony
11	100	9.9	771	2	granulocyte colony
12	98	9.7	581	2	granulocyte colony
13	95	9.4	206	2	prolactin receptor
14	95	9.4	616	2	prolactin receptor
15	95	9.4	97	2	prolactin receptor
16	93.5	9.3	432	2	pseudo-prolactin r
17	93	9.2	460	2	interleukin-11 rec
18	93	9.2	440	2	interleukin-6 rece
19	91.5	9.1	856	2	interleukin-6 rece
20	91	9.0	880	2	protein-tyrosine k
21	91	9.0	876	2	protein-tyrosine k
22	90.5	9.0	837	2	granulocyte colony
23	89	8.8	462	1	interleukin-6 rece
24	89	8.8	830	2	prolactin receptor
25	88	8.7	880	2	prolactin receptor
26	88	8.7	303	2	prolactin receptor
27	88	8.7	292	2	prolactin receptor
28	87	8.6	608	2	prolactin receptor
29	87	8.6	831	2	prolactin receptor
30	85.5	8.5	894	1	prolactin receptor
31	85.5	8.5	610	2	protein-tyrosine k
32	85.5	8.5	150	2	lactogen receptor
33	85.5	8.5	610	2	lactogen receptor
34	85.5	8.5	412	2	prolactin receptor
35	85.5	8.5	310	2	prolactin receptor
36	82.5	8.2	754	2	finger protein neu
37	81	8.1	372	1	ciliary neurotroph
38	81	8.1	547	1	intercellular adhe
39	81	8.1	372	2	ciliary neurotroph

40	80	8.0	468	1	A41242	interleukin-6 rece
41	79.5	7.9	834	2	S66498	M-sema F protein p
42	79.5	7.9	894	2	JC4797	leptin receptor pr
43	79.5	7.9	1162	2	PC4184	leptin receptor, O
44	79.5	7.9	805	3	JC4897	leptin receptor, O
45	79	7.9	630	2	I51086	prolactin receptor

ALIGNMENTS

RESULT 1
149699
glycoprotein 130 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Aug-1996 #sequence, revision 02-Aug-1996 #text_change 07-Feb-1997
C/Accession: 149699; 148370
R:Salto, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.
J. Immunol. 148, 4066-4071, 1992
A>Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp
A/Reference number: 148370; MVID:92291532
A/Accession: 149699
A>Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-917 <RES>
A/Cross-references: GB:M83336; NID:9193591; PID:9193592
A/Accession: 148370
A>Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-917 <RES>
A/Cross-references: EMBL:X62646; NID:9840816; PID:9840817
C/Genetics:
C/Gene: gp130
C/Keywords: glycoprotein

Query Match 14.3%; Score 144; DB 2; Length 917;
Best local similarity 26.5%; Pred. No. 3e-06;
Matches 39; Conservative 26; Mismatches 70; Indels 12; Gaps 3;

QY 2 PTLIGSSLSQATCSIRHGT---DTGATREGILYTFNGRRRLPSESLRLNLTSLALANLN 58
DB 36 PVOQSGNFTALCYLKEACIQHYVNSYTVMTNAAVREQVTYINRTTSVTFTDVV 95
QY 59 GSRQSGDNLVCHARDGSIAGSLYGLPPEKFNISCSRMKNDTCWTEGANGETP 118
DB 96 LPVQGLCNLTLSRGQIEQNYGYTMTSGFPDPKPTNITLCIVNEGKNLCCWDPR--ETI 153
QY 119 LHTNYSIKYRLRLVRSEKHXKGVPHCE 145
DB 154 LEMNYTLK-----SEWATEKFPDQ 173

RESULT 2
A36337
membrane glycoprotein gp130 precursor - human
C:Species: Homo sapiens (man)
C>Date: 12-Apr-1991 #sequence, revision 12-Apr-1991 #text_change 24-Sep-1998
C/Accession: A36337
R:Hibi, M.; Murakami, M.; Salto, M.; Hirano, T.; Taga, T.; Kishimoto, T.
Cell 63, 1149-1157, 1990
A>Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
A/Reference number: A36337; MVID:91084844
A/Accession: A36337
A>Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-918 <HIB>
A/Cross-references: GB:M57230; NID:9186353; PID:9186354
C/Genetics:
A/Gene: GDB:IL6ST; GP130
A/Cross-references: GDB:126725; OMIM:600694
A/Map position: 5q11-5q11
C/Keywords: glycoprotein; membrane protein

C:Keywords: receptor

Query Match 11.2%; Score 112.5; DB 2; Length 719;

Best Local Similarity 25.4%; Pred. No. 0.0028;

Matches 29; Conservative 27; Mismatches 41; Indels 17; Gaps 5;

DB 1 DPTLLIGSLQATCSHGDTPGATAEGLYWTFNGRRRLPSELRLINT--STLALANLNLN 58

DB 253 DKVYLAASNNITICM-----SPTKVLSC-----QIGNTLRPLHLHGYVAIHILNIP 300

DB 59 GSRQSGDNLYCHARDGSIAGSCLYVGLPPEKPNISCSWRNKKDLTCRWTPG 112

DB 301 VS-ENSGTNIIFITDD--VYGVTFAGYPPDPVQKISCETHDIKEITCSWNP 351

RESULT 7

Interleukin-11 receptor alpha chain - human

C:Species: Homo sapiens (man)

C:Date: 29-May-1998 #sequence, revision 29-May-1998 #text, change 16-Dec-1998

C:Accession: I37891; G01970; G01971

C:Cherel M.; Sorel, M.; Lebeau, B.; Dubois, S.; Moreau, J.F.; Bataille, R.; Mnyielie,

A:Title: Molecular cloning of two isoforms of a receptor for the human hematopoietic cy

A:Reference number: I37891, PMID:95399754

A:Accession: I37891

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-422 <RES>

A:Cross-references: EMBL:238102; NID:9995653; PID:9995654

A:Van Leuven, F.

A:Reference number: G08959

A:Accession: G01970

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-422 <VAN>

A:Cross-references: EMBL:032323; NID:9975334; PID:9975335

A:Van Leuven, F.

A:Reference number: G08961

A:Accession: G01971

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-422 <VAN>

A:Cross-references: EMBL:032324; NID:9975336; PID:9975337

A:Genetics:

A:Antons: 34/1; 54/2; 111/1; 149/2; 160/2; 216/1; 270/3; 318/1; 358/1; 390/2; 418/1

A:Superfamily: cytokine receptor homology

F:120-310/Domain: cytokine receptor homology <CRS>

Query Match 10.7%; Score 107.5; DB 2; Length 422;

Best Local Similarity 26.3%; Pred. No. 0.0046;

Matches 40; Conservative 24; Mismatches 67; Indels 21; Gaps 7;

DB 7 GSSLQATCSHGDTPGATA-EGLYWTFNG--RRLPSELRLINTSTLALANLNGSROQ 63

DB 41 GRSVKLCC-----PGVTAGDPVSMFRDGEPLKLGDPDSGLHETLVAQDSTDEGR--- 92

DB 64 SGONLVCHARDGSIAGSCLYVGLPPEKPNISCSWRNKKDLTCRWTPGAGHGEFLHTN 123

DB 92 ----YICQILDGALGCTVTQLQISPPARPV-VSCQADYENFSCWSPSO--ISGLPTRY 144

DB 124 SLKYKLLVSEKHXMGVPHCEPSLMPYPOG 155

DB 145 LTVYRKKTVLGADSGQRSPSTGP--WCPDP 174

RESULT 8

A40144

prolactin receptor long form precursor, hepatoma and breast cancer cells - human

C:Species: Homo sapiens (man)

C:Date: 17-Jul-1992 #sequence, revision 17-Jul-1992 #text, change 24-Sep-1998

C:Accession: A40144

R:Bouthin, J.M.; Edey, M.; Shirots, M.; Jolicoeur, C.; Lesueur, L.; All, S.; Gould, D

Mol. Endocrinol. 3, 1455-1461, 1989

A:Title: Identification of a cDNA encoding a long form of prolactin receptor in human

A:Reference number: A40144, PMID:90114212

A:Accession: A40144

A:Molecule type: mRNA

A:Residues: 1-622 <BDU>

A:Cross-references: GB:M31661; NID:9190361; PID:9190362

A:Genetics:

A:Gene: GDB:PRLR

A:Map position: 5p13.3-5p13.1

A:Keywords: glycoprotein; transmembrane protein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-622/Product: prolactin receptor, long form #status predicted <MAP>

F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.1%; Score 101.5; DB 2; Length 622;

Best Local Similarity 46.2%; Pred. No. 0.028;

Matches 24; Conservative 3; Mismatches 22; Indels 3; Gaps 2;

DB 77 ILASCLYVGLPPEKPNISCSWRNKKDLTCRWTPGAGHGEFLHTNYSKY 127

DB 15 LFLNTCLNLGLPPEKPNISCSWRNKKDLTCRWTPGAGHGEFLHTNYSKY 64

RESULT 9

granulocyte colony-stimulating factor receptor D7 precursor - human

C:Species: Homo sapiens (man)

C:Date: 12-Feb-1993 #sequence, revision 12-Feb-1993 #text, change 12-Dec-1997

C:Accession: JH0329; G31608

R:Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.

J. Exp. Med. 172, 1559-1570, 1990

A:Title: Expression cloning of a human granulocyte colony-stimulating factor receptor

A:Reference number: JH0329, PMID:91079757

A:Accession: JH0329

A:Molecule type: mRNA

A:Residues: 1-783 <LAP>

A:Cross-references: GB:X55720; NID:931698; PID:931699

A:Experimental source: placenta

A:Keywords: glycoprotein; transmembrane protein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-783/Product: granulocyte colony-stimulating factor receptor D7 #status predicted

F:62-637/Domain: extracellular #status predicted <EXTR>

F:64-783/Domain: transmembrane #status predicted <TRA>

F:93,128,134,389,474,579,610/Binding site: carbohydrate (Asn) (covalent) #status pred

Query Match 9.9%; Score 100; DB 2; Length 783;

Best Local Similarity 26.7%; Pred. No. 0.051;

Matches 51; Conservative 27; Mismatches 87; Indels 26; Gaps 11;

DB 2 PTLIGSLQATCSHGDTPGATA-GLYTFNGRRLPSELRLN--ISTLALANLN 58

DB 34 PIVHGLPITASCLITKONCSHDPEDQILRLGAELOPGROORLSDGOESITLTPHLN 93

DB 59 GSRQSGDNLYCHARDGSIAGSCLYVGLPPEKPNISCSWRNKKDLTCRWTPGAGH 114

DB 94 HTQA----FLSCLLNGNNSLQILDOVELRAGYPPALPHNLSCMLNLTSSLIQWEPGP- 149

DB 115 GEFTFLHTNYSKYLR--LYRSEKHXMGVPHCEPSLMPYPOG 162

DB 149 -ETHLPTSEFLKSKRGKNGQOTGDSILDCVPRDGGSHCCIPRKHLLY-QNNGIIVQAE 206

DB 163 DLGSHQSPRL 173

DB 207 NALGTSMSPOL 217

Matches 29; Conservative 8; Mismatches 21; Indels 28; Gaps 3;

OY 42 SRLNTSLALALANNGSRQSGDNLVCHARDGSLAGSCLVGLPPEKPNISCSRN 101

Db 7 SRVVFILLFLFSLVSLNG--QS-----PPKPKLVKCRSPG 40

OY 102 MKDLTCRMTPGAHGTFELHTNYSKY 127

Db 41 KETFCWMEPGADG--LPTNYLTLY 64

RESULT 13

A57018

prolactin receptor - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-Jul-1996

C/Accession: A57018

R/Ref: G. Wells, J.A.

A/Title: prolactin receptor antagonists that inhibit the growth of breast cancer cell 14

A/Reference number: A57018; MUID:95286597

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Cross-references: GB:578505; NID:9999114; PID:9999115

Query Match 9.4%; Score 95; DB 2; Length 206;

Best Local Similarity 51.28; Pred. No. 0.033;

Matches 21; Conservative 1; Mismatches 17; Indels 2; Gaps 1;

OY 87 LPPEKPNISCSRNMDLTCRMTPGAHGTFELHTNYSKY 127

Db 2 LPPEKPNISCSRNMDLTCRMTPGAHGTFELHTNYSKY 127

RESULT 14

A30304

prolactin receptor 2 precursor - rabbit

N/Alternate names: prolactin receptor, mammary gland

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Mar-1998

C/Accession: A30304; A60380

R/Ref: M. Jolicoeur, C. Levi-Meynueis, C. Dusanter-Fourt, I. Petridou, B. Boutin,

Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116, 1989

A/Title: Identification and sequence analysis of a second form of prolactin receptor by

A/Reference number: A30304; MUID:89184578

A/Accession: A30304

A/Molecule type: mRNA

A/Residues: 1-616 <EDE>

A/Cross-references: GB:J04510; NID:9165669; PID:9165670

R/Waters, M.J.; Spencer, S.A.; Hanlin, G.; Henzel, W.J.; Wood, W.I.

Int. J. Biochem. 22, 1089-1095, 1990

V/Title: Purification and partial sequence of the rabbit mammary gland prolactin receptor

V/Reference number: A60380; MUID:91146782

V/Accession: A60380

V/Molecule type: protein

V/Residues: 41-58, 'X', 60-66; 90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108, 150-164, 'XX', 167

V/Note: The amino end of the mature protein was blocked

V/Keywords: blocked amino end; glycoprotein; transmembrane protein

V/1-24/Domain: signal sequence #status predicted <SIG>

V/25-616/Product: prolactin receptor 2 #status predicted <MAT>

V/235-258/Domain: transmembrane #status predicted <TM>

V/159, 104, 132, 347, 389, 411/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.4%; Score 95; DB 2; Length 616;

Best Local Similarity 50.08; Pred. No. 0.12;

Matches 20; Conservative 2; Mismatches 16; Indels 2; Gaps 1;

OY 88 LPPEKPNISCSRNMDLTCRMTPGAHGTFELHTNYSKY 127

Db 1 LPPEKPNISCSRNMDLTCRMTPGAHGTFELHTNYSKY 127

Db 27 PPKKPEIFKCRSPKETFCTCWRPGADG--LPTNYLTLY 64

RESULT 15

157699

pseudo-prolactin receptor precursor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 02-Aug-1996

C/Accession: 157699

R/Davis, J.A.; Linzer, D.I.H.

Mol. Endocrinol. 3, 674-680, 1989

A/Title: Expression of multiple forms of the prolactin receptor in mouse liver.

A/Reference number: 157699; MUID:89261824

A/Accession: 157699

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-97 <RES>

A/Cross-references: GB:M2957; NID:9200477; PID:9200478

Query Match 9.4%; Score 95; DB 2; Length 97;

Best Local Similarity 33.08; Pred. No. 0.014;

Matches 30; Conservative 9; Mismatches 20; Indels 32; Gaps 4;

OY 37 LPSESLNTSLALANNGSRQSGDNLVCHARDGSLAGSCLVGLPPEKPNIS 96

Db 1 MPSALAYL---LVLSISLNG--QS-----PPKPEIFK 30

OY 97 CWSRNMDLTCRMTPGAHGTFELHTNYSKY 127

Db 31 CRSPDKETFTCWRNPGSDG--LPTNYSLTLY 59

Search completed: September 16, 1999, 20:42:11

Job time: 5404 sec.

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OM protein - protein search, using sw model

Run on: September 17, 1999, 03:10:14 ; Search time 35.09 Seconds

(without alignments)
149,840 Million cell updates/sec

Title: US-09-037-657-29

Sequence: 1 DPTLLIGSSLIQATCSIHGDT.....SHQSPRLSKIXCPHTGCPGR 186

Scoring table: BLOSUM62

Searched: 77977 seqs, 28268293 residues

Database: SwissProt_37.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	144	14.3	917	1	IL6_MOUSE
2	133.5	13.3	918	1	IL6B_HUMAN
3	130	12.9	918	1	IL6B_RAT
4	115	11.4	1097	1	LIFR_HUMAN
5	112.5	11.2	1092	1	LIFR_MOUSE
6	101.5	10.1	632	1	PRR_HUMAN
7	100	9.9	836	1	GCSR_HUMAN
8	98	9.7	581	1	PRR_BOVIN
9	95	9.4	461	1	PRR_RABIT
10	93	9.2	460	1	IL6A_MOUSE
11	91	9.0	880	1	TYO3_MOUSE
12	90.5	9.0	837	1	GCSR_MOUSE
13	89	8.8	462	1	IL6A_RAT
14	89	8.8	830	1	PRR_COLT
15	88.5	8.8	581	1	PRR_CEREL
16	88	8.7	608	1	PRR_MOUSE
17	88	8.7	880	1	TYO3_RAT
18	87	8.6	831	1	PRR_CHICK
19	85.5	8.5	610	1	PRR_RAT
20	85.5	8.5	887	1	PRR_HUMAN
21	82	8.2	831	1	PRR_MELGA
22	81	8.1	372	1	CNTR_HUMAN
23	81	8.1	372	1	CNTR_RAT
24	81	8.1	547	1	IC3_HUMAN
25	80	8.0	468	1	IL6A_HUMAN
26	79	7.9	630	1	PRR_ORENT
27	77.5	7.7	270	1	YFHX_ECOLI
28	76.5	7.6	704	1	CRAR_MOUSE
29	76.5	7.6	1363	1	ILPR_BRAIA
30	75.5	7.5	550	1	MYCO_STRCT
31	74.5	7.4	1220	1	DPOL_HSVB
32	74	7.4	437	1	AFIR_ASPL
33	74	7.4	362	1	CNTR_CHICK
34	74	7.4	1165	1	LPRR_HUMAN
35	73.5	7.3	1162	1	LPRR_MOUSE
36	73	7.3	515	1	NEF2_DROME
37	73	7.3	1805	1	NEF2_RAT
38	72	7.2	444	1	AFIR_ASPPA
39	72	7.2	532	1	SREP_PENCH
40	71.5	7.1	2481	1	UN52_CAEEL
41	71	7.1	854	1	ENV_STVCE
42	71	7.1	1038	1	IT4A_HUMAN
43	71	7.1	367	1	NAR3_HUMAN

ALIGNMENTS

RESULT	ID	IL6_MOUSE	STANDARD	PRT	917 AA	P30026 dengue virus P40395 saccharomyc
44	71	7.1	1127	1	POLG_DEN2D	
45	71	7.1	1056	1	RIC1_YEAST	
1	IL6_MOUSE					
AC	000560					
DT	01-FEB-1995 (REL. 31, CREATED)					
DT	01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)					
DT	15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)					
DE	INTERLEUKIN-6 RECEPTOR BETA PRECURSOR (IL-6R-BETA) (INTERLEUKIN 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).					
GN	IL6ST.					
OS	MUS MUSCULUS (MOUSE).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;					
OC	RODENTIA; SCIOGONATHI; MORIDAE; MORINAE; MUS.					
RP	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN-ICR; TISSUE-MACROPHAGE;					
RX	MEDLINE: 92291532.					
RA	SAITO M., YOSHIDA K., HIBI M., TAGA T., KISHIMOTO T.;					
RT	Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp130, and its regulated expression in vivo.					
RL	J. IMMUNOL. 148:4066-4071(1992).					
CC	1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6R (ALPHA CHAIN) COMPLEX, RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6-BINDING SITES, AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN EMBRYONIC DEVELOPMENT.					
CC	1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.					
CC	1- TISSUE SPECIFICITY: FOUND IN TISSUES SUCH AS BRAIN, HEART, THYMUS, SPLEEN, KIDNEY, LUNG AND LIVER. FOUND IN ALL THE CELL LINES TESTED EXCEPT BAF-B03. EXPRESSION NOT RESTRICTED TO IL-6-RESPONSIVE CELLS.					
CC	1- DEVELOPMENTAL STAGE: IN EMBRYONIC STEM CELLS IT IS FOUND FROM DAY 6 OF GESTATION. IT REACHES A PEAK ON DAY 8 AND GRADUALLY DECLINES DURING THE REST OF EMBRYOGENESIS.					
CC	1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE IG-LIKE DOMAIN.					
CC	1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.					
CC	THIS SWISS-PROT ENTRY IS COPYRIGHTED. IT IS PRODUCED THROUGH A COLLABORATION between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-slb.ch/announce/ or send an email to license@isb-slb.ch).					
CC	EMBL: X62646; G840817; -					
DR	EMBL: M83366; G193592; -					
DR	MGI: 96560; IL6ST.					
DR	PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.					
DR	PIRAT: P40189; 180V.					
DR	HSSP: P40189; 180V.					
KW	RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL; REPEAT.					
FT	SIGNAL	1	22			
FT	CHAIN	23	917			
FT	DOMAIN	23	617			
FT	TRANSSEM	618	639			
FT	DOMAIN	640	917			
FT	DOMAIN	26	120			
FT	DOMAIN	124	220			
FT	DOMAIN	221	322			
FT	DOMAIN	323	420			
FT	DOMAIN					

FT DOMAIN 422 515 FIBRONECTIN TYPE-III.
 FT DOMAIN 516 611 FIBRONECTIN TYPE-III.
 FT DOMAIN 723 741 SER-RICH.
 FT DISULFID 134 144 BY SIMILARITY.
 FT DISULFID 172 180 BY SIMILARITY.
 FT CARBOHYD 43 43 POTENTIAL.
 FT CARBOHYD 61 61 POTENTIAL.
 FT CARBOHYD 83 83 POTENTIAL.
 FT CARBOHYD 131 131 POTENTIAL.
 FT CARBOHYD 157 157 POTENTIAL.
 FT CARBOHYD 225 225 POTENTIAL.
 FT CARBOHYD 388 388 POTENTIAL.
 FT CARBOHYD 476 476 POTENTIAL.
 FT CARBOHYD 551 551 POTENTIAL.
 SQ SEQUENCE 917 AA; 102452 MW; A5DD259 CRC32;

Query Match 14.3%; Score 144; DB 1; Length 917;
 Best Local Similarity 26.5%; Pred. NO. 1.5e-06;
 Matches 39; Conservative 26; Mismatches 70; Indels 12; Gaps 3;

2 PTLIGSSIAQTCSHG---DTPGATAGLTYTFNGRRLPSELRLNTSLALANLN 58
 36 PTVORGSNFTALCYLKEKACLOHYVNAIYWKTHNAVPREQVIVRTSSVFTDV 95
 59 GSROSGDNLYCHARDGSIAGSLYGLPPEKPNISCSRMKDLCTRTPGAGHET 118
 96 LPSVQLTNIILSFQIEQNYGVETMLSGFPDKPTNLICIVNEGNNMLCQWDPGR--ET 153
 119 LHTNLSKYLRLVSEKMKVCPHCE 145
 154 LETNYTLK-----SEWATERFPDQ 173

RESULT 2
 IL6B_HUMAN STANDARD; PRT; 918 AA.
 AC P40189;
 DT 01-FEB-1995 (REL. 31, LAST CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
 DE 6 SIGNAL TRANSDUCER (MEMBRANE GLYCOPROTEIN 130) (GP130) (ONCOSATIN M
 DE RECEPTOR) (CDW130) (CD130 ANTIGEN).
 GN IL6ST.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MYELOMA, AND PLACENTA;
 RX MEDLINE: 91084844.
 RA HIRI M., MURAKAMI M., SAITO M., HIRANO T., TAGA T., KISHIMOTO T.;
 RT "Molecular cloning and expression of an IL-6 signal transducer,
 RT gp130.";
 RL CELL 63:1149-1157(1990).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.
 RX MEDLINE: 98169383
 RA BRAVO J., STANTON D., HEATH J.K., JONES E.Y.;
 RT "Crystal structure of a cytokine-binding region of gp130.";
 RL EMBO J. 17:1665-1674(1998).
 CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
 CC IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
 CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
 CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
 CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
 CC EMBRYONIC DEVELOPMENT (BY SIMILARITY).
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: FOUND IN ALL THE TISSUES AND CELL LINES
 CC EXAMINED. EXPRESSION NOT RESTRICTED TO IL-6 RESPONSIVE CELLS.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS

CC ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- DATABASE: NAME=PROM; NOTE=CD guide CD130 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/ncbi/cd/cd130.htm".

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CC EMBL: M57230; G186354; -
 CC PIR: A36337; A36337.
 CC PDB: 1BOU; 26-AUG-98.
 DR MIM; 600694; -
 DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR PFAM; PF00041; fn3; 3.
 KW RECEPTOR, TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
 KW REPEAT: 3D-STRUCTURE.

FT SIGNAL 1 22
 FT CHAIN 23 918
 FT DOMAIN 23 619
 FT TRANSMEM 620 641
 FT DOMAIN 642 918
 FT DOMAIN 124 222
 FT DOMAIN 223 324
 FT DOMAIN 325 423
 FT DOMAIN 424 517
 FT DOMAIN 518 613
 FT DOMAIN 725 755
 FT DISULFID 134 144
 FT DISULFID 172 182
 FT DISULFID 43 43
 FT CARBOHYD 83 83
 FT CARBOHYD 131 131
 FT CARBOHYD 157 157
 FT CARBOHYD 227 227
 FT CARBOHYD 379 379
 FT CARBOHYD 383 383
 FT CARBOHYD 390 390
 FT CARBOHYD 553 553
 FT CARBOHYD 564 564
 SQ SEQUENCE 918 AA; 103522 MW; 7CC06F05 CRC32;

Query Match 13.3%; Score 133.5; DB 1; Length 918;
 Best Local Similarity 27.3%; Pred. NO. 1.6e-05;
 Matches 35; Conservative 22; Mismatches 66; Indels 5; Gaps 2;

2 PTLIGSSIAQTCSHG---DTPGATAGLTYTFNGRRLPSELRLNTSLALANLN 58
 36 PTVOLNSFTAVCYLKEKCDYFHVANAIYWKTNFTPKQYITINASSVFTDIA 95
 59 GSROSGDNLYCHARDGSIAGSLYGLPPEKPNISCSRMKDLCTRTPGAGHET 118
 96 LHTNLSKYLRLVSEKMKVCPHCE 145
 154 LETNYTLK 161

RESULT 3
 IL6B_RAT STANDARD; PRT; 918 AA.
 AC P40189;
 DT 01-FEB-1995 (REL. 31, LAST CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)

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Best Local Similarity: 26.0%; Pred. No. 3,6e-05;
Matches 39; Conservative 24; Mismatches 72; Indels 12; Gaps 3;

OY      2 PTLIGSSIGATCSINH--DTPGATAGLGYTFNGRRRLPSELSRLNSTALANLN 58
Db      36 PVRQSGSNFATCVLKEKGLQVYSVNATIVYKTNINVAFKQVYINNTASSVFTDV 95
OY      59 GSRQSSDNLVCHARDOSIAGSGLYGLPPEKPFNISCWSRMDLTCRMTPGAGHET 118
Db      96 FQVNYLTGNTISGQIEQNYGQITILSGYDPDIPTLSCIVNEGKMLQLDPR--ET 153
OY      119 LHTYSLKYKLRIVSEKHXKGYPHC 144
Db      154 LFTYITLK-----SEWATERFPDC 172

RESULT 4
LIFR_HUMAN
ID LIFR_HUMAN STANDARD; PRT: 1097 AA.
AC P42702;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE LEUKEMIA INHIBITORY FACTOR RECEPTOR PRECURSOR (LIF-R).
GN LIFR
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PLACENTA;
RX MEDLINE; 92007727.
RA GEARING D.P., THOT C.J., VANDENBOS T., GIMPEL S.D., DELANEY P.B.,
RA KING J., PRICE V., COSMAN D., BECKMANN M.P.;
RT "Leukemia inhibitory factor receptor is structurally related to the
RT IL-6 signal transducer, gp130."
RL EMOB J. 10:2839-2848(1991).
CC - FUNCTION: SIGNAL-TRANSDUCING MOLECULE. MAY HAVE A COMMON PATHWAY
CC WITH GP130. THE SOLUBLE FORM INHIBITS THE BIOLOGICAL ACTIVITY OF
CC LIF BY BLOCKING ITS BINDING TO RECEPTORS ON TARGET CELLS.
CC - SUBUNIT: HETERODIMER COMPOSED OF LIFR AND GP130.
CC - INTRACELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THERE IS A
CC MEMBRANE-BOUND AND A SECRETED FORM.
CC - ALTERNATIVE PRODUCTS: THE SECRETED AND THE MEMBRANE-BOUND FORMS
CC MAY ARISE BY ALTERNATIVE SPLICING.
CC - SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC ONE IG-LIKE DOMAIN.
CC - SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC - SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC - SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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CC -----
DR EMBL; X61615; G34366; .
DR MIM; 151443; .
DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
DR PFAM; PF00041; fn3; 4.
KV RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
KV ALTERNATIVE SPLICING; REPEAT.
FT CHAIN 1 44 POTENTIAL.
FT DOMAIN 45 1097 LEUKEMIA INHIBITORY FACTOR RECEPTOR.
FT TRANSSEM 834 858 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 859 1097 CYTOPLASMIC (POTENTIAL).
FT DISULFID 55 65 BY SIMILARITY.
FT CARBOHYD 64 64 POTENTIAL.
FT CARBOHYD 85 85 POTENTIAL.
FT CARBOHYD 131 131 POTENTIAL.

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FT CARBOHYD 143 143 POTENTIAL.
 FT CARBOHYD 191 191 POTENTIAL.
 FT CARBOHYD 243 243 POTENTIAL.
 FT CARBOHYD 303 303 POTENTIAL.
 FT CARBOHYD 390 390 POTENTIAL.
 FT CARBOHYD 407 407 POTENTIAL.
 FT CARBOHYD 426 426 POTENTIAL.
 FT CARBOHYD 445 445 POTENTIAL.
 FT CARBOHYD 481 481 POTENTIAL.
 FT CARBOHYD 489 489 POTENTIAL.
 FT CARBOHYD 572 572 POTENTIAL.
 FT CARBOHYD 652 652 POTENTIAL.
 FT CARBOHYD 663 663 POTENTIAL.
 FT CARBOHYD 680 680 POTENTIAL.
 FT CARBOHYD 729 729 POTENTIAL.
 FT CARBOHYD 787 787 POTENTIAL.
 SO SEQUENCE 1097 AA; 123742 MW; 412CA634 CRC32;

Query Match 11.4%; Score 115; DB 1; Length 1097;
 Best Local Similarity 23.4%; Pred. No. 0.0013;
 Matches 36; Conservative 28; Mismatches 46; Indels 44; Gaps 7;

OY 1 DPTLLIGSSIAATCSI-----HGDPTAGTAEGLYTFNGRRLPSELRLNTSTL 50
 DB 258 DRYVLLGSDITFCVSOEKVLSALIGHTNCPILHLDG-----ENV 297
 OY 51 ALALANLNGSROSGDNLVCHARDSILAGSLVGLPPEKPFNISCWSRNKDKLTCHWTG 110
 DB 258 AIKININISVS-ASSGTNVYFTEDN--IGCVIIFAGYPPDPTQQLNCEHDLKEICSWN 354
 OY 111 PG-----AHGETFLTNLSKYKLLPASE 135
 DB 355 PGRVYALVGRPRATSYTLVE-SFGSKY-VRLKRAE 386

RESULT 5
 LIFR_MOUSE STANDARD; PRT: 1092 AA.
 AC P42703;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE LEUKEMIA INHIBITORY FACTOR RECEPTOR PRECURSOR (LIF-R) (D-FACTOR/LIF RECEPTOR).
 GN LIFR.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; MUS.
 RN (1)
 RP SEQUENCE FROM N.A. (SECRETED FORM).
 RX MEDLINE: 92007727.
 RA KING J., PRICE V., COSMAN D., BECKMANN M.P.;
 RA Leukemia inhibitory factor receptor is structurally related to the
 RT IL-6 signal transducer, gp130.";
 RL EMBO J. 10:2839-2848(1991).
 RN (2)
 RP SEQUENCE FROM N.A. (SECRETED FORM).
 RC SPRAIN-ICR; TISSUE-LAYER;
 RX MEDLINE: 94039833.
 RA TOMIDA M., YAMAMOTO-YAMAGUCHI Y., HOZUMI M.;
 RA "Pregnancy associated increase in mRNA for soluble D-factor/LIF
 RT receptor in mouse liver";
 RL FEBS LETT. 334:193-197(1993).
 RN (3)
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94334302.
 RA TOMIDA M., YAMAMOTO-YAMAGUCHI Y., HOZUMI M.;
 RA "Three different cDNAs encoding mouse D-factor/LIF receptor";
 RL J. BIOCHEM. 115:557-562(1994).
 CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. MAY HAVE A COMMON PATHWAY
 CC WITH GP130. THE SOLUBLE FORM INHIBITS THE BIOLOGICAL ACTIVITY OF

CC LIF BY BLOCKING ITS BINDING TO RECEPTORS ON TARGET CELLS.
 CC -1- SUBUNIT: HETERODIMER COMPOSED OF LIFR AND GP130.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THERE IS A
 CC MEMBRANE-BOUND AND A SECRETED FORM.
 CC -1- TISSUE SPECIFICITY: PLACENTA, LIVER, KIDNEY, HEART, LUNG, BRAIN,
 CC AND EMBRYOS. THE LIVER MAY BE THE PRIMARY SITE OF SYNTHESIS OF
 CC THE SECRETED FORM.
 CC -1- ALTERNATIVE PRODUCTS: THE SECRETED AND THE MEMBRANE-BOUND FORMS
 CC MAY ARISE BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 CC or send an email to license@isb-sib.ch).

CC DR EMBL: S73496; G688386;
 CC DR EMBL: S73495; G688384;
 CC DR EMBL: D26177; G825506;
 CC DR EMBL: D17444; G441494;
 CC MGD: MGI:96788; LIFR.
 CC PROSITE, PS00241: RECEPTOR_CYTOKINES_1; FALSE_NEG.
 CC PFM: PFM0041; fn3; 4.
 CC DR PFM: PFM0041; fn3; 4.
 CC KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
 CC KW ALTERNATIVE SPLICING; REPEAT.
 CC FT SIGNAL 1 43
 CC FT CHAIN 44 1092
 CC FT DOMAIN 44 828
 CC FT TRANSMEM 829 853
 CC FT DOMAIN 854 1092
 CC FT DISULFID 53 63
 CC FT CARBOHYD 164 164
 CC FT CARBOHYD 199 199
 CC FT CARBOHYD 228 238
 CC FT CARBOHYD 261 261
 CC FT CARBOHYD 385 385
 CC FT CARBOHYD 402 402
 CC FT CARBOHYD 421 421
 CC FT CARBOHYD 440 440
 CC FT CARBOHYD 453 453
 CC FT CARBOHYD 476 476
 CC FT CARBOHYD 567 567
 CC FT CARBOHYD 647 647
 CC FT CARBOHYD 658 658
 CC FT CARBOHYD 675 675
 CC FT CARBOHYD 724 724
 CC FT CARBOHYD 782 782
 CC FT CARBOHYD 718 718
 CC FT VARSPLIC 720 1092
 CC FT VARSPLIC 1092 122573 MW; 07DC092F CRC32;
 SO SEQUENCE

Query Match 11.2%; Score 112.5; DB 1; Length 1092;
 Best Local Similarity 25.4%; Pred. No. 0.0024;
 Matches 29; Conservative 27; Mismatches 41; Indels 17; Gaps 5;

OY 1 DPTLLIGSSIAATCSIHGDPTAGTAEGLYTFNGRRLPSELRLNT--STALALANLN 58
 DB 253 DRYVLLGSDNITFCM-----SPYVLSG-----QIGNLRLLHIXGVVAHILHNT 300
 OY 59 GSRQSGDNLVCHARDSILAGSLVGLPPEKPFNISCWSRNKDKLTCHWTG 112
 DB 301 VS-ENSGTNIIFITDD--YGVTVFAGYPPDVPOKLSCTHDLKEICSWNG 351

RESULT 6
 PRLR_HUMAN

ID PRIR_HUMAN STANDARD: PRT; 622 AA.
 DT 01-AUG-1990 (REL. 15, CREATED)
 DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
 GN PRLR.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 90114212.
 RA BOUTIN J.-M., EDERY M., SHIROTA M., JOLICOEUR C., LESUEUR L.,
 RA ALI S., GOULD D., DJIANE J., KELLY P.A.;
 RT "Identification of a cDNA encoding a long form of prolactin receptor
 RT in human hepatoma and breast cancer cells."
 RL MOL. ENDOCRINOL. 3:1455-1461(1989).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 25-235.
 RX MEDLINE; 95075462.
 RA SOMERS W., ULTSCH M., DE VOS A.M., KOSSIAKOFF A.A.;
 RT "The x-ray structure of a growth hormone-prolactin receptor complex."
 RL NATURE 372:478-481(1994).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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 CC or send an email to license@isb-sdb.ch).
 CC
 CC EMBL; M31661; G190362; -
 DR PIR; A40144; A40144.
 DR PDB; 1BP3; 23-SEP-98.
 DR MIM; 176761; -
 DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
 DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
 DR PFAM; PF00041; fn3; 2.
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT; 3D-STRUCTURE.
 FT SIGNAL 1 24
 FT CHAIN 25 622
 FT DOMAIN 25 234
 FT TRANSMEM 25 258
 FT DOMAIN 259 622
 FT DOMAIN 25 122
 FT DOMAIN 123 227
 FT DISULFID 36 46
 FT DISULFID 75 86
 FT CARBOHYD 59 59
 FT CARBOHYD 104 104
 FT CARBOHYD 233 233
 FT SEQUENCE 622 AA; 69505 MW; 6924E155 CRC32;

Query Match 10.1%; Score 101.5; DB 1; Length 622;
 Best Local Similarity 46.2%; Pred. No. 0.015; Indels 3; Gaps 2;
 Matches 24; Conservative 3; Mismatches 22;

QY 77 ILAAGCLVYG-LPPEKFNISWNSMDLTCRWTPGARGETFLTNLSKY 137
 DB 15 LFLNLTCLNGQLPCKPKEIFKCRSPNKEFTCMWRPGIDGG--LPTNLSLY 64

RESULT 7
 GCSR_HUMAN STANDARD; PRT; 836 AA.

AC 099062;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE GRANULOCYTE COLONY STIMULATING FACTOR RECEPTOR PRECURSOR (G-CSF-R)
 GN CSF3R OR GCSFR.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RX MEDLINE; 91011257.
 RA LARSEN A., DAVIS T., CURTIS B.M., GIMBEL S., SIMS J.E., COSMAN D.,
 RA PARK L., SORESENSEN E., MARCH C.J., SMITH C.A.;
 RT "A cDNA clone expressed in natural killer and T cells that likely
 RT encodes a secreted protein."
 RL J. EXP. MED. 172:1559-1570(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RX MEDLINE; 91062348.
 RA FUKUNAGA R., SETO Y., MIZUSHIMA S., NAGATA S.;
 RT "Three different mRNAs encoding human granulocyte colony-stimulating
 RT factor receptor."
 RL PROC. NATL. ACAD. SCI. U.S.A. 87:8702-8706(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92091782.
 RA SETO Y., FUKUNAGA R., NAGATA S.;
 RT "Chromosomal gene organization of the human granulocyte colony-
 RT stimulating factor receptor."
 RL J. IMMUNOL. 148:259-266(1992).
 RN [4]
 RP DOMAINS STRUCTURE.
 RX MEDLINE; 92007729.
 RA FUKUNAGA R., ISHIZAKA-IKEDA E., PAN C.-X., SETO Y., NAGATA S.;
 RT "Functional domains of the granulocyte colony-stimulating factor
 RT receptor."
 RL EMBO J. 10:2855-2865(1991).
 RN [5]
 RP STRUCTURE BY NMR OF 227-334.
 RX MEDLINE; 97331327.
 RA YAMASAKI R., NAITO S., AMAGUCHI H., OHKUBO T., OTA Y.;
 RT "Solution structure of an extracellular domain containing the WxWxS
 RT motif of the granulocyte colony-stimulating factor receptor and its
 RT interaction with ligand."
 RL NAT. STRUCT. BIOL. 4:498-503(1997).
 RN [6]
 RP 3D-STRUCTURE MODELLING OF 125-331.
 RX MEDLINE; 98037802.
 RA LAYTON J.E., IARIA J., SMITH D.K., TREUTLEIN H.R.;
 RT "Identification of a ligand-binding site on the granulocyte colony-
 RT stimulating factor receptor by molecular modeling and mutagenesis."
 RL J. BIOL. CHEM. 272:29735-29741(1997).
 CC -1- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR (G-
 CC CSF). IN ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION
 CC EVENTS AT THE CELL SURFACE.
 CC -1- SUBUNIT: DIMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE GCSFR-2 FORM,
 CC WHICH LACKS THE TRANSMEMBRANE DOMAIN, MAY REPRESENT A SOLUBLE FORM
 CC OF THE RECEPTOR.
 CC -1- TISSUE SPECIFICITY: ONE OR SEVERAL FORMS HAVE BEEN FOUND IN
 CC BONE MARROW CELLS, PLACENTA, AND PERIPHERAL BLOOD GRANULOCYTES.
 CC THE GCSFR-2 FORM HAS BEEN FOUND ONLY IN LEUKEMIA U937 CELLS. THE
 CC GCSFR-3 FORM IS HIGHLY EXPRESSED IN PLACENTA.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST FOUR FORMS, GCSFR-1 (SHOWN UNDER),
 CC GCSFR-2, GCSFR-3 AND GCSFR-4/D7, ARE PROBABLY PRODUCED BY
 CC ALTERNATIVE SPLICING OF THE SAME GENE. THEY DIFFER IN THEIR C-
 CC TERMINAL PORTION.
 CC -1- DISEASE: DEFECTS IN CSF3R ARE A CAUSE OF KOSTMANN SYNDROME;

FT CARBOHYD 59 59 POTENTIAL.
 FT CARBOHYD 132 132 POTENTIAL.
 SQ SEQUENCE 581 AA; 65153 MW; COECA0A2 CRC32;

Query Match 9.7%; Score 98; DB 1; Length 581;
 Best Local Similarity 33.7%; Pred. No. 0.03;
 Matches 29; Conservative 8; Mismatches 21; Indels 28; Gaps 3;

OY 42 SRLNLTALANLNGSRQSGDNLVCHARGSLAGSCLVGLPEPEFNIQSMRN 101

DB 7 SRVFFLLFLSLNG--QS-----PPEPKLVKCRSPG 40

OY 102 MNDLCRWTPGAGETFLHTNYSKY 127

DB 41 KEFTCWMERGADG--LPTNLTLY 64

RESULT 9

PRLR RABIT STANDARD; PRI; 616 AA.

AC P14787:

DT 01-APR-1990 (REL. 14, CREATED)

DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)

DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).

GN PRLR.

OS ORYCTOLAGUS CUNICULUS (RABBIT).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

OC LAGOMORPHA; LEPORIDAE; ORYCTOLAGUS.

OC (1)

OC SEQUENCE FROM N.A.

OC TISSUE-MAMMARY GLAND;

OC MEDLINE: 89184578.

OC EDERY M., JOLICOEUR C., LEVI-MEYREIS C., DUSANTER-FOURT I.,

OC PETRIDOU B., BOUTIN J.M., LESDEUR L., KELLY P.A., DJIANE J.,

OC "Identification and sequence analysis of a second form of prolactin

OC receptor by molecular cloning of complementary DNA from rabbit

OC mammary gland."

OC PROC. NATL. ACAD. SCI. U.S.A. 86:2112-2116(1989).

OC [2]

OC 3D-STRUCTURE MODELLING OF 30-228.

OC HALABY D., THOREAU E., DJIANE J., MORNON J.P.;

OC "Homology modeling of rabbit prolactin hormone complexed with its

OC receptor."

OC PROTEINS 27:459-468(1997).

OC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE

OC PROLACTIN.

OC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

OC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

OC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

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OC EMBL: J04510; GI65670;

OC PIR: A30304; A30304.

OC PDB: 1AN3: 03-DEC-97.

OC PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.

OC PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.

OC PFAM: PF00041; fn3; 2.

OC RECEPTOR: TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT: 3D-STRUCTURE.

OC SIGNAL 1 24 BY SIMILARITY.

OC CHAIN 25 616 PROLACTIN RECEPTOR.

OC DOMAIN 25 234 EXTRACELLULAR (POTENTIAL).

OC TRANSMEM 235 258 POTENTIAL.

OC DOMAIN 259 616 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 25 122 FIBRONECTIN TYPE-III.
 FT DOMAIN 124 227 FIBRONECTIN TYPE-III.
 FT DISULFID 36 46 BY SIMILARITY.
 FT DISULFID 75 86 BY SIMILARITY.
 FT CARBOHYD 59 59 POTENTIAL.
 FT CARBOHYD 104 104 POTENTIAL.
 FT CARBOHYD 132 132 POTENTIAL.
 SQ SEQUENCE 616 AA; 68840 MW; FB0170B1 CRC32;

Query Match 9.4%; Score 95; DB 1; Length 616;
 Best Local Similarity 50.0%; Pred. No. 0.064;
 Matches 20; Conservative 2; Mismatches 16; Indels 2; Gaps 1;

OY 88 PPEKPNISGSRNMDLTCRWTPGAGETFLHTNYSKY 127

DB 27 PGKPFIFKCRSPKETFCTWWRPGADG--LPTNLTLY 64

RESULT 10

IL6A MOUSE STANDARD; PRI; 460 AA.

AC P22272:

DT 01-AUG-1991 (REL. 19, CREATED)

DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)

DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA).

GN IL6RA OR IL6R.

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

OC RODENTIA; SCITROGNATHI; MORIDAE; MORINAE; MUS.

OC [1]

OC SEQUENCE FROM N.A.

OC STRAIN-BALB/C; TISSUE-SPLEEN;

OC MEDLINE: 90278354.

OC KISHIMOTO T., TOTSUKA T., SAITO M., YAMASAKI K., TAGA T., HIRANO T.,

OC "Functional murine interleukin 6 receptor with the intracellular A

OC particle gene product at its cytoplasmic domain. Its possible role in

OC plasmacytogenesis."

OC J. EXP. MED. 171:2001-2009(1990).

OC [2]

OC SEQUENCE FROM N.A.

OC STRAIN-C3H; TISSUE-LIVER;

OC FIORILLO M.T., CILIBERTO G., DENTE L.;

OC SUBMITTED (JUL-1990) TO EMBL/GENBANK/DBJ DATA BANKS.

OC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6

OC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL.

OC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.

OC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

OC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS

OC ONE IG-LIKE DOMAIN.

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OC or send an email to license@isb-sdb.ch).

OC EMBL: X51975; G49726;

OC EMBL: X53802; G52693;

OC PIR: J10145; J10145.

OC PIR: S14543; S14543.

OC MED: MGI:105304; IL6RA.

OC PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.

OC PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.

OC PFAM: PF00041; fn3; 1.

OC PFAM: PF00047; fn3; 1.

OC HSSP: P16471; 1B23.

OC RECEPTOR: TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL.

FT SIGNAL 1 19
 FT CHAIN 20 460 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
 FT DOMAIN 21 357 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 358 385 POTENTIAL.
 FT DOMAIN 386 460 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 40 99 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 47 92 POTENTIAL.
 FT DISULFID 117 128 BY SIMILARITY.
 FT DISULFID 162 173 BY SIMILARITY.
 FT CARBOHYD 32 32 POTENTIAL.
 FT CARBOHYD 55 55 POTENTIAL.
 FT CARBOHYD 150 150 POTENTIAL.
 FT CARBOHYD 374 374 A -> R (IN REF. 2).
 FT CONFLICT 374 374
 SQ SEQUENCE 460 AA; 50454 MW; 0B9F5F46 CRC32;

Query Match 9.2%; Score 93; DB 1; Length 460;
 Best Local Similarity 29.3%; Pred. No. 0.072;
 Matches 34; Conservative 22; Mismatches 38; Indels 22; Gaps 9;

Db 36 TSLPGATVTLIC-----PGKEAAGNTIHWYSGSO-----NREWTGTGTLARDVOL 84
 3 TLIGSSIAQTCISIHGDTPGATAEG---LYWTNGRLPSELSTLALALANLNG 59
 60 SROSGNLVCHARDGSLAGSC-LYVGLPPEKPFNSCSNRN-MKDLGCRWEGA 113
 85 S-DTGDYL-CSLNDH--LVGTPLVDVPEEP-KLSCEKPNLVNAICWRPSS 134

RESULT 11
 TYO3_MOUSE STANDARD; PRT; 880 AA.

AC P5144;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE DTK) (TK19-2).
 OS TYRO3 OR DTK OR RSE.
 OS MUS MUSCULUS (MUSCLE).
 OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.

EN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE-BRAIN;
 RC MEDLINE; 94193774.
 RX MARK M.R., SCADDEN D.T., WANG Z., GU Q., GODDARD A., GODOMSKI P.J.;
 RA "RSE, a novel receptor-type tyrosine kinase with homology to Axl/Tfco, is expressed at high levels in the brain."
 RT J. BIOL. CHEM. 269:10720-10728(1994).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE-BRAIN;
 RC MEDLINE; 95161079.
 RX CROSIER P.S., LEWIS P.M., HALL L.R., VITAS M.R., MORRIS C.M.,
 RA BEIER D.R., WOOD C.R., CROSIER K.E.;
 RT "Isolation of a receptor tyrosine kinase (DTK) from embryonic stem cells: structure, expression, and activity of Tyro 3, a neural adhesion-related receptor tyrosine kinase."
 RT GROWTH FACTORS 11:125-136(1994).
 RL [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN-C57BL/6;
 RX MEDLINE; 94336210.
 RX LAI C., GORE M., LEMKE G.;
 RT "Structure, expression, and activity of Tyro 3, a neural adhesion-related receptor tyrosine kinase."
 RT ONCOGENE 9:2567-2578(1994).
 RL [4]
 RN SEQUENCE FROM N.A.
 RP STRAIN-BALB/C; TISSUE-BRAIN;
 RX MEDLINE; 95240399.
 RX SCHULZ N., PAULHIC C., LEE L., ZHOU R.;
 RT "Isolation and expression analysis of tyro3, a murine growth factor

RT receptor tyrosine kinase preferentially expressed in adult brain."
 RL BRAIN RES. MOL. BRAIN RES. 28:273-280(1995).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-BRAIN;
 RX SASAKI M.;
 RT SUBMITTED (JUN-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 RL -1- FUNCTION: MAY BE INVOLVED IN CELL ADHESION PROCESSES, PARTICULARLY IN THE CENTRAL NERVOUS SYSTEM.
 CC -1- TISSUE SPECIFICITY: ABUNDANT IN THE BRAIN AND LOWER LEVELS IN OTHER TISSUES.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. THE EXTRACELLULAR DOMAINS CONTAINS 2 IG-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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EMBL; U05683; G469519; -
 DR EMBL; U18933; G622983; -
 DR EMBL; X78103; G473097; ALT_INIT.
 DR EMBL; U18342; G687626; ALT_INIT.
 DR EMBL; AB000828; D1019943; -
 DR MGI; MGI:104294; TYRO3.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PRAM; PF00047; fn3; 2.
 DR PRAM; PF00069; pkinaase; 1.
 DR HSP; P11362; 1FGI.
 DR RECEPTOR; GLYCOPROTEIN; TYROSINE-PROTEIN KINASE; ATP-BINDING;
 KW TRANSFERASE; PHOSPHORYLATION; TRANSMEMBRANE; SIGNAL; REPEAT;
 KW IMMUNOGLOBULIN FOLD.
 FT SIGNAL 1 30
 FT CHAIN 31 880
 FT DOMAIN 31 419
 FT TRANSMEM 420 440
 FT DOMAIN 441 880
 FT DOMAIN 34 115
 FT DOMAIN 131 200
 FT DOMAIN 214 301
 FT DOMAIN 305 401
 FT DOMAIN 508 785
 FT NP_BIND 514 522
 FT BINDING 540 540
 FT ACT_SITE 645 645
 FT MOD_RES 676 676
 FT CARBOHYD 53 53
 FT CARBOHYD 75 75
 FT CARBOHYD 181 181
 FT CARBOHYD 220 220
 FT CARBOHYD 230 230
 FT CARBOHYD 283 283
 FT CARBOHYD 356 356
 FT CARBOHYD 370 370
 FT CONFLICT 630 630
 FT CONFLICT 811 811
 SQ SEQUENCE 880 AA; 96222 MW; 476973C9 CRC32;

Query Match 9.0%; Score 91; DB 1; Length 880;
 Best Local Similarity 22.0%; Pred. No. 0.24;
 Matches 41; Conservative 18; Mismatches 53; Indels 74; Gaps 7;

QY 11 QATCSHGDTPGATAGLTW---TENGRLPSELSRLNTSLALALANLNGSSQSD 66
 DB 147 QLSCEAVGPPEPVY---ITWNRGLTKVGGPAPSP-----SYLVNTGYGTQT-- 190
 QY 67 NIVCHAROGSILAGS---CLVGLPPEKPFNISCNRNKKDLTCMTGPAHEFTLH--- 121
 DB 190 EESCEARNKGLATSRPAIVRLQAPPAEFNTVTTISSYNSVAMVPGADGLALLHSGT 249
 QY 121 -----TNTSLKYLRLVSEKXHMKGVPCEPSL 148
 DB 250 VGVNAPGEWEALAVVVPPTCLLRNAPATNTSLNR-----CANAL 294
 QY 149 MEYPOG 154
 DB 295 GPSPYG 300

RESULT 12
 GCSR_MOUSE STANDARD: PRT: 837 AA.

AC P40223;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE GRANULOCYTE COLONY STIMULATING FACTOR RECEPTOR PRECURSOR (G-CSF-R).
 GN CSF3R OR CSF3R.
 OS MUS MUSCULUS (MOUSE).
 OC EURARVOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIROGNATHI; MORIDAE; MORINAE; MUS.
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 90235283.
 RA FUNUNAGA R., ISHIZAKA-IKEDA E., SETO Y., NAGATA S.;
 RT "Expression cloning of a receptor for murine granulocyte colony-
 stimulating factor.";
 RL CELL 61:341-350(1990).
 RN (2)
 RP STRUCTURE BY NMR OF 225-333.
 RX MEDLINE: 97331327.
 RA YANASAKI K., NAITO S., ANAGUCHI H., OHKUBO T., OTA Y.;
 RT "Solution structure of an extracellular domain containing the WXXWS
 motif of the granulocyte colony-stimulating factor receptor and its
 interaction with ligand.";
 RL NAT. STRUCT. BIOL. 4:498-504(1997).
 CC -1- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR. IN
 ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION EVENTS AT
 THE CELL SURFACE.
 CC -1- SUBUNIT: DIMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: FOUND IN BONE MARROW.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 entities requires a license agreement (See <http://www.1sb-slb.ch/announce/>
 or send an email to license@1sb-slb.ch).
 CC
 DR EMBL: M58288; G193455; -
 DR PIR: A34898; A34898;
 DR PDB: 1GCF; 22-OCT-97.
 DR PDB: 1CTO; 22-OCT-97.
 DR MGI: 88533; CSFGR.
 DR PROSITE: PS00241; RECEPTOR CYTOKINES_1; 1.
 DR PROSITE: PS00340; RECEPTOR CYTOKINES_2; 1.
 DR PFM: PF00041; fn3; 3.
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
 REPEAT; 3D-STRUCTURE.

FT SIGNAL 1 25
 FT CHAIN 26 837
 FT TRANS 26 626
 FT TRANS 627 650
 FT TRANS 651 837
 FT DOMAIN 26 118
 FT DOMAIN 122 228
 FT DOMAIN 229 333
 FT DOMAIN 334 431
 FT DOMAIN 432 528
 FT DOMAIN 529 624
 FT DISULFID 132 143
 FT DISULFID 249 296
 FT DISULFID 267 310
 FT CARBOHYD 51 51
 FT CARBOHYD 94 94
 FT CARBOHYD 129 129
 FT CARBOHYD 186 186
 FT CARBOHYD 279 279
 FT CARBOHYD 392 392
 FT CARBOHYD 408 408
 FT CARBOHYD 474 474
 FT CARBOHYD 487 487
 FT CARBOHYD 582 582
 FT CARBOHYD 613 613
 SQ SEQUENCE 837 AA; 93406 MW; D55F84D4 CRC32;

Query Match 9.08; Score 90.5; DB 1; Length 837;
 Best Local Similarity 23.88; Pred. No. 0.26; Indels 21; Gaps 8;
 Matches 45; Conservative 26; Mismatches 95;

QY 2 PFLIGSSLOATCSHGDTPGATAEG-LYWFNGRLT-PSELSRL--NTSLALALANL 57
 DB 34 PVRRLGDEVLASCTISPCSKIDQAKILMLRDEPIQGRDQHLLPDTQESLITPLRL 93
 QY 58 NGSQSSDNLVCHARDOSILAGSCLVGLPPEKPFNISCNR-NKKDLTCMTGANGGE 116
 DB 94 NYT-QALFELCPWEDSVQLLDOALAGYPAPSPNSLCLMHLTNSLYCOMEGP--E 150
 QY 117 TFLATNYSLKYLRLVSEKXHMKGVPHC-----EPSLWPPGPGPLSLMDL 164
 DB 151 THLTSLFKFSRBRADQYGGDTIPDCVAKRKNCSIPKRLLL-QYMAIVQAEEM 209
 QY 165 GGSQSPRL 173
 DB 210 LGSSSPRL 218

RESULT 13
 IL6A_RAT STANDARD: PRT: 462 AA.

AC P22273;
 DT 01-AUG-1991 (REL. 19, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA).
 GN IL6R.
 OS RATTUS NORVEGICUS (RAT).
 OC EURARVOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIROGNATHI; MORIDAE; MORINAE; RATTUS.
 RN (1)
 RP SEQUENCE FROM N.A.
 RX STRAIN-FISHER 344; TISSUE-LIVER;
 RX MEDLINE: 91060602.
 RA BAUMANN M., BAUMANN H., FEY G.H.;
 RT "Molecular cloning, characterization and functional expression of the
 rat liver interleukin 6 receptor.";
 RL J. BIOL. CHEM. 265:19853-19862(1990).
 RN (2)
 RP IDENTIFICATION OF PROBABLE FRAMESHIFT IN 227-261.
 RA GIBSON T.;

Search completed: September 17, 1999, 03:10:15
Job time: 295 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:40:09 ; Search time 68.96 seconds
(without alignments)
165.996 Million cell updates/sec

Title: US-09-037-657-29

Perfect score: 1006
Sequence: 1 DPTLLIGSSLIQNCISIHGDT.....SHQSPRLSKIXCPHTGCGPR 186

Scoring table: BLOSUM62

Searched: 201082 seqs, 61543640 residues

Database :

- 1: SP_ARCHAEA:*
- 2: SP_BACTERIA:*
- 3: SP_FUNGI:*
- 4: SP_HUMAN:*
- 5: SP_INVERTEBRATE:*
- 6: SP_MAMMAL:*
- 7: SP_MHC:*
- 8: SP_ORGANELLE:*
- 9: SP_PHAGE:*
- 10: SP_PLANT:*
- 11: SP_PROTOZOA:*
- 12: SP_VIRUS:*
- 13: SP_VERTEBRATE:*
- 14: SP_UNCLASSIFIED:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	658	65.4	422	4	075462	075462 homo sapien
2	167.5	16.7	881	13	057519	057519 xenopus lae
3	110.5	11.0	862	4	099665	099665 homo sapien
4	108	10.7	971	11	070458	070458 mus musculu
5	107.5	10.7	970	11	088821	088821 mus musculu
6	107.5	10.7	422	4	016542	016542 homo sapien
7	107.5	10.7	1093	11	070535	070535 ratcus norv
8	99.5	9.9	581	6	046561	046561 ovls arles
9	98	9.7	266	6	018880	018880 bos tauris
10	95	9.4	206	4	016334	016334 homo sapien
11	93.5	9.3	432	11	064385	064385 mus musculu
12	93.5	9.3	432	11	P70225	P70225 mus musculu
13	93	9.2	440	11	000343	000343 mus musculu
14	92.5	9.2	979	4	099650	099650 homo sapien
15	91.5	9.1	866	11	062121	062121 mus musculu
16	91	9.0	876	11	060752	060752 mus musculu
17	90	8.9	874	11	P97378	P97378 mus musculu
18	88.5	8.8	198	6	018985	018985 cervus elap
19	86.5	8.6	340	12	086893	086893 male dwarf
20	83.5	8.3	6658	5	076281	076281 drosophila
21	83	8.3	1896	4	060468	060468 homo sapien
22	83	8.3	1571	4	060469	060469 homo sapien
23	82.5	8.2	754	5	027273	027273 drosophila
24	81.5	8.1	1395	5	044924	044924 drosophila
25	81	8.0	372	11	088507	088507 mus musculu
26	80.5	8.0	1165	6	002671	002671 sus scrofa
27	80	7.9	346	13	093404	093404 oreochromis
28	79.5	7.9	834	11	064151	064151 mus musculu
29	78.5	7.8	1180	4	015051	015051 homo sapien

30	78.5	7.8	917	11	060625	060625 mus musculu
31	78	7.8	1299	4	015179	015179 homo sapien
32	77.5	7.7	270	2	P76995	P76995 escherichia
33	77.5	7.7	1299	4	092823	092823 homo sapien
34	77.5	7.7	753	5	026306	026306 drosophila
35	77	7.7	1127	12	P89532	P89532 dengue viru
36	76.5	7.6	1404	4	015080	015080 homo sapien
37	76.5	7.6	2222	5	097394	097394 drosophila
38	76	7.6	313	12	088195	088195 sugarcane m
39	75	7.5	1241	4	060500	060500 homo sapien
40	75	7.5	310	12	088198	088198 sugarcane m
41	75	7.5	313	12	088199	088199 sugarcane m
42	75	7.5	515	12	09YTX2	09YTX2 sugarcane m
43	74.5	7.4	262	4	043561	043561 homo sapien
44	74.5	7.4	233	4	043919	043919 homo sapien
45	74	7.4	958	4	092920	092920 homo sapien

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	422 AA.
ID	075462			
AC	075462:			
DT	01-NOV-1998 (TRENBLREL.08, Created)			
DT	01-NOV-1998 (TRENBLREL.08, Last sequence update)			
DT	01-MAY-1999 (TRENBLREL.10, Last annotation update)			
DE	CYTOKINE-LIKE FACTOR-1 PRECURSOR.			
GN	CLF-1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
CC	Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	ELSON G.C.A., GRABER P., LOSBERGER P., HERREN S., GRETENER D.,			
RA	MENOLD L.N., WELLS T.N.C., ROSCO-VILBOIS M.H., GAUCHAT J.F.;			
RT	"CLF-1, a Novel Soluble Protein Shares Homology with Members of the			
RT	Cytokine Type-1 Receptor Family."			
RL	J. Immunol. 0:0-0(1998).			
DR	EMBL; AF059293; AAC2835.1; ..			
KW	PFAM; PF00041; fn3; 2.			
DR	Signal.			
FT	SIGNAL	1	37	POTENTIAL.
FT	CHAIN	38	422	CYTOKINE-LIKE FACTOR-1.
SQ	SEQUENCE	422 AA;	46301 MW;	87759BC9 CRC32.
Query Match		65.4%;	Score 658;	DB 4;
Best Local Similarity		84.5%;	Pred. No. 2.7e-62;	Length 422;
Matches 125;	Conservative	4;	Mismatches 13;	Indels 6;
Gaps				2;
DB	1 DPTLLIGSSLIQNCISIHGDTGPAAGAEGLYTFNGRRRLPRLSLRLNSTALAINNGS 60			
DB	47 DPTLLIGSSLIQNCISIHGDTGPAAGAEGLYTFNGRRRLPRLSLRLNSTALAINNGS 106			
DB	61 ROOSGDMVCHARDSTILASCLYVGLPEKPEFNIQSCSRNMDLTCRTPGAAGETFLH 120			
DB	107 RORSGDMVCHARDSTILASCLYVGLPEKPEFNIQSCSRNMDLTCRTPGAAGETFLH 166			
DB	121 TNYSLAKTKRL-----VRSEKMGCVPH 143			
DB	167 TNYSLAKTKRLMYGQDNTCEYHTVG-PH 193			
RESULT	2			
ID	057519	PRELIMINARY:	PRT:	881 AA.
AC	057519:			
DT	01-JUN-1998 (TRENBLREL.06, Created)			
DT	01-JUN-1998 (TRENBLREL.06, Last sequence update)			
DT	01-MAY-1999 (TRENBLREL.10, Last annotation update)			
DE	GP130P1.			

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QY      1 DPTLLIGSSLQATCSIHG-----DFGATAEGLYWTFNGRRLPSELRLNTST 49
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     154 DKVLEEGSNV-TICLMYGQWYVNSCKLQDEP-----IHGEQLDSHVSLKLNW 202

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OY 50 LALALANLNGSRQSGDNVCHARDG-STLASCCLYVGLPPEKPNISCSWRNMDLTCR 108
Db 203 VFLS-----DGTINMCOATKPKRIFCTVLFVSKYLEEPKNSVCEETBDEKTLDCS 253
OY 109 WTPGAGGETFL-----HTNYSL 125
Db 254 WEPGV--DTLTLMKROKRONYTL 274

RESULT 6
ID 016542 PRELIMINARY; PRT; 422 AA.
AC 016542: 014626:
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE INTERLEUKIN-11 RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=MUSCLE;
MEDLINE: 95399754.
RA CHEREL M., SOREL M., LEBEAU B., DUBOIS S., MOREAU J.F., BATAILLE R.,
RA MINVILLE S., JACQUES Y.;
RT Molecular cloning of two isoforms of a receptor for the human
RT hematopoietic cytokine interleukin-11."
RL Blood 86:2534-2540(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA VAN LEUVEN F., STAS L., HILLIKER C., MIYAKE Y., GOSSLER A.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 3-390 FROM N.A.
RC TISSUE=PLACENTA.
RA CHEREL M., SOREL M., DUBOIS S., LEBEAU B., MOREAU J., JACQUES Y.,
RA MINVILLE S.;
RT Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RL EMBL: U32324; AAB36492.1; -
RL EMBL: Z38102; CAAB6224.1; -
RL EMBL: U32323; AAB36491.1; -
RL EMBL: Z46595; CAAB6570.1; -
RL PFAM: PF00041; fn3; 2.
RL PFAM: PF00047; fn3; 1.
SQ SEQUENCE 422 AA; 45222 MW; 29011292 CRC32;

Query Match 10.7%; Score 107.5; DB 4; Length 422;
Best Local Similarity 26.3%; Pred. No. 0.0013;
Matches 40; Conservative 24; Mismatches 67; Indels 21; Gaps 7;

Y 7 GSSLATCSIHGTPTGATA-EGLYWTFNG--RRLPSLSRLNTSTLALANLNGSRQ 63
b 41 GRVVKLC-----PGVTADDPVSWFDEGPKLLQGPDSGLGHELYLAQDSDEG--- 92
64 SGNLVCARHARDGSIILGSCLYVGLPPEKPNISCSWRNMDLTCRTPGAGGETFLHTNT 123
b 92 -----YICQLDGLAGLGTWTLQGLYPPARPV-VSCQADADYENFSCWSPSO--ISGLPTRY 144
Y 124 SLKYLRLVREXEHMAGVPHCEPSLMPYPOG 155
b 145 LITSYRKTYVLGADSQRRSPSTGP--WPCPODP 174

RESULT 7
ID 070535 PRELIMINARY; PRT; 1093 AA.
AC 070535:
DT 01-AUG-1998 (TREMblrel. 07, Created)
DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
DT 01-MAY-1999 (TREMblrel. 10, Last annotation update)
DE LEUKEMIA INHIBITOR FACTOR RECEPTOR ALPHA-CHAIN.

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OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTER-IMMICH; TISSUE=LIVER.
RX MEDLINE: 98007878.
RA AITAMA J., IKEDA-NAIKI S., OHGANE J., MIN K.S., INAKURA T., SASAI K.,
RA SHIOYA K., OGAWA T.;
RT Molecular cloning of rat leukemia inhibitory factor receptor
RT alpha-chain gene and its expression during pregnancy."
RL Biochim. Biophys. Acta 1353:266-276(1997).
DR EMBL: D86345; BAA25907.1; -
DR PFAM: PF00041; fn3; 4.
SQ SEQUENCE 1093 AA; 122394 MW; 23638887 CRC32;

Query Match 10.7%; Score 107.5; DB 11; Length 1093;
Best Local Similarity 24.1%; Pred. No. 0.004;
Matches 28; Conservative 23; Mismatches 44; Indels 21; Gaps 4;

OY 1 DPTLLIGSLQATC---SINGDPGATAEGLYTFNGRRRLPSLSRLNTSTLALAN 56
Db 254 DKVLAGSNMTICISTRTKVLASGIGNTFRLHLHG-----ETVAINITLN 299
OY 57 LNSGROSGDNVCHARDG-STLASCCLYVGLPPEKPNISCSWRNMDLTCRTPG 112
Db 300 IPVS-ENSGSNVIFSTVDD--VGTGVFAGYPPDPVKLSLSETHLMEIISWNP 352

RESULT 8
ID 046561 PRELIMINARY; PRT; 581 AA.
AC 046561:
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-MAY-1999 (TREMblrel. 10, Last annotation update)
DE PROLACTIN RECEPTOR LONG FORM PRECURSOR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Caprinae; Ovis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98001468.
RA BIGNON C., BINART N., ORMANDY C., SCHULER L.A., KELLY P.A.,
RA DJIANE J.;
RT "Long and short forms of the ovine prolactin receptor: cDNA cloning
RT and genomic analysis reveal that the two forms arise by different
RT alternative splicing mechanisms in ruminants and in rodents."
RL J. Mol. Endocrinol. 19:109-120(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA BIGNON C., DJIANE J.;
RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF041257; AAB96795.1; -
RL DR PFAM: PF00041; fn3; 2.
FT SIGNAL.
FT CHAIN 1 24 POTENTIAL.
FT SEQUENCE 581 AA; 65235 MW; 6792ATC7 CRC32;

Query Match 9.9%; Score 99.5; DB 6; Length 581;
Best Local Similarity 45.3%; Pred. No. 0.014;
Matches 24; Conservative 4; Mismatches 18; Indels 7; Gaps 2;

OY 76 STLASCCLYVGLPPEKPNISCSWRNMDLTCRTPGAGGETFLHTNYSLKX 128
Db 20 SLNNGS-----PPEKPLIKCRSPKEKFTCWEPGADG--LPNTYLLTRY 65

RESULT 9

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018880
ID 018880 PRELIMINARY; PRT; 296 AA.
AC 018880;
DT 01-JAN-1998 (TREMELREL. 05, Created)
DT 01-JAN-1998 (TREMELREL. 05, Last sequence update)
DE 01-NOV-1998 (TREMELREL. 08, Last annotation update)
DE PROLACTIN RECEPTOR SHORT FORM.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97375450.
RA SCHUIJER L.A., NAGEL R.J., GAO J., HORSEMAN N.D., KESSLER M.A.;
RT "Prolactin receptor heterogeneity in bovine fetal and maternal
RT tissues";
RL Endocrinology 138:3187-3194(1997).
DR EMBL: AF027403; AAB83999.1;
DR PFAM: PF00041; fn3; 2.
SQ SEQUENCE 296 AA; 33854 MW; 8B40CCD8 CRC32;

Query Match 9.7%; Score 98; DB 6; Length 296;
Best Local Similarity 33.7%; Pred. No. 0.0088;
Matches 29; Conservative 8; Mismatches 21; Indels 28; Gaps 3;

OY 42 SRLNLTALALANNGSGDNLNCHARGSLIAGSLVGLPPEKPFNISGSRN 101
DB 7 SRVFLILFLVSLNG--QS-----PPEKPKLVKCRSPG 40

OY 102 MMDLTCRWTPGAGETFLHTNYSIKY 127
DB 41 KETFTCWMEPGADG--LPTNYLTLY 64

RESULT 10
O16354 PRELIMINARY; PRT; 206 AA.
AC 016354;
DT 01-NOV-1996 (TREMELREL. 01, Created)
DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)
DE 01-NOV-1996 (TREMELREL. 08, Last annotation update)
DE PROLACTIN RECEPTOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95286597.
RA FUH G., WELLS J.A.;
RT "Prolactin receptor antagonists that inhibit the growth of breast
RT cancer cell lines";
RL J. Biol. Chem. 270:13133-13137(1995).
DR EMBL: X78505; AAB34470.1;
DR PFAM: PF00041; fn3; 2.
FT NON-TER 1
SQ SEQUENCE 206 AA; 23950 MW; D7E57266 CRC32;

Query Match 9.4%; Score 95; DB 4; Length 206;
Best Local Similarity 51.2%; Pred. No. 0.012;
Matches 21; Conservative 1; Mismatches 17; Indels 2; Gaps 1;

OY 87 LPPEKPFNISGSRNKKDLTCRWTPGAGETFLHTNYSIKY 127
DB 2 LPPEKPFNISGSRNKKDLTCRWTPGAGETFLHTNYSIKY 40

RESULT 11
O64385 PRELIMINARY; PRT; 432 AA.
AC 064385;
SQ SEQUENCE 432 AA; 46655 MW; F65B3060 CRC32;

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DT 01-JAN-1998 (TREMELREL. 05, Created)
DT 01-JAN-1998 (TREMELREL. 05, Last sequence update)
DE 01-NOV-1998 (TREMELREL. 08, Last annotation update)
DE INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 1 PRECURSOR (NRL) (ETL2)
DE (IL-11RALPHA) (IL11RA1).
GN IL11RA1 OR IL11RA OR ETL2 OR ETL2/IL11 REC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95045367.
RA HILTON D.J., HILTON A.A., RAICEVIC A., RAKAR S., HARRISON-SMITH M.,
RA GOUCH N.M., BEGLEY C.G., METCALF D., NICOLA N.A., WILSON T.A.;
RT "Cloning of a murine IL-11 receptor alpha-chain: requirement for
RT gp130 for high affinity binding and signal transduction.";
RL EMBO J. 13:4765-4775(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95045367.
RA HILTON D.J., HILTON A.A., RAICEVIC A., RAKAR S., HARRISON-SMITH M.,
RA GOUCH N.M., BEGLEY C.G., METCALF D., NICOLA N.A., WILSON T.A.;
RT "Cloning of a murine IL-11 receptor alpha-chain: requirement for
RT gp130 for high affinity binding and signal transduction.";
RL EMBO J. 13:4765-4775(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97129000.
RA BILINSKI P., HALT M.A., NEHAUS H., GISEL C., HEATH J.K.,
RA GOSSLER A.;
RT "Two differentially expressed interleukin-11 receptor genes in the
RT mouse genome.";
RL Blochem J. 320:359-363(1996).
CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11.
CC -1- BINDS TO IL-11 WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A
CC SIGNAL.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC CONTAINS ONE IG-LIKE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
DR EMBL: X74953; CAAS2908.1;
DR EMBL: U14412; AAB53248.1;
DR EMBL: X94162; CA63873.1;
DR EMBL: X94163; CA63873.1; JOINED.
DR MGD: MGI:107426; IL11RA1.
DR PFAM: PF00041; fn3; 2.
DR PFAM: PF00047; fn3; 1.
FT Receptor; Transmembrane; Glycoprotein; Immunoglobulin fold; Signal.
FT SIGNAL 1
FT CHAIN 23
FT DOMAIN 24 432
FT DOMAIN 367
FT TRANSMEM 368 393
FT DOMAIN 394 432
FT DOMAIN 41 102
FT CARBOHYD 127 127
FT CARBOHYD 194 194
FT CARBOHYD 194 194
SQ SEQUENCE 432 AA; 46655 MW; F65B3060 CRC32;

Query Match 9.3%; Score 93.5; DB 11; Length 432;
Best Local Similarity 27.9%; Pred. No. 0.042;
Matches 39; Conservative 19; Mismatches 63; Indels 19; Gaps 8;

OY 21 PGATA-EGLYWTFNGRRLPSELSRLN--TSLA--LALANLNGSGDNLNCHARG 75
DB 49 PGVSAAGTPVSMFRDGD-----SRLLOQPSDGLHRLVLAQVDSFDE---GTIVCQTLIDG 99

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QY 76 SLIAGSCLVGPPEKPFENISCSNMKDLTCRWTGAGETFLHTNYSKYLRLVRS 135
 DB 100 VSGGWTLKLGPPARP-EVSCQADVENSCTWSFGQ--VSLPTFRILTSYRKTLPGA 156
 QY 136 XHMGVPCPESLMPYPOGP 155
 DB 157 ESORESPSTGCP--WPCPODP 174

RESULT 12
 P70225 PRELIMINARY: PRT: 432 AA.

AC P70225 009074: 02, Created)
 AD 01-FEB-1997 (TREMELREL. 02, Last sequence update)
 DT 01-FEB-1997 (TREMELREL. 08, Last annotation update)
 DT 01-NOV-1998 (TREMELREL. 08, Last annotation update)
 DE INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 2 PRECURSOR (IL11RA2)
 DE (IL-11BETA) (INTERLEUKIN-11 RECEPTOR BETA CHAIN).
 OS IL11RA2 OR IL-11BETA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CD1: TISSUE-TESTIS;
 RX MEDLINE; 97129000.
 RA BILINSKI P., HALL M.A., NEUHAUS H., GISSEL C., HEATH J.K.,
 RA GOSSLER A.;
 RT "Two differentially expressed interleukin-11 receptor genes in the
 RT mouse genome.";
 RL Biochem. J. 320:359-363(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CD-1: TISSUE-TESTIS;
 RX MEDLINE; 96278810.
 RA ROBB L., HILTON D.J., WILSON T.A., BEGLEY C.G.;
 RT "Structural analysis of the gene encoding the murine interleukin-11
 RT receptor alpha-chain and a related locus.";
 RL J. Biol. Chem. 271:13754-13761(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CD-1: TISSUE-TESTIS;
 RX MEDLINE; 97230451.
 RA ROBB L., HILTON D.J., BROOK-CARTER P.T., BEGLEY C.G.;
 RT "Identification of a second murine interleukin-11 receptor
 RT alpha-chain gene (IL11RA2) with a restricted pattern of expression.";
 RL Genomics 40:387-394(1997)
 CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11.
 CC -1- SUBUNIT: HETERODIMER OF TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC -1- SIMILARITY: BELONGS TO THE IMMUGLOBULIN SUPERFAMILY.
 CC -1- CONTRAINS ONE IG-LIKE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 DR EMBL; X94157; CAA63872.1; JOINED.
 DR EMBL; X94158; CAA63872.1; JOINED.
 DR EMBL; X94159; CAA63872.1; JOINED.
 DR EMBL; X94160; CAA63872.1; JOINED.
 DR EMBL; X94161; CAA63872.1; JOINED.
 DR EMBL; X98519; CAA67144.1; JOINED.
 DR EMBL; U69491; AAC5111.1; JOINED.
 DR MGD; MGI:109123; IL11RA2.
 DR PFAM; PF00041; fn3; 2.
 DR PFAM; PF00047; fn3; 1.
 DR PFAM; PF00047; fn3; 2.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin fold; Signal.
 FT SIGNAL 1 23
 FT CHAIN 1 23
 FT DOMAIN 24 432
 FT TRANSMEM 368 393
 FT DOMAIN 394 432
 FT DOMAIN 41 102
 FT CARBOHYD 127 127
 FT CARBOHYD 194 194

FT CONFLICT 200 200 S -> P (IN CAA63872).
 FT CONFLICT 384 384 V -> L (IN CAA63872).
 SQ SEQUENCE 432 AA; 46721 MW; C4FD7DEC CRC32;

Query Match 9.3%; Score 93.5; DB 11; Length 432.
 Best Local Similarity 27.9%; Pred. No. 0.042;
 Matches 39; Conservative 19; Mismatches 63; Indels 19; Gaps 8;

QY 21 PGATA-EGLYWTFNGRRRLPSELRLN--TSILA--LALANNGSRQSGDNLVGHARDG 75
 DB 49 PGVSAGTPVSWFRDGD-----SRLLGPDSSGLGRLVLAQVDSDE--GTYVQTLDG 99
 QY 76 SLIAGSCLVGPPEKPFENISCSNMKDLTCRWTGAGETFLHTNYSKYLRLVRS 135
 DB 100 VSGGWTLKLGPPARP-EVSCQADVENSCTWSFGQ--VSLPTFRILTSYRKTLPGA 156
 QY 136 XHMGVPCPESLMPYPOGP 155
 DB 157 ESORESPSTGCP--WPCPODP 174

RESULT 13
 000343 PRELIMINARY: PRT: 440 AA.

AC 000343
 AD 01-NOV-1996 (TREMELREL. 01, Created)
 DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)
 DT 01-NOV-1998 (TREMELREL. 08, Last annotation update)
 DE INTERLEUKIN 6 RECEPTOR, ALPHA PRECURSOR
 DE (MUTANT INTERLEUKIN-6 RECEPTOR).
 GN IL6RA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RX MEDLINE; 90278354.
 RA SDGITA T., TOTSUKA T., SAITO M., YAMASAKI K., TAGA T., HIRANO T.,
 RA KISHIMOTO T.;
 RT "Functional murine interleukin 6 receptor with the intracisternal A
 RT particle gene product at its cytoplasmic domain. Its possible role in
 RT plasmacytomaogenesis.";
 RL J. Exp. Med. 171:2001-2009(1990).
 CC -1- THIS PROTEIN IS A ABNORMAL INTERLEUKIN-6 RECEPTOR.
 CC IN THE CDNA ENCODING THE ABNORMAL INTERLEUKIN-6 RECEPTOR THE
 CC REGION CORRESPONDING TO ITS INTRACITOPLASMIC DOMAIN WAS REPLACED
 CC WITH A LONG TERMINAL REPEAT OF THE INTRACISTERNAL A PARTICLE
 CC (IAP) GENE, A MEMBER OF THE ENDOGENOUS PRORETROVIRAL-LIKE
 CC ELEMENTS PRESENT IN THE GENOME OF MUS MUSCULUS.
 DR EMBL; X51976; CAA36238.1; JOINED.
 DR PIR; J01444; J01444.
 DR MGD; MGI:105304; IL6RA.
 DR PFAM; PF00041; fn3; 1.
 DR PFAM; PF00047; fn3; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin fold; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 440
 FT DOMAIN 1 385
 FT DOMAIN 20 357
 FT DOMAIN 43 96
 FT TRANSMEM 358 385
 FT DOMAIN 386 440
 FT DOMAIN 386 440
 FT DISULFID 47 92
 FT CARBOHYD 32 32
 FT CARBOHYD 55 55
 FT CARBOHYD 150 150
 SQ SEQUENCE 440 AA; 47901 MW; EB5E7B93 CRC32;

Query Match 9.2%; Score 93; DB 11; Length 440;

Best Local Similarity 29.3%; Pred. No. 0.048;
Matches 34; Conservative 22; Mismatches 38; Indels 22; Gaps 9;

QY 3 TLIGSSQATCSIHGDPGATAGC---LYWTFNGRLPSELSTLALANLING 59
DB 36 TSLGATVTLIC-----PGKEAGNWTIHVYSGSQ-----NEMTTGTIVLRVQL 84
QY 60 SROOSGNLVCHARDGSLAGSC-LYVGLPPEKPFNISCWERN-MKDLTCRWTPGA 113
DB 85 S-DTGDTL-CSLNDH--LVGTVPILVDVPEEP-KLSCFKNPLVNAICEMRPS 134

RESULT 14

Q99650 PRELIMINARY; PRT; 979 AA.
AC Q99650;
DT 01-MAY-1997 (TREMblrel. 03, Created)
DT 01-NOV-1997 (TREMblrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE ONCOSMOTIN-M SPECIFIC RECEPTOR BETA SUBUNIT.
GN OSMB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA MOSLEY B., DE IMOS C., FRIEND D., BOIANI N., THOMA B., PARK L.,
RA COSMAN D.;
RL J. Biol. Chem. 271:32635-32643(1996).
DR EMBL; U60805; AAC50946.1;
DR PFM; PFM0041; fn3; 4
SQ SEQUENCE 979 AA; 110508 MW; 965DE8BC CRC32;

Query Match

Best Local Similarity 33.9%; Pred. No. 0.14;
Matches 21; Conservative 10; Mismatches 26; Indels 5; Gaps 2;

QY 56 NLNCSR--QOSGNLVCHARDGSI---LAGSCLVGLPPEKPFNISCWERNMDLTCRW 110
DB 199 NLNCPVPIRNKGTNYCEASQGNVSEGMKGVILEPVSYLEPKDFSCETEDFTLHCTWD 258
QY 111 PG 112
DB 259 PG 260

RESULT 15

062121

PRELIMINARY; PRT; 856 AA.

AC Q62121;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAY-1999 (TREMblrel. 10, Last annotation update)
DE PROTEIN TYROSINE KINASE.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 94150990.
RA FUJIMOTO J., YAMAMOTO T.;
RT "btl, a mouse gene encoding a novel receptor-type protein-tyrosine
kinase, is preferentially expressed in the brain."
RL Oncogene 9:693-698(1994).
DR EMBL; D17393; BAA04216.1;
DR MGI; MGI:104294; TRO3.
DR PFM; PFM0041; fn3; 2.
DR PFM; PFM0047; fn3; 2.
DR PFM; PFM0069; PKinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

SQ SEQUENCE 856 AA; 93930 MW; 2DFBFC94 CRC32;

Query Match

Best Local Similarity 23.0%; Pred. No. 0.15;
Matches 48; Conservative 24; Mismatches 62; Indels 75; Gaps 11;

QY 11 QATCSIHGDPGATAGELYWTFNGRLPSELSTLALANLINGSRQSGDNLVC 70
DB 143 QLSCEAVGPEPEPT---LYW-WRG-----LTNKGPAPEPFVL-NVTGVTQRT--EFSC 169
QY 71 HARDGSLAGS---CLYVGLPPEKPFNISCWERNMDLTCRWTPGAHGETFLH----- 121
DB 190 EARNINGLATSRPAIVRLQAPPAPEFTVTTISYNASVAVWPGADGALLHSCVQVA 249
QY 121 -----TYSIKYKRLVRSXHNKGVPHCEPSLMYP 152
DB 250 HARGEMBALAVVPVPPFTCLNLAIPATVYSLVR-----CANAL----- 291
QY 153 QGPGP--LHSLXDLGSHOSPRLSKIXCP 179
DB 291 -GPSPTRLGALSDKPS--AAELRLISMP 316

Search completed: September 16, 1999, 20:40:11
Job time: 5562 sec

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: September 17, 1999, 03:08:16 ; Search time 64.1 Seconds

(without alignments)
11.086 Million cell updates/sec

Title: US-09-037-657-32

Perfect score: 139

Sequence: 1 MVLASSTSIHMLLMLFHLGLQASIS 30

Scoring table: BLOSUM62

Searched: 188963 segs, 23686106 residues

Database: A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	139	100.0	166	1 P50161	Sequence encoded b
2	139	100.0	30	1 M10638	Murine IL-3 signal
3	139	100.0	30	1 M09823	Interleukin-3 sign
4	139	100.0	359	1 M56260	Construct containi
5	139	100.0	30	1 M55017	Murine IL3 signal
6	48	34.5	694	1 M31267	Drosophila frizzele
7	46	33.1	116	1 R71911	Antifer specific pro
8	45	32.4	96	1 M46836	Bacillus thuringie
9	45	32.4	652	1 M30637	Human 7-transmembr
10	45	32.4	521	1 M30638	Partial human 7-tr
11	43	30.9	1268	1 M58774	Human breast cancer
12	43	30.9	481	1 M55029	G-protein coupled
13	43	30.9	542	1 M55030	G-protein coupled
14	42	30.2	266	1 M71460	Protein encoded by
15	42	30.2	306	1 M90236	E. coli antibiotic
16	42	30.2	299	1 M90237	E. coli antibiotic
17	42	30.2	266	1 M90238	E. coli antibiotic
18	42	30.2	51	1 Y02760	Human secreted pro
19	42	30.2	55	1 Y12970	Protein sequence c
20	41.5	29.9	428	1 M63713	Human hR1 protein
21	41.5	29.9	427	1 M98017	Human calcium acti
22	41	29.5	315	1 R43568	Mouse MSH-R. Melan
23	41	29.5	709	1 R99801	CRIL-7 nerve prote
24	41	29.5	315	1 M37826	Mouse melanocyte s
25	41	29.5	315	1 M87864	Mouse melanocyte s
26	40	28.8	336	1 R28149	Sugar beet beta-1,
27	40	28.8	1276	1 R35199	Mouse multidrug re
28	40	28.8	30	1 R63638	Sheep erythropoiet
29	40	28.8	32	1 R65246	N-terminal of 48 k
30	40	28.8	508	1 R75757	BAV3 ORF2 product
31	40	28.8	523	1 M78915	Bovine butyrophili
32	40	28.8	248	1 M94567	Mouse major periph
33	40	28.8	45	1 Y12940	Amino acid sequenc
34	39.5	28.4	132	1 P70411	ORF 8 gene product
35	39.5	28.4	244	1 M29149	Human high affinity
36	39.5	28.4	244	1 M29149	Human beta subunit
37	39	28.1	1093	1 R05332	Human lymphotoxin
38	39	28.1	1093	1 R56879	Human myotonic dys
39	39	28.1	206	1 R82672	CD45 associating p
40	39	28.1	1989	1 R99640	Peripheral nervous
41	39	28.1	1977	1 R99641	Peripheral nervous
42	39	28.1	467	1 M00382	Bacillus cellulase
43	39	28.1	467	1 M05731	Cellulase. Cellula

ALIGNMENTS

44	39	28.1	81	1 M30082
45	39	28.1	164	1 M38705

Rat persepilin, GDN
S. pneumoniae phos

RESULT 1
ID P50161 standard; Protein; 166 AA.
AC P50161;
DE 27-NOV-1991 (first entry)
DE Sequence encoded by cDNA clone exhibiting multi-lineage cellular
DE growth factor activity.
DE Growth factor; multi-lineage; mast cell; haematopoietic.
OS Mus musculus.
PN EP-138133-A.
PD 24-APR-1985.
PF 29-SEP-1984; US-539050.
PR 04-OCT-1983; US-539050.
PR 19-MAR-1984; US-539050.
PA (SCHE) SCHERING CORP.
PA (DNAX-) DNAX RES INST MOLEC.
PI Tokota T, Lee FD, Remnick DM, Aral KI;
DR WPI: 85-100349/17.
DR N-PSDB; N50199.
PT New poly(peptide(s) having growth factor activities - are prepd.
PT by recombinant DNA procedures
PS Claim 5; Fig 1; 64pp; English.
CC The cDNA is derived from messenger RNA isolated from a mouse T-cell
CC line after activation with concanavalin A. The cDNA was cloned by
CC incorporation into a plasmid vector, which then transformed into
CC E.coli. The plasmid vector also contained DNA segments from the SV40
CC virus, permitting expression of the cDNA after transfection into a
CC mammalian host cell, such as monkey COS-7 cells. The polypeptide
CC includes a potential leader sequence of about 19 AAs.
SO Sequence 166 AA.

Query Match 100.0%; Score 139; DB 1; Length 166;
Best local Similarity 100.0%; Pred. No. 7.2e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1 MVLASSTSIHMLLMLFHLGLQASIS 30
Db 1 MVLASSTSIHMLLMLFHLGLQASIS 30

RESULT 2
ID M10638 standard; Peptide; 30 AA.
AC M10638;
DE 23-JUN-1997 (first entry)
DE Murine IL-3 signal sequence.
DE LERK; ligand for eph-related kinase; ERK; NLERK;
KW receptor protein tyrosine kinase; cell proliferation;
KW cell differentiation; cell survival; nerve cell; interleukin-3;
KW IL-3; signal peptide; protein secretion.
OS Mus sp.
PN M09704091-A1.
PD 06-FEB-1997.
PF 19-JUL-1996; AU0460.
PR 20-JUL-1995; AU-004263.
PR 27-NOV-1995; AU-006847.
PR 22-DEC-1995; AU-007299.
PR 05-FEB-1996; AU-007890.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PI Nicotiana glauca.
DR WPI: 97-132632/12.
PT Nucleic acid mol. encoding ligand for eph-related kinase - useful
PT for treatment of, pref. neuronal, cells to increase survival,
PT proliferation and differentiation
PS Example 3; Page 30; 71pp; English.

CC A peptide sequence (W10638) comprises the signal sequence of
 CC mouse interleukin-3 (IL-3). Mammalian expression vector pEF-BOS
 CC was engineered to contain DNA for the IL-3 signal sequence and for
 CC a FLAG epitope. PCR fragments (see also T60970-72) coding for
 CC mature or soluble NLERK2 (see also W10637), a novel ligand for
 CC eph kinase (LERK), were cloned into the vector to allow prodn. of
 CC recombinant NLERK2 proteins in transfected COS cells.
 SQ Sequence 30 AA;

Query Match 100.0%; Score 139; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 1e-14;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MYLASSTSIHTMLLMFLHGLQASIS 30
 DB 1 MYLASSTSIHTMLLMFLHGLQASIS 30

RESULT 3
 ID W09823 standard; Peptide; 30 AA.
 AC W09823;
 DT 15-JUL-1997 (first entry)
 DE Interleukin-3 signal peptide.
 KW Interleukin-3; IL-3; signal peptide; NR4; haemopoietin receptor;
 OS Mus sp.
 PN W09715663-A1.
 PD 01-MAY-1997.
 PR 23-OCT-1996; AU00668.
 PR 23-OCT-1995; AU-006135.
 PR 22-DEC-1995; AU-007276.
 PR 09-SEP-1996; AU-002208.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PI Hilton DJ, Metcalf D, Nicola NA, Willson T, Zhang JG;
 DR WPI; 97-259018/23.
 PT DNA encoding animal haemopoietin receptor which interacts with
 PT Interleukin-13 - useful to treat asthma, allergy or condition
 PS Excerpted by IGE Production
 PS Example 2; Page 56; 93pp; English.
 CC Using PCR, a derivative of novel haemopoietin receptor NR4 cDNA was
 CC generated which encoded the interleukin-3 signal peptide (W09823)
 CC and an N-terminal FLAG epitope tag (W09824) preceding the mature
 CC coding region (Thr27-Pro424) of murine NR4 (see also W09821). The
 CC PCR product was cloned into the mammalian expression vector
 CC pEF-BOS.
 SQ Sequence 30 AA;

Query Match 100.0%; Score 139; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 1e-14;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MYLASSTSIHTMLLMFLHGLQASIS 30
 DB 1 MYLASSTSIHTMLLMFLHGLQASIS 30

RESULT 4
 ID W56260 standard; Protein; 359 AA.
 AC W56260;
 DT 16-SEP-1998 (first entry)
 DE Construct containing mature interleukin-13 binding protein.
 KW Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis;
 KW autoimmune disease; antibody; immunotherapy.
 OS Homo sapiens.
 PN W09810638-A1.
 PD 19-MAR-1998.
 PF 10-SEP-1997; AU00591.
 PR 27-FEB-1997; AU-005374.
 PR 10-SEP-1996; AU-002262.

PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PI Hilton DJ, Nicola NA, Simpson RJ, Zhang J;
 DR WPI; 98-207062/18.
 DR N-PSD; V22701.
 PT New isolated interleukin-13 binding protein - used to develop
 PT products for therapy e.g. for allergic conditions such as asthma or
 PT for diagnosis or detection
 PS Example 14; Page 52-53; 69pp; English.

CC The IL-13 binding protein and related therapeutic molecules can be used
 CC in the antagonism of at least one IL-13 activity. They can be used for
 CC treating IL-13 mediated conditions such as certain allergic conditions
 CC such as asthma or to inactivate locally administered IL-13 after IL-13
 CC treatment. The products can also be used as diagnostic agents, e.g. for
 CC detecting autoimmune diseases. The antibodies can also be used for
 CC immunotherapy and may also be used as a diagnostic tool.
 SQ Sequence 359 AA;

Query Match 100.0%; Score 139; DB 1; Length 359;
 Best Local Similarity 100.0%; Pred. No. 1.7e-13;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MYLASSTSIHTMLLMFLHGLQASIS 30
 DB 1 MYLASSTSIHTMLLMFLHGLQASIS 30

RESULT 5
 ID W55017 standard; Protein; 30 AA.
 AC W55017;
 DT 28-SEP-1998 (first entry)
 DE Murine IL3 signal sequence.
 KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
 KW cell survival; therapeutic; neuronal proliferation; drug screening;
 OS Mouse.
 PN W09811225-A2.
 PD 19-MAR-1998.
 PF 11-SEP-1997; G02479.
 PR 11-SEP-1996; AU-002246.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PA (DZIE) DZIELEMSKA H E.
 PI Alexander W, Fabry L, Farley A, Hilton DJ, Kikuchi Y,
 PI Kojima T, Meda W, Nash A, Nicola NA, Rakar S, Willson T,
 PI Zhang J;
 DR WPI; 98-260970/23.
 PT New isolated haemopoietin receptor - used for developing products
 PT for modulating proliferation, differentiation and survival of cells,
 PS e.g. neuronal cells
 PS Claim 29(1); Page 54; 182pp; English.
 CC The mouse IL3 signal sequence was used to study the expression of mouse
 CC NR6.1. NR6.1 is a form of NR6 a novel Haemopoietin receptor (HR).
 CC Interaction between the novel HR and a ligand facilitates proliferation,
 CC differentiation and survival of a wide variety of cells. The HR and it's
 CC derivatives can be used for modulating the activity of the receptors e.g.
 CC to regulate development, maintenance or regeneration in an array of
 CC different cells and tissues in vitro and in vivo. They can be present in
 CC therapeutics used for modulating neuronal proliferation, differentiation
 CC and survival. The products can also be used for detection and diagnosis,
 CC e.g. for cancers or predisposition to cancers, or for drug screening.
 SQ Sequence 30 AA;

Query Match 100.0%; Score 139; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 1e-14;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MYLASSTSIHTMLLMFLHGLQASIS 30
 DB 1 MYLASSTSIHTMLLMFLHGLQASIS 30

RESULT 6

W31267 standard; Protein; 694 AA.

AC W31267; (first entry)

DE Drosophila frizzled-2 protein (Wnt receptor).

KW Wnt receptor; Drosophila frizzled-2 protein; Dfz2 gene; wingless receptor; Wg receptor; signal transduction; cancer; cell growth; cell proliferation.

OS Drosophila melanogaster.

Key location/Qualifiers

FT Misc_difference 268 /note= "encoded by CAC"

FT Misc_difference 269 /note= "encoded by CAC"

FT Misc_difference 348 /note= "encoded by TGC"

FT Misc_difference 348 /note= "encoded by TA (apparent 1 nucleotide deletion of codon)"

FT Misc_difference 488 /note= "encoded by TTA"

FT Misc_difference 632 /note= "encoded by CTG"

FT Misc_difference 633 /note= "encoded by GCG"

FT Misc_difference 671 /note= "encoded by GCG"

FT /note= "encoded by CG (apparent 1 nucleotide deletion of codon)"

MO9739357-A1.

PD 23-OCT-1997.

PF 11-APR-1997; U06049.

PR 12-APR-1996; US-015307.

PA (UYXO) UNIV JOHNS HOPKINS.

PA (STRD) UNIV LELAND STARFORD JUNIOR.

PI Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J, Nusse R, Samos CH, Wang Y, WPI; 97-526631/48.

DR N-PSDB; T89885.

PT Identification of Wnt receptor binding modulators - useful for treatment of cancer and growth, development or proliferation related disorders

PS Claim 2; Page 23-25; 61pp; English.

CC This protein comprises the Drosophila frizzled-2 protein encoded by the Dfz2 gene (see T89885). It is a receptor for wingless (Wg) acting as a signal transducing molecule, and is an example of a Wnt receptor (WntR). Other novel frizzled family members have been identified in human, mouse and Caenorhabditis elegans (see W31268-74) and are considered also to be Wnt receptors. Wnt proteins involved in a novel, claimed method of screening for compounds which modulate the binding of a Wnt polypeptide (secreted for CC receptors used in a novel, claimed method of screening for Wnt is involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal). CC Modulators identified by the claimed method are useful for treatment of diseases related to these conditions.

SO Sequence 694 AA.

Query Match 34.5%; Score 48; DB 1; Length 694;
Best Local Similarity 31.0%; Pred. No. 16;
Matches 9; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 MYLASSSTSIHMLLLMLLFLHGLQAST 29

DB 383 LTLRESSTGPHSCTLVFLTYFFGMASST 411

RESULT 7

R71911 standard; Protein; 116 AA.

AC R71911; (first entry)

DE 22-NOV-1995 (first entry)

DE Anther specific protein.

KW Anther specific gene; Brassica napus; antisense RNA; Cruciferae;

KW Pollen formation; male sterile plant.

OS Brassica napus.

PN 307059573-A.

PD 07-MAR-1995.

PR 20-AUG-1993; 206459.

PR 20-AUG-1993; JP-206459.

PA (MITS) MITSUBISHI CORP.

PA (MITU) MITSUBISHI KASEI CORP.

DR WPI; 95-135897/18.

DR N-PSDB; Q87926.

PT A gene expressed specifically in anther(s) - used for the preparation of male sterile Cruciferae plants

PS Claim 1; Page 5; 6pp; Japanese.

CC This sequence is encoded by an anther specific gene derived from Brassica napus. This gene may be expressed as antisense RNA in a CC Cruciferae plant causing pollen formation to be modified. This is esp. useful in the production of male sterile plants.

SO Sequence 116 AA.

Query Match 33.1%; Score 46; DB 1; Length 116;
Best Local Similarity 38.5%; Pred. No. 4.3;
Matches 10; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 5 SRTTSIHMLLLMLLFLHGLQASTS 30

DB 2 SKTKYSSFCCLLVFFLNSQFALS 27

RESULT 8

W46836 standard; Protein; 96 AA.

AC W46836;

DE 11-JUN-1998 (first entry)

DE Bacillus thuringiensis toxin designated 85N2.

KW Toxin; lepidopteran pest; control; Agrotis ipsilon; black cutworm; Heliothis virescens; Helicoverpa zea.

OS Bacillus thuringiensis.

Key location/Qualifiers

FT Misc_difference 23 /label= unknown

FT /note= "encoded by TAA"

FT Misc_difference 24 /label= unknown

FT /note= "encoded by TAA"

FT Misc_difference 37 /label= unknown

FT /note= "encoded by TAA"

FT Misc_difference 39 /label= unknown

FT /note= "encoded by TAG"

FT Misc_difference 45 /label= unknown

FT /note= "encoded by TAG"

FT Misc_difference 47 /label= unknown

FT /note= "encoded by TAG"

FT Misc_difference 49 /label= unknown

FT /note= "encoded by TGA"

FT Misc_difference 81 /label= unknown

FT /note= "encoded by TAA"

FT Misc_difference 84 /label= unknown

FT /note= "encoded by TAA"

FT /label= unknown

FT /note= "encoded by TAG"

PN W09800546-A2.

PD 08-JAN-1998.

PF 01-JUL-1997; U11658.

PR 01-JUL-1996; US-674002.

PA (MYCO) MYCOGEN CORP.

PI Narva KE, Schnepf HE, Stockhoff BA, Walz M, Wicker C; WPI; 98-086971/08.

RESULT 11
 ID W58774 standard; Protein: 1268 AA.
 AC W58774.
 DT 21-JUL-1998 (first entry)
 DE Human breast cancer gene CH1-9a11-2 protein fragment #1.
 KW Breast cancer; CH1-9a11-2; malignant transformation; diagnostic; therapeutic; screening.
 OS Homo sapiens.
 PN W09738085-A2.
 PD 16-OCT-1997.
 PF 09-APR-1997; U059330.
 PR 10-JUL-1996; US-678280.
 PR 09-APR-1996; US-015167.
 PR 05-JUN-1996; WO-009286.
 PR 06-JUN-1996; US-019202.
 PA (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.
 PI Chen L, Smith H;
 DR WPI: 97-512705/47.
 DR N-PSDB: V10696.
 PT Breast cancer genes - used to develop products to design or screen diagnostic reagents or therapeutic compounds
 PS Claim 17; Fig 24; 118pp; English.
 CC W58774-W58804 are translated protein fragments from the novel human breast cancer gene, CH9-2a11-2 isolated from a 3.5 kb DNA fragment. This fragment can be used for identifying genes and gene products that are intimately related to malignant transformation or maintenance of the malignant properties of cancer cells. It can also be used to design or screen diagnostic reagents or therapeutic compounds. Kits are included within the scope of the invention.
 SO Sequence 1268 AA;

Query Match 30.9%; Score 43; DB 1; Length 1268;
 Best Local Similarity 50.0%; Pred. No. 1.8e+02;
 Matches 11; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 4 ASSTSIHTMLLMFLHGL 25
 17 AIALRTIGHIALRLRLMLGL 38

RESULT 12
 ID W55029 standard; Protein: 481 AA.
 AC W55029;
 DT 17-SEP-1998 (first entry)
 DE G-protein coupled receptor; short form.
 KW G-protein coupled receptor; gene therapy; abnormality detection;
 OS Homo sapiens.
 PN EP-845529-A2.
 PD 03-JUN-1998.
 PF 27-OCT-1997; 308562.
 PR 29-OCT-1996; JP-286823.
 PA (TAKE) TAKEDA CHEM IND LTD.
 PI Fukusumi S, Hinuma S, Kawamata Y;
 DR WPI: 98-288746/26.
 DR N-PSDB: V271174.
 PT New human G-protein coupled receptor protein - and corresponding DNA, ligands, antibodies, etc
 PS Claim 1; Page 42-44; 65pp; English.
 CC This sequence represents a human G-protein coupled receptor of the invention. The protein or cells expressing the DNA encoding it can be used to screen for agonists or antagonists of the receptor, which can be used as drugs for treating various diseases (none disclosed). The DNA can also be used for practice drug design based on comparisons with structurally analogous ligands and receptors. DNA encoding the protein can be used for gene therapy for diseases caused by a deficiency of the receptor. The DNA can also be used to detect abnormalities in the gene encoding the receptor. The protein or fragment can be used to determine levels of receptor ligands in vivo. The antibody can be used in assays to detect the protein.

SO Sequence 481 AA;

Query Match 30.9%; Score 43; DB 1; Length 481;
 Best Local Similarity 28.6%; Pred. No. 61;
 Matches 8; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

OY 3 LASSTSIHTMLLMFLHGLQASIS 30
 123 VTSSYSAYAILMLALVFAVGIVGNTLS 150

RESULT 13
 ID W55030 standard; Protein: 542 AA.
 AC W55030;
 DT 17-SEP-1998 (first entry)
 DE G-protein coupled receptor; long form.
 KW G-protein coupled receptor; gene therapy; abnormality detection;
 OS Homo sapiens.
 PN EP-845529-A2.
 PD 03-JUN-1998.
 PF 27-OCT-1997; 308562.
 PR 29-OCT-1996; JP-286823.
 PA (TAKE) TAKEDA CHEM IND LTD.
 PI Fukusumi S, Hinuma S, Kawamata Y;
 DR WPI: 98-288746/26.
 DR N-PSDB: V271175.
 PT New human G-protein coupled receptor protein - and corresponding DNA, ligands, antibodies, etc
 PS Claim 2; Page 45-47; 65pp; English.
 CC This sequence represents a human G-protein coupled receptor of the invention. The protein or cells expressing the DNA encoding it can be used to screen for agonists or antagonists of the receptor, which can be used as drugs for treating various diseases (none disclosed). The DNA can also be used for practice drug design based on comparisons with structurally analogous ligands and receptors. DNA encoding the protein can be used for gene therapy for diseases caused by a deficiency of the receptor. The DNA can also be used to detect abnormalities in the gene encoding the receptor. The protein or fragment can be used to determine levels of receptor ligands in vivo. The antibody can be used in assays to detect the protein.
 SO Sequence 542 AA;

Query Match 30.9%; Score 43; DB 1; Length 542;
 Best Local Similarity 28.6%; Pred. No. 70;
 Matches 8; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

OY 3 LASSTSIHTMLLMFLHGLQASIS 30
 184 VTSSYSAYAILMLALVFAVGIVGNTLS 211

RESULT 14
 ID W71460 standard; Protein: 266 AA.
 AC W71460;
 DT 07-DEC-1998 (first entry)
 DE Protein encoded by ORF 266.
 KW Multiple antibiotic resistance operon; mar; antisense;
 OS Escherichia coli.
 PN US5817793-A.
 PD 06-OCT-1998.
 PF 08-AUG-1994; 225480.
 PR 08-APR-1994; US-225480.
 PR 28-AUG-1992; US-938085.
 PA (TUFT) TUFTS COLLEGE.
 PI Levy SB;
 DR WPI: 98-556472/47.
 DR N-PSDB: V60383.

PT DNA encoding activator of multiple antibiotic resistance operon -
 PT and anti-sense molecule for lowering antibiotic resistance of
 PT bacteria
 PS Disclosure: Columns 35-38; 22pp; English.
 CC The present sequence represents the protein encoded by open
 CC reading frame (ORF) 266 of *Escherichia coli* multiple antibiotic
 CC resistance (mar) operon. Antisense molecules directed against the
 CC mar operon can be used to lower the resistance of bacteria to
 CC antibiotics.
 SQ Sequence 266 AA;

Query Match 30.2%; Score 42; DB 1; Length 266;
 Best Local Similarity 30.3%; Pred. No. 44;
 Matches 10; Conservative 9; Mismatches 10; Indels 4; Gaps 1;

OY 1 MYLASTTSHTMLL---LMLFHLGLQASI 29
 DB 161 LILDGSAIMHSLVITDMITLIMYLAFAVATI 193

RESULT 15

W90236
 ID W90236 standard; protein; 306 AA.
 AC W90236;
 DT 30-MAR-1999 (first entry)
 DE E. coli antibiotic efflux protein fragment #2.
 KW Antibiotic efflux gene; fermentation; L-cysteine; L-cysteine; toxic;
 OS N-acetyl-serine; thiazolidine derivative; cellular clearance; secretion.
 PN *Escherichia coli*.
 FN EP-885962-A1.
 PD 23-DEC-1998.
 PF 22-MAY-1998; 109269.
 PR 19-JUN-1997; DE-026083.
 PA (CONE) CONSORTIUM ELEKTROCHEM IND GMBH.
 PI Leinfelder W, Winterhalter C;
 DR WPI; 99-047559/05.
 PT Microbial strain over-expressing antibiotic efflux gene - for
 PT producing L-cysteine, L-cysteine, N-acetyl-serine and/or thiazolidine
 PT derivatives
 PS Claim 5; Page 16-17; 33pp; German.
 CC This sequence is a fragment of an antibiotic efflux protein from
 CC *Escherichia coli* strain K12 which is used as a method resulting in a
 CC novel microbial strain which is suitable for the fermentative production
 CC of L-cysteine, L-cysteine, N-acetyl-serine and/or thiazolidine derivatives
 CC and over-expresses at least one gene coding for a protein that mediates
 CC cellular clearance of antibiotics or other substances that are toxic for
 CC the microorganism. A process is described for producing L-cysteine, in
 CC which intracellularly produced L-cysteine reacts with an intracellular
 CC ketone or aldehyde in a microorganism to form a thiazolidine derivative.
 CC The thiazolidine derivative is secreted from the microorganism by
 CC means of a protein that mediates cellular clearance of antibiotics or
 CC other substances that are toxic for the microorganism, and optionally
 CC after separating the thiazolidine derivative. L-cysteine is recovered by
 CC equilibrium displacement of the reaction equilibrium between L-cysteine
 CC and the thiazolidine derivative in the direction of L-cysteine.
 SQ Sequence 306 AA;

Query Match 30.2%; Score 42; DB 1; Length 306;
 Best Local Similarity 30.3%; Pred. No. 52;
 Matches 10; Conservative 9; Mismatches 10; Indels 4; Gaps 1;

OY 1 MYLASTTSHTMLL---LMLFHLGLQASI 29
 DB 201 LILDGSAIMHSLVITDMITLIMYLAFAVATI 233

Search completed: September 17, 1999, 03:08:19
 Job time: 310 sec

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: September 16, 1999, 20:41:11 ; Search time 53.94 Seconds

(without alignments)
5.489 Million cell updates/sec

Title: US-09-037-657-32

Perfect score: 139
Sequence: 1 WVLASSTSIHTMLLMFHLGLASIS 30

Scoring table: BLOSUM62

Searched: 106577 seqs, 9868381 residues

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/2/1aa/5A.CONB.pep.*
- 2: /cgn2_6/ptodata/2/1aa/5B.CONB.pep.*
- 3: /cgn2_6/ptodata/2/1aa/PTUS9.CONB.pep.*
- 4: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	43	30.9	30	4	5304637-4	Patent No. 5304637
2	42	30.2	396	1	US-08-208-007A-13	Sequence 13, Appl
3	42	30.2	266	1	US-08-225-480-7	Sequence 7, Appl
4	41	29.5	315	1	US-07-866-979-4	Sequence 4, Appl
5	41	29.5	315	2	US-08-466-906B-4	Sequence 4, Appl
6	40	28.8	308	2	US-08-164-292B-18	Sequence 18, Appl
7	40	28.8	22	2	US-08-446-875-6	Sequence 6, Appl
8	40	28.8	581	2	US-08-724-334A-3	Sequence 3, Appl
9	40	28.8	30	3	PCT-US94-04361-31	Sequence 31, Appl
10	39.5	28.4	244	2	US-07-869-933-32	Sequence 32, Appl
11	39.5	28.4	244	2	US-08-201-879A-3	Sequence 3, Appl
12	39	28.1	206	1	US-08-197-793-2	Sequence 2, Appl
13	39	28.1	206	2	US-08-638-176-2	Sequence 2, Appl
14	39	28.1	467	2	US-08-727-348-2	Sequence 2, Appl
15	39	28.1	206	3	PCT-US95-01618-2	Sequence 2, Appl
16	38.5	27.7	1873	1	US-08-435-675B-4	Sequence 4, Appl
17	38.5	27.7	1873	1	US-08-336-257A-7	Sequence 7, Appl
18	38.5	27.7	954	2	US-08-749-169A-3	Sequence 3, Appl
19	38	27.3	408	1	US-07-916-901-2	Sequence 2, Appl
20	38	27.3	78	1	US-07-778-413E-12	Sequence 12, Appl
21	38	27.3	353	1	US-08-118-270-45	Sequence 45, Appl
22	38	27.3	78	1	US-08-340-102-12	Sequence 12, Appl
23	38	27.3	402	1	US-08-444-734A-6	Sequence 6, Appl
24	38	27.3	114	1	US-08-352-324A-3	Sequence 3, Appl
25	38	27.3	408	1	US-08-351-473B-3	Sequence 3, Appl
26	38	27.3	78	1	US-08-330-163-8	Sequence 8, Appl
27	38	27.3	93	1	US-08-480-449-2	Sequence 2, Appl
28	38	27.3	402	1	US-08-087-722A-15	Sequence 15, Appl
29	38	27.3	111	1	US-08-417-460-4	Sequence 4, Appl
30	38	27.3	879	1	US-08-554-612C-1	Sequence 1, Appl
31	38	27.3	78	2	US-08-482-111-8	Sequence 8, Appl
32	38	27.3	78	2	US-08-436-420-32	Sequence 32, Appl
33	38	27.3	114	2	US-08-862-607-3	Sequence 3, Appl
34	38	27.3	419	2	US-08-270-581-2	Sequence 2, Appl
35	38	27.3	148	2	US-08-791-924-3	Sequence 4, Appl
36	38	27.3	114	2	US-08-468-819-4	Sequence 4, Appl
37	38	27.3	400	2	US-08-103-170-9	Sequence 9, Appl
38	38	27.3	24	2	US-08-103-170-30	Sequence 30, Appl
39	38	27.3	353	3	PCT-US93-08528-45	Sequence 45, Appl

40	38	27.3	93	3	PCT-US95-07294-2	Sequence 2, Appl
41	38	27.3	114	3	PCT-US95-16144-3	Sequence 3, Appl
42	37.5	27.0	1968	1	US-07-745-206A-7	Sequence 7, Appl
43	37.5	27.0	426	1	US-08-455-550-21	Sequence 21, Appl
44	37.5	27.0	1968	2	US-08-455-543A-45	Sequence 45, Appl
45	37.5	27.0	1968	2	US-08-223-305C-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
5304637-4
Patent No. 5304637
APPLICANT: DORSSERS, LAMBERTUS C.J.; WAGEMAKER, GERARD; VOS, YONNE J.; VAN LEEN, ROBERT M.; PERSSON, MARIA L.N.
TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF HUMAN INTERLEUKIN-3 AND KOTELINS THEREOF
NUMBER OF SEQUENCES: 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/494,182
FILING DATE: 13-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 249,184
FILING DATE: 16-AUG-1988
SEQ ID NO: 4:
LENGTH: 139
5304637-4

Query Match 30.9%; Score 43; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVLASSTSI 10
DB 1 WVLASSTSI 10

RESULT 2
US-08-208-007A-13
Sequence 13, Application US/08208007A
Patent No. 5501969
GENERAL INFORMATION:
APPLICANT: HASTINGS, ET AL.
TITLE OF INVENTION: Human Osteoclast-Derived Cathepsin
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
STREET: 6 BROOKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/208,007A
FILING DATE: March 8, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 5501969e
FILING DATE: No. 5501969e
ATTORNEY/AGENT INFORMATION:
NAME: PERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-95
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS: LINEAR
MOLECULE TYPE: PROTEIN
US-08-208-007A-13

Query Match 30.2% Score 42; DB 1; Length 396;
Best Local Similarity 69.2% Pred. No. 46;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 12 TWLILMLFHG 24
Db 3 TLLELLVLELG 15

RESULT 3
US-08-225-480-7
Sequence 7, Application US/08225480
Patent No. 3817793
GENERAL INFORMATION:

APPLICANT: LEVY, STUART B.
TITLE OF INVENTION: MULTIPLE ANTIBIOTIC RESISTANCE OPERON
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,480
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,085
FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: T0359/7003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 266 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-225-480-7

Query Match 30.2% Score 42; DB 2; Length 266;
Best Local Similarity 30.3% Pred. No. 30;
Matches 10; Conservative 9; Mismatches 10; Indels 4; Gaps 1;

OY 1 MWLASSTSIHTMLL-----LMLFHGLDAST 29
Db 161 LIIDGSKMHSVLTIDMTTILSLMIAFVATI 193

RESULT 4
US-07-866-979-4
Sequence 4, Application US/07866979
Patent No. 5532347
GENERAL INFORMATION:

APPLICANT: Cone, Roger D
TITLE OF INVENTION: Mountjoy, Kathleen G
TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/866,979
FILING DATE: 19920410
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: No. 5532347nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,154
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-866-979-4

Query Match 29.5% Score 41; DB 1; Length 315;
Best Local Similarity 41.4% Pred. No. 50;
Matches 12; Conservative 4; Mismatches 9; Indels 4; Gaps 1;

OY 3 LASSTSI---HTMLLMLFHGLQA 27
Db 171 IVSSTLEITYKHTAVLCLVTFFLAMLA 199

RESULT 5
US-08-466-906B-4

Sequence 4, Application US/08466906B
Patent No. 5849871
GENERAL INFORMATION:

APPLICANT: Cone, Roger D
TITLE OF INVENTION: Mountjoy, Kathleen G
TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,906B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: No. 5849871nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,154-H
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-466-906B-4

Query Match 29.5% Score 41; DB 2; Length 315;
Best Local Similarity 41.4%; Pred. No. 50;
Matches 12; Conservative 4; Mismatches 9; Indels 4; Gaps 1;

OY 3 LASSTST---HTMLLLMLFLHGLA 27
DB 171 IVSSLTFTTYKHYKVALCLVTFELMMA 199

RESULT 6
US-08-164-292B-18
Sequence 18; Application US/08164292B
Patent No. 5820868
GENERAL INFORMATION:
APPLICANT: MITTAL, SURESH K.
APPLICANT: GRAHAM, FRANK L.
APPLICANT: PREVEC, LUDVIG
APPLICANT: BABIUK, LORNE A.
TITLE OF INVENTION: RECOMBINANT PROTEIN PRODUCTION IN BOVINE
TITLE OF INVENTION: ADENOVIRUS EXPRESSION VECTOR SYSTEM
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 345 California Street
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94104-2675
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,292B
FILING DATE: 09-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GRACEY, NANCY J.
REGISTRATION NUMBER: 28,216
REFERENCE/DOCKET NUMBER: 29310-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 677-7000
TELEFAX: (415) 677-7522
TELEX: 34-0154
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 308 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-164-292B-18

Query Match 28.8% Score 40; DB 2; Length 308;
Best Local Similarity 45.5%; Pred. No. 68;
Matches 10; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

OY 4 ASSTSTHTMLLLMLFLHGL 25
DB 19 ASSPTSMKGFLLIFSLVHCP 40

RESULT 7
US-08-446-875-6
Sequence 6; Application US/08446875
Patent No. 5858751
GENERAL INFORMATION:
APPLICANT: Paulson, James C.
APPLICANT: Wen, Xiaohong
APPLICANT: Livingston, Brian Duane
APPLICANT: Gillespie, William
APPLICANT: Keim, Sorge
APPLICANT: Burlingame, Alma L.
APPLICANT: Medzihadszky, Katalin
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Identification and Synthesis of Sialyltransferases
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Poma, Smith, Lande & Rose
STREET: 2029 Century Park East, Suite 3800
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,875
FILING DATE: July 12, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/102,385
FILING DATE: August 4, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 111-197
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 788-5000
TELEFAX: (310) 277-1297
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: porcine
FEATURE:
NAME/KEY: Region
LOCATION: 1..22
OTHER INFORMATION: /label=48KDa
OTHER INFORMATION: /note="amino terminal amino acid sequence of the
OTHER INFORMATION: porcine 48 KDa Gal Beta1,3 GalNAc alpha 2,3
OTHER INFORMATION: sialyltransferase"
FEATURE:
NAME/KEY: Domain
LOCATION: 5..20
OTHER INFORMATION: /note="putative signal-anchor
OTHER INFORMATION: domain"

ZIP: 22313-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/869,933
 FILING DATE: 19920416
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 40399/154 NIHD
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703)836-9300
 TELEFAX: (703)836-4109
 TELEX: 899149
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 244 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: homo sapien
 STRAIN: FCRI beta subunit
 US-07-869-933-32

Query Match

Best Local Similarity 39.3%; Score 39.5; DB 2; Length 244;

Matches 11; Conservative 7; Mismatches 7; Indels 3; Gaps 1;

QY 3 LASTSTSHMTLLMLLFLHGLQASIS 30
 Db 174 MASSTSEIVVMFLRI--LGLSAYS 198

RESULT 11

US-08-201-879A-3
 Sequence 3, Application US/08201879A
 Patent No. 5807988
 GENERAL INFORMATION:
 APPLICANT: KINET, Jean-Pierre
 APPLICANT: JOUVIN, Marie-Helene
 TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
 TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/201,879A
 FILING DATE: 24-FEB-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/869,933
 FILING DATE: 16-APR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/03419
 FILING DATE: 16-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 40399/234/NIHD
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)672-5300
 TELEFAX: (202)672-5399
 TELEX: 904136

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
 LENGTH: 244 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-201-879A-3

Query Match

Best Local Similarity 39.3%; Score 39.5; DB 2; Length 244;

Matches 11; Conservative 7; Mismatches 7; Indels 3; Gaps 1;

QY 3 LASTSTSHMTLLMLLFLHGLQASIS 30
 Db 174 MASSTSEIVVMFLRI--LGLSAYS 198

RESULT 12

US-08-197-793-2
 Sequence 2, Application US/08197793
 Patent No. 5510461

GENERAL INFORMATION:

APPLICANT: Meuer, S.
 APPLICANT: Schraven, B.
 APPLICANT: Schoenhaut, D.
 APPLICANT: Ratonsky, S.
 TITLE OF INVENTION: pp32: A Newly Identified CD45-Associated
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 STATE STREET, SUITE 510
 CITY: BOSTON
 STATE: MASSACHUSETTS
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/197,793
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/668,019;
 FILING DATE: 19-APR-1991
 APPLICATION NUMBER: 08/004,199
 FILING DATE: 13-JAN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: DeConti, Giulio A., Jr.
 REGISTRATION NUMBER: 31,503
 REFERENCE/DOCKET NUMBER: BEI-006CNCNP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 206 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-197-793-2

Query Match

Best Local Similarity 28.1%; Score 39; DB 1; Length 206;

OY 4 ASSTSIHTMLLLMLFHLGL 25
: | | : : | | | : | |
Db 31 SSSVIV--LLELLELLLATGL 50

Search completed: September 16, 1999, 20:41:12
Job time: 5441 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:42:11 ; Search time 49.27 Seconds
(without alignments)
24.395 Million cell updates/sec

Title: US-09-037-657-32

Sequence: 1 MVLASTTSITMILLIMFLHLGIQASIS 30

Scoring table: BLOSUM62

Searched: 122810 seqs, 40065486 residues

Database:

PIR_60:
1: PIR1:
2: PIR2:
3: PIR3:
4: PIR4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	139	100.0	166	1	ICMS3	Interleukin-3 prec
2	96	69.1	166	1	S07369	Interleukin-3 prec
3	96	69.1	166	1	JC6566	Interleukin-3 beta
4	52	37.4	677	2	S33664	flagella-associated
5	50.5	36.3	437	2	S34959	NADH dehydrogenase
6	48.5	34.9	443	2	F30010	NADH dehydrogenase
7	48	34.5	654	2	S71786	wingless receptor
8	47	33.8	244	2	B69318	nitrate reductase,
9	47	33.8	160	2	B71171	hypothetical prote
10	46	33.1	2073	1	BMASBE	b1me protein Eme
11	46	33.1	451	1	S36152	isocitrate dehydro
12	46	33.1	342	2	F69261	conserved hypochet
13	46	33.1	633	2	AS4366	sodium/phosphate c
14	45	32.4	309	1	S34198	IGE Fc receptor II
15	45	32.4	574	2	S58992	NADH dehydrogenase
16	45	32.4	279	2	E64109	dimethylsulfoxide
17	44	31.7	142	1	S42722	interleukin-3 prec
18	44	31.7	142	1	S42721	interleukin-3 prec
19	44	31.7	130	2	S55171	hypothetical prote
20	43.5	31.3	323	2	A70029	hypothetical prote
21	43	30.9	436	2	S77639	hypothetical prote
22	43	30.9	357	2	H64855	exopolysaccharide
23	43	30.9	493	2	S73890	probable membrane
24	43	30.9	114	2	G71161	hypothetical prote
25	43	30.9	408	2	E70380	Na+/H+-exchanging
26	42.5	30.6	115	2	S26158	NADH dehydrogenase
27	42.5	30.6	115	2	S41842	NADH dehydrogenase
28	42	30.2	500	2	S16872	cytochrome P450 2D
29	42	30.2	396	2	A34401	cathepsin E (EC 3.
30	42	30.2	182	2	S17723	H+-transporting AT
31	42	30.2	70	2	S00408	legumin Ii beta ch
32	42	30.2	266	2	H64907	probable membrane
33	42	30.2	598	2	S75728	ubiquitinol--cytochr
34	41.5	29.9	357	2	A45619	probable abc trans
35	41.5	29.9	631	2	H70154	NADH dehydrogenase
36	41.5	29.9	119	2	S40617	nitrogen regulatio
37	41	29.5	469	1	RGEBCG	nitrogen regulatio
38	41	29.5	468	1	RGEBCG	nitrogen regulatio
39	41	29.5	328	1	QOBEF6	HVLA protein - hu

40	41	29.5	500	2	J00258	cytochrome P450 1s
41	41	29.5	434	2	J00451	cytochrome P450 2C
42	41	29.5	117	2	S58996	NADH dehydrogenase
43	41	29.5	1099	2	A55405	adenylate cyclase
44	41	29.5	118	2	S16762	gonadotropin alpha
45	41	29.5	118	2	A60626	glycoprotein hormo

ALIGNMENTS

RESULT 1

ICMS3

Interleukin-3 precursor - mouse
N:Alternate names: hematopoietic growth factor; IL-3; mast-cell growth factor; multi-

C:Species: Mus musculus (house mouse)

C:Date: 18-Apr-1984 #sequence, revision 18-Apr-1984 #text, change 05-Sep-1997

C:Accession: A25481, A01851, A21022, I59024, I53994

R:Campbell, H.D.; Ymer, S.; Fung, M.C.; Young, I.G.

Eur. J. Biochem. 150, 297-304, 1985

A:Title: Cloning and nucleotide sequence of the murine interleukin-3 gene.

A:Reference number: A25481; MUID:85257655

A:Accession: A25481

A:Molecule type: DNA

A:Residues: 1-166 <CAM>

A:Cross-references: GB:X0732; NID:952673; PID:952674

R:Fung, M.C.; Hapel, A.D.; Ymer, S.; Cohen, D.R.; Johnson, R.M.; Campbell, H.D.; Yoon

Nature 307, 233-237, 1984

A:Title: Molecular cloning of cDNA for murine interleukin-3.

A:Reference number: A01851; MUID:84117447

A:Accession: A01851

A:Molecule type: mRNA

A:Residues: 1-166 <FUN>

A:Cross-references: GB:R01850; NID:9198334; PID:9309405

R:Experimental source: myelomonocytic leukemia cell line WEHI-3

R:Yokota, T.; Lee, F.; Renwick, D.; Hall, C.; Araki, N.; Mosmann, T.; Nabel, G.; Canto

Proc. Natl. Acad. Sci. U.S.A. 81, 1070-1074, 1984

A:Title: Isolation and characterization of a mouse cDNA clone that expresses mast-cell

A:Reference number: A21022; MUID:84144843

A:Accession: A21022

A:Molecule type: mRNA

A:Residues: 1-145, 'A', 147-166 <YOK>

A:Cross-references: GB:R01668; NID:9199083; PID:9387421

R:Knepfer, T.P.; Ardognet, B.; Schreurs, J.; Delnizer, M.L.

Biochemistry 31, 11651-11659, 1992

A:Title: Determination of the glycosylation patterns, disulfide linkages, and protein

A:Reference number: A38860; MUID:93015774

A:Accession: A38860

A:Contents: annotation

A:Note: disulfide bonds were shown between Cys residues at 43 and either 106 or 105, enesis; the disulfide bond 105-166 is not conserved in most orthologs

R:Myatake, S.; Yokota, T.; Lee, F.; Araki, K.

Proc. Natl. Acad. Sci. U.S.A. 82, 316-320, 1985

A:Title: Structure of the chromosome 1 gene for murine interleukin 3.

A:Reference number: I59024; MUID:85113192

A:Accession: I59024

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-166 <RES>

A:Cross-references: GB:R03233; NID:9198338; PID:9387385

R:Todoroko, K.; Yamamoto, A.; Amanuma, H.; Ikawa, Y.

Gene 39, 103-107, 1985

A:Title: Isolation and characterization of a genomic DDD mouse interleukin-3 gene.

A:Reference number: I53994; MUID:86083183

A:Accession: I53994

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-70, 'R', 72-166 <RE2>

A:Cross-references: GB:M20128; NID:9198384; PID:9387387

C:Comment: This glycoprotein, produced by bone marrow cells, by mitogen or antigen-ac

citation of hematopoietic cells.

C:Genetics: 55/3; 69/3; 101/3; 115/3

A:introns: 55/3; 69/3; 101/3; 115/3

C:superfamily: Interleukin-3

A:Gene: NDA

A:Genome: mitochondrion

A:Genetic code: SGC6

C:Superfamily: NADH dehydrogenase (ubiquinone) chain 4

C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 36.3%; Score 50.5; DB 2; Length 437;

Best Local Similarity 34.4%; Pred. No. 12;

Matches 11; Conservative 11; Mismatches 7; Indels 3; Gaps 1;

QY 1 MVLASSTSIHTMLLMFHR--LGLQASI 29

Db 131 LVIVSSISIMCIIICIIIFHFNLMQSF 162

RESULT 6

F30010

NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Leishmania tarentolae mitochondrion

C:Species: Leishmania tarentolae

C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Aug-1997

C:Accession: F30010

R:de la Cruz, V.F.; Neckelmann, N.; Simpson, L.

J. Biol. Chem. 259, 15136-15147, 1984

A:Title: Sequences of six genes and several open reading frames in the kinetoplast maxic

A:Reference number: A22848; M01D:85079995

A:Accession: F30010

A:Molecule type: DNA

A:Residues: 1-443

A:Cross-references: GB:M10126

C:Genetics:

A:Genome: mitochondrion

A:Genetic code: SGC6

C:Superfamily: NADH dehydrogenase (ubiquinone) chain 4

C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 34.9%; Score 48.5; DB 2; Length 443;

Best Local Similarity 34.4%; Pred. No. 22;

Matches 11; Conservative 11; Mismatches 7; Indels 3; Gaps 1;

QY 1 MVLASSTSIHTMLLMFHR--LGLQASI 29

Db 137 LVIFSSISIMCIIICIIIFHFNLMQSF 168

RESULT 7

F30010

NADH dehydrogenase precursor fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 17-Jul-1998

C:Accession: S71786; S78444

R:Bhanot, P.; Bink, M.; Harryman Samos, C.; Hsieh, J.C.; Wang, Y.; Meeke, J.P.; Andrew,

ature 362, 225-230, 1996

A:Title: A new member of the frizzled family from Drosophila functions as a wingless rec

A:Reference number: S71786

A:Accession: S71786

A:Molecule type: DNA

A:Residues: 1-694 <BNA>

A:Cross-references: EMBL:065589

A:Note: mRNA was also sequenced

A:Status: preliminary; nucleic acid sequence not shown

A:Experimental source: strain 073

A:Note: this accession replaces an interim accession for a sequence replaced by GenB

C:Genetics:

A:Gene: ditz2

A:Genome: transmembrane protein

Query Match

Best Local Similarity 31.0%; Pred. No. 37;

Matches 9; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 MVLASSTSIHTMLLMFHR--LGLQASI 29

Db 383 LLNBSSTGPHSCVFLVLYFFGMAS 411

RESULT 8

B69318

nitrate reductase, gamma subunit (narI) homolog - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Jun-1998

C:Accession: B69318

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Overbeek, R.; Cotton, M.D.; Spriggs, T.; Arlrich, P.; Kaine, B.P.; Sykes,

Smith, H.O.; Wiese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch

A:Reference number: A69250; M01D:98049343

A:Accession: B69318

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-244 <KLE>

A:Cross-references: GB:AE001066; GB:AE000782; M01D:92689389; PID:92650071; TIGR:AF0546

Query Match

Best Local Similarity 60.0%; Pred. No. 20;

Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 16 LLNBSSTGPHSCVFLVLYFFGMAS 103

Db 89 ILNMFHIGLIVSLS 103

RESULT 9

B71171

hypothetical protein PH0566 - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii

C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 14-Aug-1998

C:Accession: B71171

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Se

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu

DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophil

A:Reference number: A71000; M01D:98344137

A:Accession: B71171

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-160 <KAW>

A:Cross-references: GB:AP000002; M01D:93236129; PID:d1030598; PID:93256972

A:Experimental source: strain 073

A:Note: this accession replaces an interim accession for a sequence replaced by GenB

C:Genetics:

A:Gene: PH0566

Query Match

Best Local Similarity 45.5%; Pred. No. 14;

Matches 10; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 MVLASSTSIHTMLLMFHR--LGLQASI 22

Db 134 LALASSEGVIFSLIALSIFH 155

RESULT 10

BMASBE

b1me protein - *Emicellia nidulans*
 C:Species: *Emicellia nidulans*, *Aspergillus nidulans*
 C>Date: 31-Dec-1991 #sequence, revision 31-Dec-1991 #text_change 24-Oct-1997
 C:Accession: A37879
 R:Engle, D.B.; Osman, S.A.; Osman, A.H.; Rosborough, S.; Xiang, X.; Morris, N.R.
 J. Biol. Chem. 265, 16132-16137, 1990
 A:Title: A negative regulator of mitosis in *Aspergillus* is a putative membrane-spanning
 A:Reference number: A37879; MUID:90375468
 A:Accession: A37879
 A:Molecule type: mRNA
 A:Residues: 1-2073 <ENG>
 A:Cross-references: GB:M59705; GB:J05607; NID:9168026; PID:9168027
 A:Note: In addition to three predicted transmembrane domains, there are several potential
 A:kinase and one sequence that resembles a nuclear localization signal
 C:Comment: This protein is part of a regulatory pathway that includes the nma protein X
 ter mitosis and prevent them from leaving mitosis.
 C:Genetics:
 A:Gene: b1me
 C:Superfamily: b1me protein
 C:Keywords: cell cycle control; mitosis; transmembrane protein
 F:1623-1643/Domain: transmembrane #status predicted <TM1>
 F:1685-1703/Domain: transmembrane #status predicted <TM2>
 F:1746-1764/Domain: transmembrane #status predicted <TM3>

Query Match 33.1%; Score 46; DB 1; Length 2073;
 Best Local Similarity 47.6%; Pred. No. 1.8e+02;
 Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

3 LASTSTSHMTLLMLFHL 23
 DB 946 LSNSESHHTPLCTILVNLHL 966

RESULT 11
 S33612
 Isoleucate dehydrogenase (NADP+) (EC 1.1.1.42) - soybean
 C:Species: Glycine max (soybean)
 C>Date: 19-Mar-1997 #sequence, revision 19-Mar-1997 #text_change 17-Mar-1999
 C:Accession: S33612
 R:Udvardi, M.K.; McDermott, T.R.; Kahn, M.L.
 Plant Mol. Biol. 21, 739-752, 1993
 A:Title: Isolation and characterization of a cDNA encoding NADP(+)-specific isocitrate
 A:Reference number: S33612; MUID:93222474
 A:Accession: S33612
 A:Molecule type: mRNA
 A:Residues: 1-451 <UDV>
 C:Superfamily: Yeast isocitrate dehydrogenase (NADP+)
 C:Keywords: NADP; oxidoreductase

Query Match 33.1%; Score 46; DB 2; Length 451;
 Best Local Similarity 36.7%; Pred. No. 47;
 Matches 11; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

1 MYLASSTSHMTLLMLFHLGLQASIS 30
 DB 3 MITSARAAIHGTCLFSLIHSHTFYSSQS 32

RESULT 12
 F69261
 conserved hypothetical protein AF0094 - *Archaeoglobus fulgidus*
 C:Species: *Archaeoglobus fulgidus*
 C>Date: 05-Dec-1997 #sequence, revision 05-Dec-1997 #text_change 05-Jun-1998
 C:Accession: F69261
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
 R. Fliedmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
 Nature 390, 364-370, 1997
 A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Sykes, S.
 Smith, H.O.; Moose, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon

A:Reference number: A69250; MUID:98049343
 A:Accession: F69261
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-342 <KLE>
 A:Cross-references: GB:AE001100; GB:AE000782; NID:92689423; PID:92650554; TIGR:AF00

Query Match 33.1%; Score 46; DB 2; Length 342;
 Best Local Similarity 30.0%; Pred. No. 37;
 Matches 9; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

1 MYLASSTSHMTLLMLFHLGLQASIS 30
 DB 1 MHIGGVVVRIRIILMLFHLGSSNNV 30

RESULT 13
 A54366
 sodium/phosphate cotransport protein, renal - North American opossum
 C:Species: *Didelphis virginiana*, *Didelphis marsupialis virginiana* (North American o
 C>Date: 07-Jul-1995 #sequence, revision 07-Jul-1995 #text_change 17-Mar-1999
 C:Accession: A54366
 R:Sorribas, V.; Markovitch, D.; Hayes, G.; Stange, G.; Forgo, J.; Blber, J.; Murer, J.
 J. Biol. Chem. 269, 6615-6621, 1994
 A:Title: Cloning of a Na/P-1 cotransporter from opossum kidney cells.
 A:Reference number: A54366; MUID:94165050
 A:Accession: A54366
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-653 <SOR>
 A:Cross-references: GB:L26308; NID:9425468; PID:9425469

Query Match 33.1%; Score 46; DB 2; Length 653;
 Best Local Similarity 36.7%; Pred. No. 65;
 Matches 11; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

1 MYLASSTSHMTLLMLFHLGLQASIS 30
 DB 355 ILLAGSLTILCTILVNLVLSVLOQOVA 384

RESULT 14
 S34198
 IGE re receptor II, low-affinity - rat
 M:Alternate names: CD23, lymphocyte IGE receptor
 C:Species: *Rattus norvegicus* (Norway rat)
 C>Date: 06-Jan-1995 #sequence, revision 06-Jan-1995 #text_change 13-Feb-1998
 C:Accession: S34198
 R:Flores-Romo, L.; Shield, J.; Humbert, Y.; Graber, P.; Audry, J.P.; Gauchat, J.F.;
 submitted to the EMBL Data Library, June 1993
 A:Description: Inhibition of an in vivo antigen-specific IGE response by antibodies
 A:Reference number: S34198
 A:Accession: S34198
 A:Molecule type: mRNA
 A:Residues: 1-309 <FLD>
 A:Cross-references: EMBL:X73579; NID:9313672; PID:9313673
 C:Superfamily: IGE receptor II; C-type lectin homology
 C:Keywords: B-cell; glycoprotein; immunoglobulin receptor; macrophage; tandem repeat
 F:1-25/Domain: intracellular #status predicted <INT>
 F:14-22/Region: stop-transfer sequence
 F:24-46/Domain: transmembrane #status predicted <TM>
 F:47-309/Domain: extracellular #status predicted <EXT>
 F:126-309/Product: soluble IGE-binding factor (29K) #status predicted <IGI>
 F:146-309/Product: soluble IGE-binding factor (25-27K) #status predicted <BFI>
 F:164-288/Domain: C-type lectin homology <LCH>
 F:192-283,260-274/Disulfide bonds: #status predicted

Query Match 32.4%; Score 45; DB 1; Length 309;
 Best Local Similarity 34.5%; Pred. No. 46;
 Matches 10; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

Y 1 MYLASSSTSIHMLLLMLFHLGLQASI 29
 b 26 LVLYGLITVWVWLLALLMLHMETEKSL 54

ESULT 15

58992

NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - earthworm (Lumbricus terrestris)
 ;Species: mitochondrion Lumbricus terrestris (common earthworm)
 ;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 21-Aug-1998
 ;Accession: S58992

Boore, J.L., Brown, W.M.
 Genetics 141, 305-319, 1995

Title: Complete sequence of the mitochondrial DNA of the annelid worm Lumbricus terrestris
 ;Reference number: S58985; MUID:96042914

Accession: S58992

Status: preliminary; nucleic acid sequence not shown; translation not shown

Molecule type: DNA

Residues: 1-574 <BOO>

Cross-references: EMBL:U24570

Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995

Genetics:

Genome: mitochondrion

Genetic code: SCC4

Superfamily: NADH dehydrogenase (ubiquinone) chain 5

Keywords: mitochondrion; NAD; oxidoreductase

Query Match

Best Local Similarity 32.4%; Score 45; DB 2; Length 574;

Matches 11; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

Y 1 MYLASSSTSIHMLLLMLFHLGLQASIS 30

b 364 MIVEASLYPPHNSIMINILFPAVGLTARTS 393

earch completed: September 16, 1999, 20:42:13
 ob time: 5406 sec

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 17, 1999, 03:10:15 ; Search time 35.09 Seconds

(without alignments)
24.168 Million cell updates/sec

Title: US-09-037-657-32

Perfect score: 139

Sequence: 1 MYLASSSTSTHTMLLMFLHLGLQASIS 30

Scoring table: BLOSUM62

Searched: 77977 seqs, 28268293 residues

Database: SwissProt_37.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	139	100.0	166	IL3_MOUSE	P01586 mus musculu
2	96	69.1	166	IL3_RAT	P04823 rattus norv
3	52	37.4	677	FLHA_BACSU	P35620 bacillus su
4	51	36.7	115	NU3M_BOVAS	P92482 equus asinu
5	51	36.7	115	NU3M_HORSE	P48654 equus caball
6	49.5	35.6	115	NU3M_CERSI	O03202 ceratotheri
7	49.5	35.6	115	NU3M_RHIUN	O09066 rhinoceros
8	49	35.3	115	NU3M_SHEEP	O78753 ovils aries
9	46	33.1	2073	BIME_EMENT	P24686 emeritella
10	45	32.4	279	DMSC_HAETN	P45002 haemophilus
11	45	32.4	574	NU3M_LUNTE	O34947 lumbricus t
12	44	31.7	142	IL3_CALJA	O28334 callithrix
13	44	31.7	117	IL3_SAGOE	P51940 drosophila
14	44	31.7	117	NU3M_DROSU	O08908 mus musculu
15	44	31.7	722	P85E_MOUSE	O63788 rattus norv
16	44	31.7	722	P85E_MOUSE	O45411 saccharomyc
17	44	31.7	130	YJ02_YEAST	P47010 burholderi
18	43	30.9	436	EPSE_BURSO	P75506 mycoplasma
19	43	30.9	493	Y130_MYCPN	F75955 escherichia
20	43	30.9	357	YCEF_ECOLI	P48912 felis silve
21	42.5	30.6	115	NU3M_FELCA	P38600 halichoerus
22	42.5	30.6	115	NU3M_HALGR	O00541 phoca vitul
23	42.5	30.6	115	NU3M_PROVI	P22479 bacillus fi
24	42	30.2	182	ATPD_BACFI	P14091 homo sapien
25	42	30.2	396	CATE_HUMAN	P12938 rattus norv
26	42	30.2	500	CPE3_RAT	P31125 escherichia
27	42	30.2	265	YDED_ECOLI	O79880 sus scrofa
28	41.5	29.9	115	NU3M_PIG	O36424 locusta mdy
29	41.5	29.9	444	NU4M_LOCM1	O11047 mycobacteri
30	41.5	29.9	631	Y08A_MYCTU	P33773 rattus norv
31	41	29.5	434	CPCO_RAT	P51829 mus musculu
32	41	29.5	1099	CYAN_MOUSE	P30983 ctenopharyn
33	41	29.5	118	GLHA_CTEID	P03737 hypophthalm
34	41	29.5	118	GLHA_HYPMO	O01127 mus musculu
35	41	29.5	315	MSHR_MOUSE	P03929 escherichia
36	41	29.5	469	NTRC_ECOLI	P03929 escherichia
37	41	29.5	469	NTRC_KLEPN	P41789 salmoeilla
38	41	29.5	469	NTRC_SALT	O04950 lumbricus t
39	41	29.5	117	NU3M_LUNTE	P09719 human cytom
40	41	29.5	310	US14_HCMVA	P43371 saccharomyc
41	41	29.5	1029	YFCS_YEAST	P39836 escherichia
42	41	29.5	332	YFES_YEAST	O09288 caenorhabdi
43	41	29.5	566	YOK4_CAEEL	

ALIGNMENTS

RESULT	ID	IL3_MOUSE	STANDARD	PRT	166 AA
AC	P01586	IL3_MOUSE	STANDARD	PRT	166 AA
DT	21-JUL-1986	(REL. 01, CREATED)			
DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)			
DT	15-DEC-1998	(REL. 37, LAST ANNOTATION UPDATE)			
DE	INTERLEUKIN-3 PRECURSOR (IL-3) (MULTIPOTENTIAL COLONY-STIMULATING FACTOR) (HEMATOPOIETIC GROWTH FACTOR) (P-CELL STIMULATING FACTOR)				
DE	(MAST-CELL GROWTH FACTOR) (MCSF).				
GN	IL3 OR IL-3.				
OS	MUSCULUS (MOUSE).				
OC	EDAROTIA; METAFOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;				
OC	RODENTIA; SCIROGNATHI; MORIDAE; MORINAE; MUS.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 85113192.				
RA	MIRAIKE S., YOKOTA T., LEE F., ARAI K.-I.;				
RT	"Structure of the chromosomal gene for murine Interleukin 3.";				
RL	PROC. NATL. ACAD. SCI. U.S.A. 82:316-320(1985).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 85257655.				
RA	CAMPBELL H.D., YMER S., FUNG M.-C., YOUNG I.G.;				
RT	"Cloning and nucleotide sequence of the murine Interleukin-3 gene.";				
RL	EUR. J. BIOCHEM. 150:297-304(1985).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 84117447.				
RA	FUNG M.-C., HAPPEL A.J., YMER S., COHEN D.R., JOHNSON R.M.,				
RT	CAMPBELL H.D., YOUNG I.G.;				
RL	"Molecular cloning of cDNA for murine interleukin-3.";				
RN	NATURE 307:233-237(1984).				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 86083183.				
RA	TODOKORO K., YAMAMOTO A., AMAMURA H., IKAWA Y.;				
RT	"Isolation and characterization of a genomic DDD mouse interleukin-3 gene.";				
RL	GENE 39:103-107(1985).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 84144843.				
RA	YOKOTA T., LEE F., RENNICK D., HALL C., ARAI N., MOSMANN T., NABEL G.,				
RT	CANTOR H., ARAI K.-I.;				
RL	"Isolation and characterization of a mouse cDNA clone that expresses mast-cell growth-factor activity in monkey cells.";				
RN	PROC. NATL. ACAD. SCI. U.S.A. 81:1070-1074(1984).				
RP	[6]				
RX	CARBOHYDRATE-BINDING SITES, AND DISULFIDE BONDS.				
RA	KNEPPER T.P., ARBOGAST B., SCHREURS J., DEINZER M.L.;				
RT	"Determination of the glycosylation patterns, disulfide linkages, and protein heterogeneities of baculovirus-expressed mouse interleukin-3 by mass spectrometry.";				
RL	BIOCHEMISTRY 31:11651-11659(1992).				
RP	FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE DIFFERENTIAL THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION, DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES.				
CC	FUNCTION: THIS CSF INDICES GRANULOCYTES, MACROPHAGES, MAST CELLS, STEM CELLS, ERYTHROID CELLS, EOSINOPHILS AND MEGAKARYOCYTES.				
CC	SUBUNIT: MONOMER.				
CC	-1- TISSUE SPECIFICITY: ACTIVATED T CELLS, MAST CELLS, NATURAL KILLER CELLS.				
CC	-1- SUBCELLULAR LOCATION: SECRETED.				

CC -1- SIMILARITY: BELONGS TO THE IL-3 FAMILY.
 CC -----
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 CC -----
 DR EMBL: K01850; G309405; -
 DR EMBL: K03233; G387385; -
 DR EMBL: X02732; G52674; -
 DR EMBL: M20128; G387387; -
 DR EMBL: M14394; G387387; JOINED.
 DR EMBL: K01668; G387421; -
 DR EMBL: A02046; G344554; -
 DR PIR: A25481; ICMS3
 DR MGI: 96552; IL3.
 DR HSSP: P08700; IJLI.
 DR CYTOKINE; GLYCOPROTEIN; GROWTH FACTOR; SIGNAL.
 KW SIGNAL
 FT CHAIN 1 26
 FT DISULFID 27 166 INTERLEUKIN-3.
 FT DISULFID 43 105
 FT CARBOHYD 105 166
 FT CARBOHYD 42 42
 FT CARBOHYD 112 112
 SQ SEQUENCE 166 AA; 18540 MW; AA9EB59F CRC32;
 Query Match 100.0%; Score 139; DB 1; Length 166;
 Best Local Similarity 100.0%; Pred. No. 3; 2e-12;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 MVLASSTSIHMLLMLFHLGLQASIS 30
 Db 1 MVLASSTSIHMLLMLFHLGLQASIS 30
 RESULT 2
 IL3_RAT STANDARD; PRT; 166 AA.
 AC P04823; P70513;
 DT 13-AUG-1987 (REL. 05, CREATED)
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE INTERLEUKIN-3 PRECURSOR (IL-3) (MULTIPOTENTIAL COLONY-STIMULATING
 DE FACTOR) (HEMATOPOIETIC GROWTH FACTOR) (P-CELL STIMULATING FACTOR)
 DE (MAST-CELL GROWTH FACTOR) (MCGF).
 GN IL3 OR IL-3.
 OS RATIUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; RATIUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86232609.
 RA COHEN D.R., HABEL A.J., YOUNG I.G.;
 RT "Cloning and expression of the rat interleukin-3 gene";
 RL NUCLEIC ACIDS RES. 14:3641-3658(1986).
 RP SEQUENCE FROM N.A.
 RA ESANDI M.C., VAN SOMEREN G.D., VAN BEKKUM D.W., VALERIO D.,
 RA NOTERBOOM J.L., BOUT A.;
 RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/CDJ DATA BANKS.
 CC -1- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE
 CC CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,
 CC DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
 CC OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES/MACROPHAGES.
 CC -1- FUNCTION: THIS CSR INDUCES GRANULOCYTES, MACROPHAGES, MAST CELLS,
 CC STEM CELLS, ERYTHROID CELLS, EOSINOPHILS AND MEGAKARYOCYTES.
 CC -1- SUBUNIT: MONOMER.
 CC -1- TISSUE SPECIFICITY: ACTIVATED T CELLS, MAST CELLS, NATURAL KILLER
 CC CELLS.

CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -----
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 CC -----
 DR EMBL: X03846; G56476; -
 DR EMBL: X03914; E10390; -
 DR EMBL: X03914; E10391; -
 DR EMBL: X03914; E10392; -
 DR EMBL: B81483; G1763673; -
 DR PIR: S07369; S07369.
 DR HSSP: P08700; IJLI.
 DR CYTOKINE; GLYCOPROTEIN; GROWTH FACTOR; SIGNAL.
 KW SIGNAL
 FT CHAIN 1 27
 FT DISULFID 28 166 INTERLEUKIN-3.
 FT DISULFID 43 106 BY SIMILARITY.
 FT DISULFID 105 166 BY SIMILARITY.
 FT CARBOHYD 60 60
 FT CARBOHYD 70 70 POTENTIAL.
 SQ SEQUENCE 166 AA; 18630 MW; 6B571582 CRC32;
 Query Match 69.1%; Score 96; DB 1; Length 166;
 Best Local Similarity 82.1%; Pred. No. 2e-06;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Oy 1 MVLASSTSIHMLLMLFHLGLQAS 28
 Db 1 MVLASSTSIHMLLMLFHLGLQAS 28
 RESULT 3
 FLHA_BACSU STANDARD; PRT; 677 AA.
 AC P35620;
 DT 01-JUN-1994 (REL. 29, CREATED)
 DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
 DT 01-FEB-1999 (REL. 31, LAST ANNOTATION UPDATE)
 DE FLAGELLAR BIOSYNTHESIS PROTEIN FLHA.
 GN FLHA.
 OS BACILLUS SUBTILIS.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 OC BACILLUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 93225816.
 RA CARPENTER P.B., ORDAL G.W.;
 RT "Bacillus subtilis flha: a flagellar protein related to a new family
 RT of signal-transducing receptors";
 RL MOL. MICROBIOL. 7:735-743(1993).
 CC -1- FUNCTION: INVOLVED IN THE EXPORT OF FLAGELLUM PROTEINS.
 CC -1- SUBCELLULAR LOCATION: INTERNAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE FLIPEP (FLAGELLA/HR/INVASION PROTEINS
 CC EXPORT PORE) FAMILY.
 CC -----
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 CC -----
 DR EMBL: X63698; G39917; -
 DR EMBL: Z99112; E1185230; -
 DR PIR: S33664; S33664.
 DR SUBTILIST; BG10542; FLHA.

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DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DE 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE MADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).
OS NMND3 OR ND3
OS EQUUS CABALLUS (HORSE).
OS MITOCHONDRION.
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
OC PERISSODACTYLA: EQUIDAE: EQUUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95047450.
RA XU X., ARNASON U.:
RT "The complete mitochondrial DNA sequence of the horse, Equus
RL caballus: extensive heteroplasmy of the control region.";
RL GENE 148:357-362(1994).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.
CC
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CC
DR EMBL: X79547; G577579;
DR PFAM: PF00507; oxidored_4; 1.
DR OXIDOREDUCTASE; NAD; UBIQUINONE; MITOCHONDRION.
SQ SEQUENCE 115 AA; 13016 MW; C4C238F9 CRC32;
-----
Query Match 36.7%; Score 51; DB 1; Length 115;
Best Local Similarity 50.0%; Pred. No. 1.6;
Matches 10; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
QY 4 ASSTSHHTMLLMLRL 23
Db 78 ASQTNTMLTLMALVLSL 97
-----
RESULT 6
NM3M_CERSI ID NM3M_CERSI STANDARD; PRT; 115 AA.
AC 00302;
DT 15-JUL-1998 (REL. 36, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE MADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).
GN NMND3 OR ND3 OR MADH3.
OS CERATOTHERIUM SIMUM (WHITE RHINOCEROS) (SQUARE-LIPPED RHINOCEROS).
OS MITOCHONDRION.
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
OC PERISSODACTYLA: RHINOCEROTIDAE: CERATOTHERIUM.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97271644.
RA XU X., ARNASON U.:
RT "The complete mitochondrial DNA sequence of the white rhinoceros,
RT Ceratotherium simum, and comparison with the mtDNA sequence of the
RL Indian rhinoceros, Rhinoceros unicornis.";
RL MOL. PHYLOGENET. EVOL. 7:189-194(1997).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.
CC
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CC
DR EMBL: Y07726; E275046;
DR PFAM: PF00507; oxidored_4; 1.

```

KM OXIDOREDUCTASE; NAD; UBIQUINONE; MITOCHONDRION.
SQ SEQUENCE 115 AA; 12980 MW; 50796E31 CRC32;

Query Match 35.6%; Score 49.5; DB 1; Length 115;
Best Local Similarity 48.1%; Pred. No. 2.5;
Matches 13; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

OY 4 ASSTSIHTMLLLMLFHLGLQASIS 30
DB 78 ASQTNLTKMTMLTLLISL-LAASIA 103

RESULT 7
NM3M_RH10N STANDARD; PRT; 115 AA.
AC 096066;

DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).
GN MTND3 OR ND3 OR NADH3.

OS RHINOCEROS UNICORNIS (GREATER INDIAN RHINOCEROS).
OG MITOCHONDRION.
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PERISSODACTYLA; RHINOCEROTIDAE; RHINOCEROS.

RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE-KIDNEY;
RX MEDLINE: 97051708.

RA XU X., JANKE A., ARNASON U.;

RT "The complete mitochondrial DNA sequence of the greater Indian rhinoceros, *Rhinoceros unicornis*, and the phylogenetic relationship among *Carnivora*, *Perissodactyla*, and *Artiodactyla* (+ *Cetacea*).";

RL MOL. BIOL. EVOL. 13:1167-1173(1996).

CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.

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CC EMBL: X97336; E237876;
DR PFAM: PF00507; oxidored_94; 1.
KW OXIDOREDUCTASE; NAD; UBIQUINONE; MITOCHONDRION.
SQ SEQUENCE 115 AA; 13044 MW; 9FE83B49 CRC32;

Query Match 35.6%; Score 49.5; DB 1; Length 115;
Best Local Similarity 48.1%; Pred. No. 2.5;
Matches 13; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

OY 4 ASSTSIHTMLLLMLFHLGLQASIS 30
DB 78 ASQTNLTKMTMLTLLISL-LAASIA 103

RESULT 8
NM3M_SHEEP STANDARD; PRT; 115 AA.
AC 078753;

DT 15-DEC-1998 (REL. 37, CREATED)

DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)

DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)

DE NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).

GN MTND3 OR ND3.

OS OVIS ARIES (SHEEP).

OG EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVIOIDEA; BOVIDAE; CAPRINAE; OVIS.

RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-MERINOLANDSCHAF; TISSUE-LIVER;

RT HIENEDLER S., LEWALSKI H., WASSMUTH R., JANKE A.;
RT "The complete mitochondrial DNA sequence of the domestic sheep (*Ovis aries*) and comparison with the other major ovine haplotype.";

RL J. MOL. EVOL. 0:0-0(1998).

CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.

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DR EMBL: AF010406; G3445514;
KW OXIDOREDUCTASE; NAD; UBIQUINONE; MITOCHONDRION.
SQ SEQUENCE 115 AA; 13102 MW; 2C610097 CRC32;

Query Match 35.3%; Score 49; DB 1; Length 115;
Best Local Similarity 50.0%; Pred. No. 2.9;
Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 4 ASSTSIHTMLLLMLFHL 23
DB 78 ASQTNLTKMTMLTLLIFL 97

RESULT 9
BIME_EMENT STANDARD; PRT; 2073 AA.
AC P24686;

DT 01-MAR-1992 (REL. 21, CREATED)

DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)

DE NEGATIVE REGULATOR OF MITOSIS.

GN BIME.

OS EMERICELLA NIDULANS (ASPERGILLUS NIDULANS).

OC EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PLECTOMYCETES;

OC EURYTILES; TRICHOCOMACEAE; EMERICELLA.

RN [1]
RP SEQUENCE FROM N.A.

RC MEDLINE: 90375468.

RA ENGLE D.B., OSMANI S.A., ROSBOROUGH S., XIANG X.,
RA MORRIS N.R.;

RT "A negative regulator of mitosis in *Aspergillus* is a putative membrane-spanning protein.";

RL J. BIOL. CHEM. 265:16132-16137(1990).

CC -1- FUNCTION: NEGATIVE REGULATOR OF MITOSIS IN *E. NIDULANS*. THIS PROTEIN IS PART OF A REGULATORY PATHWAY THAT INCLUDES THE NIMA PROTEIN KINASE. IT IS REQUIRED TO PREVENT PREMATURE ENTRY INTO MITOSIS AND PREVENT THEM FROM LEAVING MITOSIS.

CC -1- SIMILARITY: TO MOUSE TSG24 AND YEAST VML12W.

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DR EMBL: M59705; G168027;
KW PIR: A37879; BMASBE.

DT TRANSMEMBRANE; MITOSIS.

FT TRANSMEM 342 353

FT TRANSMEM 1623 1643

FT TRANSMEM 1685 1703

FT TRANSMEM 1746 1764

NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

POTENTIAL.

POTENTIAL.


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1 MYLASSSTSIHTMLLLMLFHLQASIS 30
  :::::|:::|:::|:::|:::|:::|
364 MIVEASLYYPHNSMINILFAVGLTAFYS 393
  :::::|:::|:::|:::|:::|:::|

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DOMAIN	1	9	PERIPLASMIC (POTENTIAL).
TRANSMEM	10	30	POTENTIAL.

```

RESULT 12
IL3_CALJA 12
ID IL3_CALJA STANDARD; PRF: 142 AA.
AC Q28334;
DT 15-DEC-1998 (REL. 37, CREATED)
DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE INTERLEUKIN-3 PRECURSOR (IL-3) (MULTIPOTENTIAL COLONY-STIMULATING
DE FACTOR) (HEMATOPOIETIC GROWTH FACTOR) (P-CELL STIMULATING FACTOR)
DE (MAST-CELL GROWTH FACTOR) (MCGF).
GN CALLITHRIX JACCHUS (COMMON MARMOSET).
OS EKAAROTA; METAFOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; PLATYRRHINI; CALLITHRICIDAE; CALLITHRIX.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94153996.
RA BURGER H., MOSTERT M.C., KOK E.M., WAGEBAKER G., DORSSERS L.C.J.;
RT "Cloning and expression of Interleukin-3 genes of chimpanzee and New
RT World monkeys."
RL BIOCHIM. BIOPHYS. ACTA 1217:195-198(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95018301.
RA BURGER H., WAGEBAKER G., LEUNISSEN J.A.M., DORSSERS L.C.J.;
RT "Molecular evolution of Interleukin-3."
RL J. MOL. EVOL. 39:255-267(1994).
CC -1- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE
CC CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,
CC DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
CC OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES (BY
CC SIMILARITY).
CC -1- FUNCTION: THIS CSF INDUCES GRANULOCYTES, MACROPHAGES, MAST CELLS,
CC STEM CELLS, ERYTHROID CELLS, EOSINOPHILS AND MEGAKARYOCYTES (BY
CC SIMILARITY).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: ACTIVATED T CELLS, MAST CELLS, NATURAL KILLER
CC CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE IL-3 FAMILY.
CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; X74877; G459436;
CC CYTOKINE; GLYCOPROTEIN; GROWTH FACTOR; SIGNAL.
KM SIGNAL 1 18 BY SIMILARITY.
FT FT CHAIN 19 142 INTERLEUKIN-3.
FT FT DISULFID 34 102 BY SIMILARITY.
FT FT CARBOHYD 33 33 POTENTIAL.
SQ SEQUENCE 142 AA; 15980 MM; A03CERD0 CRC32;

Query Match 31.7%; Score 44; DB 1; length 142;
Best Local Similarity 55.6%; Pred. No. 17;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

O7 11 HTMILLMLPRLGQAS 28
| :||||:| |||:
Db 3 HPIPLLTLVSPGLQAA 20

RESULT 13
IL3_SAGOE
AC P51445; STANDARD; PRF: 142 AA.

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DE 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE INTERLEUKIN-3 RECEPTOR (IL-3) (MULTIPOTENTIAL COLONY-STIMULATING FACTOR) (HEMATOPOIETIC GROWTH FACTOR) (P-CELL STIMULATING FACTOR) (MAST-CELL GROWTH FACTOR) (MCGF).
GN IL3.
OS SAGUINUS OEDIPUS (COTTON-TOP TAMARIN).
OC EUMARIOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUETHERIA; PRIMATES; PLATYRRHINI; CALLITRICHIDAE; SAGUINUS.
RN [1].
RX MEDLINE: 94153996.
RA BURGESS H., MOSTERT M.C., KOK E.M., WAGEMAKER G., DORSSESS L.C.J.; "Cloning and expression of Interleukin-3 genes of chimpanzee and New World monkeys."
RT BIOCHIM. BIOPHYS. ACTA 1217:195-198(1994).
RL [2].
RN [2].
RX MEDLINE: 95018301.
RA BURGERS H., WAGEMAKER G., LEUNISSEN J.A.M., DORSSESS L.C.J.; "Molecular evolution of interleukin-3."
RL J. MOL. EVOL. 39:255-267(1994).
CC -1 FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. DIFFERENTIATION AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. CC -1 FUNCTION: THIS CSF INDUCES GRANULOCYTES, MACROPHAGES, MAST CELLS, STEM CELLS, ERYTHROID CELLS, EOSINOPLIDS AND MEGAKARYOCYTES. CC -1 SUBUNIT: MONOMER (BY SIMILARITY). CC -1 TISSUE SPECIFICITY: ACTIVATED T CELLS, MAST CELLS, NATURAL KILLER CELLS (BY SIMILARITY). CC -1 SUBCELLULAR LOCATION: SECRETED. CC -1 SIMILARITY: BELONGS TO THE IL-3 FAMILY.
CC ---
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outpost at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
DR EMBL; X74878; E211706; -.
DR EMBL; X74879; E211706; JOINED.
DR HSSP; P08700; IJLI.
KV CYTOKINE; GLYCOPROTEIN; GROWTH FACTOR; SIGNAL.
FT SIGNAL. 1 18 BY SIMILARITY.
FT CHAIN 19 142 INTERLEUKIN-3.
FT DISULFD 34 102 BY SIMILARITY.
FT CARBOHYD 33 33 POTENTIAL.
FT CARBOHYD 88 88 POTENTIAL.
FT CARBOHYD 108 108 POTENTIAL.
SQ SEQUENCE 142 AA; 16085 MW; B2C52180 CRC32;

Query Match      31.7%; Score 44; DB 1; Length 142;
Best Local Similarity 55.6%; Pred. No. 17;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY    11 HTMLLLLMFLGLGQAAS 28
     1 :|||||: ||||:
Db     3 HPPIIIIIIIVSPGIQAA 20

RESULT 14
NM3M.DROSU STANDARD: PRG: 117 AA.
AC PS1940:
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DT NADH-UBIOQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).

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Query Match      31.7%  Score 44;  DB 1;  Length 117;
Best Local Similarity 42.9%  Pred. NO. 14;
Matches 9;  Conservative 7;  Mismatches 5;  Indels 0;  Gaps 0;

y      2 VLASSTSTSHMTLLMLLFH 22.
      :::|||||:::|::|::|
b      86 IMTSTSTIFILLIGLYH 106

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Query Match 31.7% Score 44; DB 1; Length 722;
Best Local Similarity 41.7%; Pred. NO. 73;
Matches 10; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 MTLASSTISIRMLLLMLTFHLG 24
   :|||:|:|:|:|:|:|:|:|:|
Db 207 LVLEPPTPLHQALTLRFLLQHLG 230

```

Search completed: September 17, 1999, 03:10:15
Job time: 295 sec

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 16, 1999, 20:40:11 ; Search time 68.96 seconds
(Without alignments)
26.774 Million cell updates/sec

Title: US-09-037-657-32

Perfect score: 139

Sequence: 1 MVLASSTSIHMTLLMLFHLGLQASIS 30

Scoring table: BLOSUM62

Searched: 201082 segs, 61543640 residues

Database:

- 1: SP_ARCHAEA:*
- 2: SP_BACTERIA:*
- 3: SP_FUNGI:*
- 4: SP_HUMAN:*
- 5: SP_INVERTEBRATE:*
- 6: SP_MAMMAL:*
- 7: SP_MHC:*
- 8: SP_ORGANELLE:*
- 9: SP_PHAGE:*
- 10: SP_PLANT:*
- 11: SP_RODENT:*
- 12: SP_VIRUS:*
- 13: SP_VERTEBRATE:*
- 14: SP_UNCLASSIFIED:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB ID	Description
1	96	69.1	169	11 P97688	P97688 rattus norv
2	51	36.7	1581	13 073809	073809 fugu rubrip
3	50.5	36.3	437	8 034191	034191 crithidia o
4	48.5	34.9	437	8 003616	003616 leishmania
5	47.5	34.5	694	5 094916	094916 drosophila
6	47.5	34.2	344	2 086662	086662 streptomyce
7	47.5	34.2	1914	4 013129	013129 homo sapien
8	47	33.8	244	1 029705	029705 archaeoglob
9	47	33.8	160	1 058301	058301 pyrococcus
10	46.5	33.5	115	8 092260	092260 canis famli
11	46	33.1	342	1 030142	030142 archaeoglob
12	46	33.1	346	2 P96480	P96480 streptococ
13	46	33.1	414	5 P91486	P91486 caenorhabd
14	45	33.1	653	6 028361	028361 didelphis m
15	45	32.4	352	5 021917	021917 caenorhabd
16	45	32.4	309	11 063097	063097 rattus norv
17	45	32.4	107	13 090286	090286 carassius a
18	44.5	32.0	267	5 018135	018135 caenorhabd
19	44	31.7	326	5 016396	016396 caenorhabd
20	44	31.7	326	5 062449	062449 caenorhabd
21	44	31.7	115	8 092244	092244 hippopotamu
22	43.5	31.3	723	2 034616	034616 bacillus su
23	43.5	31.3	751	11 060816	060816 mus musculu
24	43	30.9	114	1 058228	058228 pyrococcus
25	43	30.9	391	2 052060	052060 salmone
26	43	30.9	408	2 067072	067072 aquifex aeo
27	43	30.9	481	4 060883	060883 homo sapien
28	43	30.9	346	8 P92575	P92575 bipes bipor
29	43	30.9	668	10 048552	048552 arabidopsis

30	43	30.9	845	10 004703	004703 solanum tub
31	42.5	30.6	379	8 020544	020544 ctenomys le
32	42.5	30.6	345	8 078884	078884 anolis rich
33	42	30.2	293	2 P74826	P74826 sphingomona
34	42	30.2	1218	2 P96057	P96057 salmonella
35	42	30.2	598	2 055378	055378 synecocyst
36	42	30.2	359	2 092785	092785 bacillus an
37	42	30.2	102	2 092521	092521 streptomyce
38	42	30.2	350	5 P91506	P91506 caenorhabd
39	42	30.2	521	5 017900	017900 caenorhabd
40	42	30.2	325	8 021349	021349 euhadra her
41	42	30.2	484	10 024325	024325 phaseolus v
42	42	30.2	412	10 080485	080485 arabidopsis
43	42	30.2	150	10 080490	080490 arabidopsis
44	42	30.2	600	11 092063	092063 mus musculu
45	41.5	29.9	650	2 052818	052818 amycolatops

ALIGNMENTS

RESULT 1
ID P97688 PRELIMINARY; PRT: 169 AA.

AC 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DE INTERLEUKIN-3 BETA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98241512.
RA DEL C ESANMI M., VAN SOMEREN G.D., VAN DER VELDE I., VAN BEKKUM D.W.,
RA VALENIO D., NOERBOOM J.L., BOUJ A.;
RT "Cloning, biological characterization and high-level expression of
RT rat interleukin-3 using recombinant adenovirus: description of a new
RT splicing variant.";
RL Gene 211:151-158(1998).
DR EMBL; U81492; AAC17704.1;
SQ SEQUENCE 169 AA; 19019 MW; 1EA42F8D CRC32;

Query Match 69.1%; Score 96; DB 11; Length 169;
Best local Similarity 82.1%; Pred. No. 2.2e-06;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MVLASSTSIHMTLLMLFHLGLQAS 28
DB 1 MVLASSTSIHMTLLMLFHLGLQAS 28

RESULT 2
ID 073809 PRELIMINARY; PRT: 1581 AA.

AC 073809;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE LRP1 (FRAGMENT).
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percormorpha;
OC Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.
RN [1]
RP SEQUENCE FROM N.A.
RA GELINER K., BRENNER S.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF006116; AAC34396.1;
DR PFM; PF00006; EGF; 8.
DR PFM; PF00057; Id1_recept_a; 11.

DR PRAM: PF00058; ldl_recept_b: 9.
 DR PROSITE; PS00010; ASX_HYDROXYL: 2.
 DR PROSITE; PS01187; EGF_CA: 2.
 DR PROSITE; PS01209; LDLRA_1: 9.
 KM Glycoprotein; EGF-like domain.
 FT NON TER 1
 SO SEQUENCE 1581 AA; 176854 MW; 0839098E CRC32;

Query Match 36.7%; Score 51; DB 13; Length 1581;
 Best Local Similarity 58.3%; Pred. No. 27;
 Matches 14; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 4 ASSTSTSIHTMLLMLFHLGLOA 27
 DB 1455 ASSTSIIVPVLLLLMLAMAVCA 1478

RESULT 3
 ID 034191 PRELIMINARY; PRT; 437 AA.
 AC 034191;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE NADH DEHYDROGENASE SUBUNIT 4.
 GN ND4.
 OS Crithidia oncopelti.
 OC Mitochondrion.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Crithidia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S-068;
 RA DMITRIY MASLOV A.;
 RL Submitted (OCT-1990) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S-068;
 RA MASLOV D.A., HORVATH A., GWANG II K., KOLESNIKOV A.A.;
 RL Submitted (AUG-1991) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X56015; CAA39491.1;
 KM Mitochondrion.
 SO SEQUENCE 437 AA; 52018 MW; 741F2793 CRC32;

Query Match 36.3%; Score 50.5; DB 8; Length 437;
 Best Local Similarity 34.4%; Pred. No. 11;
 Matches 11; Conservative 11; Mismatches 7; Indels 3; Gaps 1;

OY 1 MYLASSSTSIHTMLLMLFHLGLOAST 29
 DB 131 LVTVSSISIMCIMIICIIIFHFNVMLQSF 162

RESULT 4
 ID 003616 PRELIMINARY; PRT; 437 AA.
 AC 003616;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3).
 GN ND4.
 OS Leishmania tarentolae (Sauruleishmania tarentolae).
 OC Mitochondrion.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE; 85079995.
 RA LA CRUZ V.F., NECKELMANN N., SIMPSON L.;
 RT "Sequences of six genes and several open reading frames in the
 Kinetoplast maxicircle DNA of Leishmania tarentolae."
 J. Biol. Chem. 259:15136-15147(1984).
 RN [1]

RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 85297791.
 RA SIMPSON A.G., NECKELMANN N., LA CRUZ V.F., MURICH M.L., SIMPSON L.;
 RT "Mapping and 5' end determination of kinetoplast maxicircle gene
 transcripts from Leishmania tarentolae."
 RL Nucleic Acids Res. 13:5977-5993(1985).
 CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
 CC -1- COFACTOR: FAD, AND IRON-SULFUR CENTRES.
 DR EMBL; M10126; -; NOT ANNOTATED_CDS.
 DR PFAM; PF00361; oxidored_q1; 1.
 KM Oxidoreductase; NAD; Ubiquinone; Mitochondrion; FAD; Iron-sulfur.
 SO SEQUENCE 437 AA; 52291 MW; EEF35AF7 CRC32;

Query Match 34.9%; Score 48.5; DB 8; Length 437;
 Best Local Similarity 34.4%; Pred. No. 20;
 Matches 11; Conservative 11; Mismatches 7; Indels 3; Gaps 1;

OY 1 MYLASSSTSIHTMLLMLFHLGLOAST 29
 DB 131 LVTFSSLSIMCIMIICIIIFHFNVMLQSF 162

RESULT 5
 ID 094916 PRELIMINARY; PRT; 694 AA.
 AC 094916;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE DFZ2.
 GN DFZ2.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
 OC Drosophilidae; Drosophila.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96353971.
 RA BHANOT P., BRINK M., SAMOS C.H., HSIEH J.C., WANG Y., MACKE J.P.,
 RA ANDREW D., NATHANS J., NUSSE R.;
 RT "A new member of the frizzled family from Drosophila functions as a
 Wingless receptor."
 RL Nature 382:225-230(1996).
 DR EMBL; U65589; AAC4723.1;
 DR FLYBASE; FB910016797; fz2.
 DR PFAM; PF01392; Fz; 1.
 SO SEQUENCE 694 AA; 75437 MW; FDTBOBB9 CRC32;

Query Match 34.5%; Score 48; DB 5; Length 694;
 Best Local Similarity 31.0%; Pred. No. 35;
 Matches 9; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

OY 1 MYLASSSTSIHTMLLMLFHLGLOAST 29
 DB 383 LMLRSTGPHSCTVFLVITTFGMASST 411

RESULT 6
 ID 086662 PRELIMINARY; PRT; 344 AA.
 AC 086662;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE PUTATIVE INTEGRAL MEMBRANE PROTEIN.
 GN SCA42.06C.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA OLIVER K., HARRIS D.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA MEDLINE: 97000351.
RA REDENBACH M., KIESER H.M., DENAPARTE D., EICHNER A., CULLUM J.,
RA KINASHI H., HOPWOOD D.A.;
RL A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb streptomyces coelicolor A3(2) chromosome."
DR EMBL: AL031182; CAA20158.1;
SQ SEQUENCE 344 AA; 35350 MW; BD06E656 CRC32;

Query Match 34.2%; Score 47.5; DB 2; Length 344;
Best Local Similarity 46.4%; Pred. No. 23;
Matches 13; Conservative 4; Mismatches 10; Indels 1; Gaps 1;
3 LASTTSIHTM-LLLMFLHGLQASIS 29
40 LPPSHLTHTAPLLSLVFSAGLOVAV 67

RESULT 7
D 013129 PRELIMINARY; PRT; 1914 AA.
C 013129;
T 01-NOV-1996 (TREMblrel. 01, Created)
T 01-NOV-1996 (TREMblrel. 01, last sequence update)
T 01-MAY-1999 (TREMblrel. 10, last annotation update)
E ZN-15 RELATED ZINC FINGER PROTEIN (RLF).
N RLF.
N Homo sapiens (Human).
C Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
C Eutheria; Primates; Catarrhini; Homiidae; Homo.
N [1]
P SEQUENCE FROM N.A.
X MEDLINE: 96132723.
X MAKEELA T.P., HELSTEN E., VESA J., HIRVONEN H., PALOTIE A.,
X PELTONEN L., ALITALO K., ALITALO K.;
T "The rearranged L-myc fusion gene (RLF) encodes a Zn-15 related zinc
finger protein."
L Oncogene 11:2699-2704(1995).
R EMBL: U23277; AAC50386.1;
R PFM: PF00096; ZF-C2H2; 14.
R PROSITE: PS00028; ZINC_FINGER_C2H2; 14.
W Zinc-finger; Metal-binding; DNA-binding.
Q SEQUENCE 1914 AA; 217898 MW; 05BE74D CRC32;

Query Match 34.2%; Score 47.5; DB 4; Length 1914;
Best Local Similarity 45.7%; Pred. No. 98;
Matches 16; Conservative 3; Mismatches 7; Indels 9; Gaps 1;
5 SSTSI-----HTMLLMFLHGLQASIS 30
1043 SSSSICASKRPTEDTMLLRLKHLKSLKNSIT 1077

DT 01-AUG-1998 (TREMblrel. 07, Last annotation update)
DE NITRATE REDUCTASE, GAMMA SUBUNIT (NARI).
GN AF0546.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE: 98049343.
RA KLEIN H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,
RA KETCHUM K.A., DODSON R.J., GINN M., HICKY E.K., PETERSON J.D.,
RA RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRIDES N.C.,
RA FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
RA KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
RA PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODER A., ZHOU L.,
RA OVERBERGER R., GOCAYNE J.D., WEIDMAN J.F., McDONALD L., UTTERBACK T.,
RA COTTON M.D., SPRIGGS T., ARTACH P., RAINE B.P., SYKES S.M.,
RA SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
RA MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
RA VENTER J.C.;
RT "The complete genome sequence of the hyperthermophilic,
RT sulphate-reducing archaeon Archaeoglobus fulgidus."
RL Nature 380:364-370(1997).
DR EMBL: AE001066; AAB90687.1;
DR TIGR: AF0546;
KW Hypothetical protein.
SQ SEQUENCE 244 AA; 27573 MW; EA12F137 CRC32;

Query Match 33.8%; Score 47; DB 1; Length 244;
Best Local Similarity 60.0%; Pred. No. 20;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
16 LLMFLHGLQASIS 30
89 ILMFLHGLQASIS 103

RESULT 9
ID 058301 PRELIMINARY; PRT; 160 AA.
AC 058301;
DT 01-AUG-1998 (TREMblrel. 07, Created)
DT 01-AUG-1998 (TREMblrel. 07, last sequence update)
DT 01-JAN-1999 (TREMblrel. 09, last annotation update)
DE 160AA LONG HYPOTHETICAL PROTEIN.
GN PH0566.
OS Pyrococcus horikoshii.
NC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OT3;
RX MEDLINE: 98344137.
RA KAWABAYASHI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,
RA YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOTAKA A., NAGAI Y.,
RA SAKAI M., OGURA K., OTSUKA R., NAKAZAWA H., TAKAMITA M., OHFUKU Y.,
RA FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,
RA AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIYUVA H.,
RA KIRUCHI H.;
RT "Complete sequence and gene organization of the genome of a
RT hyper-thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
RL DNA Res. 5:55-76(1998).
DR EMBL: AP000002; BAA29655.1;
SQ SEQUENCE 160 AA; 18153 MW; 7E023984 CRC32;

Query Match 33.8%; Score 47; DB 1; Length 160;
Best Local Similarity 45.5%; Pred. No. 14;
Matches 10; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
1 MYLASTSIHTM-LLLMFLHGLQASIS 22
:||||| :||||| :|||

DB 134 LALASSEGVFFSLILALSTFH 155

RESULT 10

092260

PRELIMINARY; PRT; 115 AA.

092260; 092260; (TREMBLrel. 10, Created)

01-MAY-1999 (TREMBLrel. 10, Last sequence update)

01-MAY-1999 (TREMBLrel. 10, Last annotation update)

DE NADH DEHYDROGENASE SUBUNIT 3 (FRAGMENT).

GN ND3.

OS Canis familiaris (Dog).

OC Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Carnivora; Fissipedata; Canidae; Canis.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 99097286.

RA KIM K.S., LEE S.E., JEONG H.W., HA J.H.;

RT "The complete nucleotide sequence of the domestic dog (Canis familiaris) mitochondrial genome."

RL Mol. Phylogenet. Evol. 10:210-220(1998).

RN [2]

RP SEQUENCE FROM N.A.

RA KIM K.S., LEE S.E., JEONG H.W., SOHN H.S., HA J.H.;

RL Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; 096639; AAD04770.1;

KW Mitochondrion.

FT NON_TER

FM 115

SQ SEQUENCE 115 AA; 12937 MW; 697D5B58 CRC32;

Query Match

Best Local Similarity 44.4%; Score 46.5; DB 8; Length 115;

Matches 12; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

OY 4 ASSTSIHTMLLMLFHLGQASIS 30

DB 78 ASQINKLTMLIMALLISL-LAASIA 103

RESULT 11

030142

PRELIMINARY; PRT; 342 AA.

030142; 030142; (TREMBLrel. 05, Created)

01-JAN-1998 (TREMBLrel. 05, Last sequence update)

01-AUG-1998 (TREMBLrel. 07, Last annotation update)

DE CONSERVED HYPOTHETICAL PROTEIN.

GN AF0094.

OS Archaeoglobus fulgidus.

OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;

OC Archaeoglobus.

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN-VC-16 / DSM 4304 / ATCC 49558;

RX MEDLINE; 98049343.

RA KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.;

RA KETCHUM K.A., DODSON R.J., GWNN M., HICKEY E.K., PETERSON J.D.;

RA RICHARDSON D.L., KERLAUGE A.R., GRAHAM D.E., KYRIDIS N.C.;

RA FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.;

RA KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTIS S.;

RA PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODER A., ZHOU L.;

RA COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYDES S.M.;

RA SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.;

RA MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.;

RA VENTER J.C.;

RT "The complete genome sequence of the hyperthermophilic

RT sulphate-reducing archaeon Archaeoglobus fulgidus."

RL Nature 390:364-370(1997).

DR EMBL; AEO01100; AAB9115.1;

DR TIGR; AF0094; .
KW Hypothetical protein.
SQ SEQUENCE 342 AA; 38629 MW; 1DAE4463 CRC32;

Query Match

Best Local Similarity 33.1%; Score 46; DB 1; Length 342;

Matches 9; Conservative 30.0%; Pred. No. 36; Mismatches 13; Indels 0; Gaps 0;

OY 1 MYLASTSIHTMLLMLFHLGQASIS 30

DB 1 MHIGGVVIRILILMLALFLGCSNVN 30

RESULT 12

P96480

PRELIMINARY; PRT; 346 AA.

P96480; P96480; (TREMBLrel. 03, Created)

01-MAY-1997 (TREMBLrel. 03, Last sequence update)

01-AUG-1998 (TREMBLrel. 07, Last annotation update)

DE HYPOTHETICAL 39.2 KD PROTEIN.

GN CAP11.

OS Streptococcus pneumoniae.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;

OC Streptococcus.

RN [1]

RP SEQUENCE FROM N.A.

RA MUNOZ R., MOLLERACH M.E., LOPEZ R., GARCIA E.;

RL Mol. Microbiol. 25:79-92(1997).

DR EMBL; Z83335; CAB05927.1;

KW Hypothetical protein.

SQ SEQUENCE 346 AA; 39177 MW; A7255E62 CRC32;

Query Match

Best Local Similarity 33.1%; Score 46; DB 2; Length 346;

Matches 7; Conservative 50.0%; Pred. No. 37; Mismatches 0; Indels 0; Gaps 0;

OY 10 IHTMLLMLFHL 23

DB 100 VYSVALLVLLFHL 113

RESULT 13

P91486

PRELIMINARY; PRT; 414 AA.

P91486; P91486; (TREMBLrel. 03, Created)

01-MAY-1997 (TREMBLrel. 03, Last sequence update)

01-NOV-1998 (TREMBLrel. 08, Last annotation update)

DE SIMILARITY TO OVAL NEURONAL CYCLE WITHDRAWAL PROTEIN.

GN T1E12.2.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;

OC Rhabditia; Rhabditidae; Rhabditidae; Pelodetinae; Caenorhabditis.

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN-BRISTOL N2;

RX MEDLINE; 94150718.

RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.;

RA BONFIELD J., BURTON J., CONNELL M., COPESEY T., COOPER J., COULSON A.;

RA GAXTON M., DEAR S., DU Z., DUREIN R., FAVELLO A., FULTON L.;

RA JONES M., KERSHAW J., KINSTER T., HILLIER L., JER M., JOHNSTON L.;

RA LIGHTNING J., LLOYD C., MCMURRAY A., MORITMORE B., O'CALLAGHAN M.;

RA PARSONS J., PERCY C., RIKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.;

RA SWALDON N., SMITH A., SONNHAMMER E., STADEN R., SUSTON J.;

RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.;

RA WATSON A., WEINSTOCK L., WILKINSON-SPOAT J., WOLDMAN P.;

RT "2.2 MD of contiguous nucleotide sequence from chromosome III of C. elegans."

RL Nature 368:32-38(1994).

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RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA DU 2., MAGGI L.;
RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA WATERSTON R.;
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL: U80440; AAB37650.1; -
SQ SEQUENCE 414 AA; 46525 MW; EB685192 CRC32;

Query Match 33.1%; Score 46; DB 5; Length 414;
Best Local Similarity 45.5%; Pred. No. 43;
Matches 15; Conservative 6; Mismatches 6; Indels 6; Gaps 2;

QY 3 LASSITS--HTMILLI---MLFHLGLQASI 29
Db LATTTTFLHSMILLFLYHFFFLALLLQTN 388

RESULT 14
ID Q28361 PRELIMINARY; PRT; 653 AA.
AC Q28361;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE NA/PI-COTRANSPORTER.
GN NAPI-4.
OS Didelphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Metatheria; Didelphimorphia; Didelphidae; Didelphis.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-EPIITHELIUM, KIDNEY;
RA MEDLINE: 94165050.
RA SORRIBAS V., MARKOVICH D., HAYES G., STANGE G., FORGO J., BIBER J.,
RA MURER H.;
RT "Cloning of a Na/Pi cotransporter from opossum kidney cells.";
RL J. Biol. Chem. 269:6615-6621(1994).
RN [2]
RP SEQUENCE OF 1-89 FROM N.A.
RC TISSUE-KIDNEY;
RA HILFKE H., HARTMANN C.M., STANGE G., MURER H.;
RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: L26308; AAA30978.1; -
DR EMBL: A0003021; CAA05806.1; -
SQ SEQUENCE 653 AA; 70551 MW; A6ED8F28 CRC32;

Query Match 33.1%; Score 46; DB 6; Length 653;
Best Local Similarity 36.7%; Pred. No. 63;
Matches 11; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 MVAASSTSIHTMILLMLFHLGLQASIS 30
Db 355 ILLAGSLTLCCLLVKLINSVLCQOVA 384

RESULT 15
ID Q21917 PRELIMINARY; PRT; 352 AA.
AC Q21917;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE CPA-7 PROTEIN.
GN
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;

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OC Rhabditina; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RA BARDILL S.;
RL Submitted (APR-1996) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPEY T., COOPER J., COULSON A.,
RA CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCKERRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAUSER E., STADEN R., SULLSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOULDMAN P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
DR EMBL: Z70686; CAA94612.1; -
DR PFM: PF00503; G-alpha; 1.
SQ SEQUENCE 352 AA; 41021 MW; 8BC25EFC CRC32;

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Query Match 32.4%; Score 45; DB 5; Length 352;
Best Local Similarity 47.1%; Pred. No. 51;
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 10 HTMILLMLFHLGLQ 26
Db 78 IHSMISIRAFVHLOIE 94

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Search completed: September 16, 1999, 20:40:13
 Job time: 5564 sec